

Table 70: Comparative Sequences relating to SAG 1280

ATACCTTTATTGAGTTTGAAAACCTTGGAATTGATTTTCTTTTGTGGATGAGGCTCATC
 ACTTCAAGAATATCCGTCCAATCACTGGACTTGGGAATGTAGCTGGAATCACCAACACAA
 CTTCTAAAAAGAACGTGGATATGGAGATGAAGGTGAGACAAGTACAGGCAGAGCATGGAG
 ATAGAAATGTGCTTTTGGGACAGGAACACCAGTTTCTAACTCTATTAGTGAACTTTCA
 CCATGATGGATTACATTC AACCTGATGTCTTGGAACGATACCTGGTATCAAATTTGACT
 CCTGGGTGGGGCTTTTGGGAATATCGAAAACCTCCATGGAAGTACCCCGACAGGAGATA
 AGTACCAACCCAAGAAACGGTTCAAGAAATTTGTCAACCTTCCTGAACTCATGCGAATCT
 ACAAGGAAACTGCCGATATTCAGACCTCAGACATGCTTGATTTACCAGTACCGGAAGCTA
 AGATTATTGCGGTGGAAAGCGAGTTAACGCAAGCTCAGAAATACTATTGGAAGAGCTGG
 TAAAGCGTTT CAGACGCTATCAAGTCAGGTAGTGTGATCCAAGTAGAGATAACATGCTTA
 AAATCACAGGAGAAGCCAGAAAACCTAGCTATTGATATGCGGTTGATTGACCCTACTTACT
 CCTTATCGGATAATCAGAAAATCCTTCAAGTAGTCGATAATGTCGAGCGGATTTACCGTG
 ATGGAGCTGGAGACAAAGCCACTCAGATGATTTTCTCAGATATTGGAACCCCTAAAAGTA
 AGGAAGAAGGGTTTGTATGTCTACAATGAACCTTAAGGACTTGTGTGTCGATCGAGGGATAC
 CAAAAGAAGAAATGCGCTTTGTCCATGATGCCAATACTGATGAGAAGAAAACTCTCTGT
 CACGCAAGGTCAATAGTGGAAGTACGGATTCTCATGGCTTCTACGGAAGGAGGGGAA
 CAGGATTAACCTCCAAATCTCGCATGAAAGCTGTCCACTATTTAGACGTTCCCTGGAGGC
 CCTCAGACATTTGCCAGCGAAATGGACGACTAATTCGACAAGGAACATGCACCAGGAGG
 TAGATATTTATCACTATATTACTAAAGGGAGCTTTGACAATTACCTCTGGCAGACGCAGG
 AGAATAAGCTAAAGTATATCACCCAGATAATGACCTCAAAGATCCTGTGAGATCAGCTG
 AAGACATTTGATGAACAAACCATGACCGCTCAGACTTTAAGGCATTTGGCAACTGGGAACC
 CTTATCTCAAACCTCAAATGGAGTTGGAAAATGAACTGACAGTTT TAGAGAATCAAAAAC
 GAGCCTTTAATCGCTCCAAAGACGAGTATCGCCATACCATTTCTATAGCGAGAAGCACC
 TCCCTATTATGGAAAAACGGTTGAGTCAATATGATAAAGATATTGCCAATCTTTGGCAA
 CCAAGTCGCAAGATTTTGTGATGCGATTTGACAATCAAGCAATGGATAATCGTGCTGAAG
 CTGGGGACTATCTGCGAAAACCTATTACCTATAACCGCTCAGAGACCAAGGAAGTCAGGA
 CACTTGCCAGCTTTAGAGGATTTGATTTAAAAATGACTACACGAGGTGCTAGTGAGCCCT
 TACCAGAAAACCTTTCTTTAATGATTGTAGGTGATAACCAGTATACTGTGCGCCCTTGATT
 TGAAATCAGACGTGGGAACCATTCACCGGATTAGTAATGCCATTGACCATATTATAGATG
 ACCAAGAAAAGACGCAAGAGCTGGTAAAGGATTTAAAAGATAAGCTACGAGTAGCCAAAG
 TAGAAGTTGATAAAGTCTTTCCAAAGGAAGAGGACTATCAGCTTGTAAGGCTAAGTATG
 ATGTTT TAGCTCCCTTGGTTGAAAAAGAAGCAGAGATTGAAGAGATAGATGCAGCTTTGG
 CCAAGTTTAGTGAAGATACAACACCCCAAAAGAAGCAACAAATAGCACTCGAGATA

SEQ ID. NO. 7002

STRAIN H36B

GGAGGGAAAATGAATCAAGAAGTCTTACTACAAATGAT
 GAGAGCCACTATTCCTCGTATAGAGCCCTTGCTTGAGGCATTTTATATT
 ACCAAGCAGAGCATTTTGATGAGGAGTGGGATAGTCTTATTCATCAGTTT
 ATGACCAATAGGCAAGAAATAAATAAGTCTGTTCAAGTACTTCACITTTGA
 GACAGATGTTTCAGCTTTTGTCCAGGCTAGTCCCTATGATACTGCTCATG
 ATCTATTGACCTATACACAAGTTTTCGGCCAAAGTGGTCTTCAAAAACCTA
 GATAAACTATCGCCGCTCGAAAAAACTTGGTGATAGAAGTGGCCTTGT
 CAATCTGGCCACTCGTTTTCATTAATTGGATTCCAATGGACACTACCAAA
 CCATATCGCCGATTCACTCTTACAAAAGAGTAGGGGAGCTAATTTGGTCT
 AATGTGTATCGTGTGGCTAATAATTTAGCGGATCGTATTAGTCGAGATAT
 TGAACAGTTTCTCTTAACTTACGAGCCTGAGCTTGAACTAGAGCTGATG
 AAACTGTTCTAGAAAATGAAGAACTGTTGATGAGCACAAAACAAGTGT
 CATCAAGCAATATCTTTTCGAGAAGAGGGCTCTCTGGTTATTGCTAGTTT
 GGATGTAGATTTGTCTCAACTAGATGTTCAAATAGGAAAAACAGTCATC
 TGCCAGCTTATGAAGAGTTATCCTTACGACGTAAATTTGAGATTCTAACA
 TATTTTGACCAAAATTCGAAATGAACGTTCCAAAGTCCCAAGTTT TAGACG
 AGGTGATTTT GACACAGAGATGGAAATGACACCAAGTCTTTGATGGCGAGG
 AATTACTTACTTATCTCGAAGCTGATGGCAGTCCCTATGAGCTGAAACGA
 ACGCTGACTACAGTCAAGAAAAGGAATTAGAAAAAATTGGACAAGCCAT
 TAGGATAGAAAATCAAGAAAAATTGACTCAGCTAsGkATTGrTTTATCTC
 AGTTTGACCCAGACCGAGTCCGTATTTTATTGkATGCAGCAGGTCTyT
 CGTTTAWAwAATGCAGACCTTGCTTCACTAGGTGGTTATCCCAAAGCCTC
 GGTAACTCAAAGTAGCCCTTGCGACAGAACTACTCCAAATGGGACTAAGTC
 ATGAAAAGGTTGAATTTTCTTTGGTAGCCAGCTTTCCATTGAAGAGCTG
 CGACAAGTTGCCTACGCCTTTTACACCAAGAACTCAGCAGAGAAGATGC
 GGAGCAATTTGAAAAAGATAAAGGTAATCAGCCAGATTTAACTCTCAGAG
 ATTGGAAAAGCAAGCTAGAGAAAGCTGAGGGAAAAGAAGTAGTTGATGAA
 GAATTCGCGGGAATACTGCTTTCAGAGAGTATTGGACACTTATCCTCT
 GGGGTCAATTGGTTTCTTATAAGGGACAGGACTTTGAGGTGATGTCGGTCA
 GCGATGCTCGAATGAACGGTTT GATTTCGGATTGAGTTAGTCAATGACTTT
 TCGGATATCATTGAACAAAATCCAGTTCTTTATGTGAGGACCTGGGAAGA
 AGTCAGTCAGGCACCTTCATCAGCCAAAGGCAGAACCAACAGAGTTAG
 AAGAAGCGGACCAAGAATTAAACCTATTCTCATTCTGGAAGAGGAGCTA
 GTTCAGAGTATTGGACTATTGGAACAGATGATT CAGAAAATGGTCATAA
 CGATACTGATCTTGAAGAAAACAGATAATCAAATTCCTGAAGAGGAAGTCG
 TCGAAACAATTCAGAGATTCCAGTAACGGACTTTTATTTTCCAGAAGAT
 TTGACGGACTTTTATCCTAAGACTGCTAGAGATAAGGTTGAGACAAACAT
 TGTGGCCATTGCTTTGGTAAAAAATCTAGAAGTAGAGCACCGCAATGCTT
 CACCAAGTGAACAAGAACTCCTTGCCAAGTATGTAGGCTGGGGTGGACTA
 GCCAATGAATTTTGTGATGACTATAATCCAAAATTTTCTAAGGAACGAGA
 AGAACTGAAGAGCCTAGTCAAGATAAAGAGTATTGCGATATGAAACAGT
 CCTCCCTGACAGCCTATTACACAGACCCATCCCTGATCCGTGAGATGTGG
 GATAAGTTGGAAAGAGATGGCTTTACAGGTGGCAAAATCCTAGATCCTTC
 CATGGGAACAGGGAATTTCTTTGCGGCTATGCCAAAACACTTAAGAGAAA
 AGAGTGAGTTGTATGGCGTAGAGTTAGATACTATTACAGGAGCTATTGCC
 AAACACCTTCATCCCAATAGTCATATTGAAATTAAGGGATTTGAGACGGT
 GGCCTTTAACGACAATAGTTTGGATTGGTGATTTCAAATGTGCCCTTTG

Table 70: Comparative Sequences relating to SAG 1280

CCAATATACGAATTGCGGATAATAGGTACGATAGGCCTTACATGATTCAT
 GACTACTTTTGTCAAAAAGTCACTTGATTGCTTCATGATGGTGGACAAGT
 AGCGATTATCTCTCCACAGGAAGTATGGATAAGCGAACAGAAAACATCT
 TACAAGATATTCGTGAGACAAGTGAATTTCTTGGTGGGGTTCGACTGCCT
 GACTCTGCCCTTTAAGGCCATTGACAGGAACGAGTGTCAACCGGATATGTT
 ATTCTTCCAGAAAACACTTAGACAAGGGATATGTGGCAGACGATTTAGCCT
 TTTCAGGTTCATTTCGTATGACAAGGATAGTCGCATTTGGCTCAATCCT
 TATTTTGATGGAGAATACAATAGCCAGGTGCTAGGAACCTACGAGGTGAG
 GAATTTTAACGGAGGAACACTTTCTGTTAAGGGGACTAGTGATGACTTGA
 TTGCAAGTGTGAAACAGCTCTAAATCACGTTAAGGCCCAAGAGAGATT
 GATAGAAATGAGGTCATCATTAACCCAGATGTGTTGACCAACAAGTCAA
 TGATACCTCCATTCCAGCTGAAATGAGGGAAAATCTAGGTCAGTACAGTT
 TTGGTTATCAGGGGTCTACAGTTTACTATCGAGATAACAAAGGCATTGCA
 GTCGGAACCAAGACGGAAGAAATCAGTTACTATGTGATGAAGAG

SEQ ID. NO. 7003

STRAIN 18RS21

GnAGGGAAAATGAATCAAGAAGTCTTACTACAAATGATGAGA
 GCCACTATTCCCTCGTGATAGAGCCTTGCTTGAGGCATTTTATATTACCA
 AGCAGAGCATTTTGATGAGGAGTGGGATAGTCTTATTCATCAGTTTATGA
 CCAATAGGCAAGAAATAAATAAGTCTGTTCAAGTACTTCACTTTGAGACA
 GATGTTTCAGCTTTTGTCCAGGCTAGTCCTTATGATACTGCTCATGATCT
 ATTGACCTATACACAAGTTTTCGGCCAAAGTGGTCTTCAAAAAGTATAGATA
 AACTATCGCCGTCTGAAAAAACTTGGTGATAGAAGTGGCCTTGTTCAAT
 CTGGCCACTCGTTTTCATTTATTTGGATTCCAATGGACACTACCAAAACCAT
 ATCGCCGGAATTCATCTTACaAAAGAGTAGGGGAGCTAATTTGGTCAATG
 TGTATCGTGTGGCTAATAATTTAGCGGATCGTATTAGTCGAGATATTGAA
 CAGTTTCTCTTAACCTACGAGCCTGAGCTTGAAACTAGAGCTGATGAAAC
 TGTTCTAGAAAATGAAGAACTGTTGATGAGCACAAAACAAGTGTTCATC
 AAGCAATATCTTTTCGAGAAGAGGGCTCTCTGGTTATTGCTAGTTTGGAT
 GTAGATTTGTCTCAACTAGATGTTCAAATAGGAAAAACAGTCATCTGCC
 AGCTTATGAAGAGTTATCTTACGACGTAAATTTGAGATTCTAACATATT
 TTGACCAAAATTCGAAATGAACGTTCCAAAGTCCCAAGTTTATAGCAGGT
 GATTTTGACACAGAGATGGAAATGACACCAGTCTTTGATGGCGAGGAATT
 ACTTACTTATCTCGAAGCTGATGGCAGTCCCTATGAGCTGAAACGAACGC
 TGACTACAGTcGAAGAAAAGGAATTAGAAAAAATTGGACAAGCCATTAGG
 ATAGAAAATCAAGAAAAAATTGACTCAGCTAGGGATTGATTTATCTCAGTT
 TGACCCAGACCGAGTCCGTATTTTATTGGATGCAGCAGGTGTTTTCTGTT
 TAAAAAATGCAGACCTTGCTTTACTAGGTGGTTATCCCAAAGCCTCGGTA
 ACTCAACTAGCCCTTGCGACAGAACTACTCCAAATGGGACTAAGTCATGA
 AAAGGTTGAATTTTCTTTGGTAGCCAGCTTTCCATTGAAGAGCTGCGAC
 AAGTTGCCCTACGCCCTTTTACACCAAGAACTCAGCAGAGAAGATGCGGAG
 CAATTTGAAAAAAGATAAAGGTAATCAGCCAGATTTAACTCTCAGAGATTG
 GAAAAGCAAGCTAGAGAAAGCTGAGGGAAAAGAGTAGTTGATGAAGAAT
 TCGCGGAAAATCCACTGGTTTCAGAGAGTATTGGACACTTATCTCTGGGG
 TCATTGGTTTCCCTATAAGGGACAGGACTTTGAGGTGATGTCGGTCAGCGA
 TGCTCGATTGAACGGTTTGATTCCGATTGAGTTAGTCAATGACTTTTCGg
 ATATCATTGAACAAAATCCAGTTCTTAtGTGAGGACCTGGGAAGAAGTC
 AGTCAGGCACCTTCATCAGCCAAAGGCAGAACCAACACAGAGTTAGAAGA
 AGCGGACCAAGAATTAACCTATTCTCATTCTGGAAGAGGAGCCAGTTC
 AGAGTATTGGACTATTGGAACCAGaTGATTGAGAAAATGGTCATAACGAT
 ACTGATCTTGAAGAAACAGATAATCAAATTCCTGAAGAGGAAGTCGTGGA
 AACAAATCCAGAGATTCCAGTAACGGACTTTTATTTTCCAGAAGATTGGA
 CGGACTTTTATCCTAAGACTGCTAGAGATAAGGTTGAGACAAACATTGTG
 GCCATTCTGTTTGGTAAAAAATCTAGAAGTAGAGCACCGCAATGCTTCACC
 AAGTGAACAAGAACTCCTTGCCAAGTATGTAGGCTGGGGTGGACTAGCCA
 ATGAATTTTTTGTATGACTATAATCCAAAATTTTCTAAGGaACGAGAAGAA
 CTGAAGAGCCTAGTCACAGATAAAGAGTATTCGGATATGAAACAGTCCTC
 CCTGACAGCCTATTACACAGACCCATCCCTGATCCGTGAGATGTGGGATA
 AGTTGGAAAGAGATGGCTTTACAGGTGGCAAAATCCTAGATCCTTCCATG
 GGAACAGGGAATTTCTTTGCGGCTATGCCAAAACACTTAAGAGAAAAGAG
 TGAGTTGTATGGCGTAGAGTTAGATACTATTACAGGAGCTATTGCCAAAC
 ACCTTCATCCCAATAGTCATATTGAAATTAAGGGATTTGAGACGGTGGCT
 TTTAACGACAATAGTTTTGATTTGGTGATTTCAAATGTGCCCTTTGCCAA
 TATACGAATTGCGGATAATAGGTACGATAGGCCTTACATGATTCATGACT
 ACTTTGTCAAAAAGTCACTTGATTGCTTCATGATGGTGGACAAGTAGCG
 ATTATCTCTTCCACAGGAAGTATGGATAAGCGAACAGAAAACATCTTACA
 AGATATTCTGTGAGACAAGTGAATTTCTTGGTGGGGTTCGACTGCCTGACT
 CTGCCCTTTAAGGCCATTGACAGGAACGAGTGTCAACCGGATATGTTATTC
 TTCCAGAAAACACTTAGACAAGGGATATGTGGCAGACGATTTAGCCTTTTC
 AGGTTCCATTTCGTATGACAAGGATAGTCGCATTTGGCTCAATCCTTATT
 TTGATGGAGAATACAATAGCCAGGTGCTAGGAACCTACGAGGTGAGGAAT
 TTTAACGGAGGAACACTTTCTGTTAAGGGGACTAGTGATGACTTGATGTC
 AAGTGTGAAACAGCTCTAAATCACGTTAAGGCCCAAGAGAGATTGATA
 GAAATGAGGTGATCATTAACCCAGATGTGTTGACCAACAAGTCAATGAT
 ACCTCCATTCCAGCTGAAATGAGGGAAAATCTAGGTGAGTACAGTTTGG
 TTATCAGGGGTCTACAGTTTACTATCGAGATAACAAAGGCATTGAGTGC
 GAACCAAGACGGAAGAAATCAGTTACTATGTGATGAAGAG

MSA Alignment Results: Pretty output

PRETTY of: /biotmp/msa31161.2{*} June 20, 2002 10:41 ..

Table 70: Comparative Sequences relating to SAG 1280

msa31161.2{327dNt_2603}	GgAGGGAAAA	TGAATCAAGA	AGTCTTACTA	CAAATGATGA	GAGCCACTAT
msa31161.2{327d_18RS21}	GnAGGGAAAA	TGAATCAAGA	AGTCTTACTA	CAAATGATGA	GAGCCACTAT
msa31161.2{327dNT_H36B}	GgAGGGAAAA	TGAATCAAGA	AGTCTTACTA	CAAATGATGA	GAGCCACTAT
Consensus	*-*****	*****	*****	*****	*****
51					
msa31161.2{327dNt_2603}	TCCTCGTGAT	AGAGCCTTGC	TTGAGGCATT	TTTATATTAC	CAAGCAGAGC
msa31161.2{327d_18RS21}	TCCTCGTGAT	AGAGCCTTGC	TTGAGGCATT	TTTATATTAC	CAAGCAGAGC
msa31161.2{327dNT_H36B}	TCCTCGTGAT	AGAGCCTTGC	TTGAGGCATT	TTTATATTAC	CAAGCAGAGC
Consensus	*****	*****	*****	*****	*****
101					
msa31161.2{327dNt_2603}	ATTTTGATGA	GGAGTGGGAT	AGTCTTATTC	ATCAGTTTAT	GACCAATAGG
msa31161.2{327d_18RS21}	ATTTTGATGA	GGAGTGGGAT	AGTCTTATTC	ATCAGTTTAT	GACCAATAGG
msa31161.2{327dNT_H36B}	ATTTTGATGA	GGAGTGGGAT	AGTCTTATTC	ATCAGTTTAT	GACCAATAGG
Consensus	*****	*****	*****	*****	*****
151					
msa31161.2{327dNt_2603}	CAAGAAATAA	ATAAGTCTGT	TCAAGTACTT	CACTTTGAGA	CAGATGTTTC
msa31161.2{327d_18RS21}	CAAGAAATAA	ATAAGTCTGT	TCAAGTACTT	CACTTTGAGA	CAGATGTTTC
msa31161.2{327dNT_H36B}	CAAGAAATAA	ATAAGTCTGT	TCAAGTACTT	CACTTTGAGA	CAGATGTTTC
Consensus	*****	*****	*****	*****	*****
201					
msa31161.2{327dNt_2603}	AGCTTTTGTC	CAGGCTAGTC	CTTATGATAC	TGCTCATGAT	CTATTGACCT
msa31161.2{327d_18RS21}	AGCTTTTGTC	CAGGCTAGTC	CTTATGATAC	TGCTCATGAT	CTATTGACCT
msa31161.2{327dNT_H36B}	AGCTTTTGTC	CAGGCTAGTC	CTTATGATAC	TGCTCATGAT	CTATTGACCT
Consensus	*****	*****	*****	*****	*****
251					
msa31161.2{327dNt_2603}	ATACACAAGT	TTTCGGCCAA	AGTGGTCTTC	AAAAACTAGA	TAAACTATCG
msa31161.2{327d_18RS21}	ATACACAAGT	TTTCGGCCAA	AGTGGTCTTC	AAAAACTAGA	TAAACTATCG
msa31161.2{327dNT_H36B}	ATACACAAGT	TTTCGGCCAA	AGTGGTCTTC	AAAAACTAGA	TAAACTATCG
Consensus	*****	*****	*****	*****	*****
301					
msa31161.2{327dNt_2603}	CCGTCTGAAA	AAAACCTGGT	GATAGAAGTG	GCCTTGTTCA	ATCTGGCCAC
msa31161.2{327d_18RS21}	CCGTCTGAAA	AAAACCTGGT	GATAGAAGTG	GCCTTGTTCA	ATCTGGCCAC
msa31161.2{327dNT_H36B}	CCGTCTGAAA	AAAACCTGGT	GATAGAAGTG	GCCTTGTTCA	ATCTGGCCAC
Consensus	*****	*****	*****	*****	*****
351					
msa31161.2{327dNt_2603}	TCGTTTTCAA	TTATTGGATT	CCAATGGACA	CTACCAAACC	ATATCGCCGG
msa31161.2{327d_18RS21}	TCGTTTTCAA	TTATTGGATT	CCAATGGACA	CTACCAAACC	ATATCGCCGG
msa31161.2{327dNT_H36B}	TCGTTTTCAA	TTATTGGATT	CCAATGGACA	CTACCAAACC	ATATCGCCGG
Consensus	*****	*****	*****	*****	*****
401					
msa31161.2{327dNt_2603}	ATTCACCTCT	ACAAAAGAGT	AGGGGAGCTA	ATTTGGTCAA	TGTGTATCGT
msa31161.2{327d_18RS21}	ATTCACCTCT	ACAAAAGAGT	AGGGGAGCTA	ATTTGGTCAA	TGTGTATCGT
msa31161.2{327dNT_H36B}	ATTCACCTCT	ACAAAAGAGT	AGGGGAGCTA	ATTTGGTCAA	TGTGTATCGT
Consensus	*****	*****	*****	*****	*****
451					
msa31161.2{327dNt_2603}	GTGGCTAATA	ATTTAGCGGA	TCGTATTAGT	CGAGATATTG	AACAGTTTCT
msa31161.2{327d_18RS21}	GTGGCTAATA	ATTTAGCGGA	TCGTATTAGT	CGAGATATTG	AACAGTTTCT
msa31161.2{327dNT_H36B}	GTGGCTAATA	ATTTAGCGGA	TCGTATTAGT	CGAGATATTG	AACAGTTTCT
Consensus	*****	*****	*****	*****	*****
501					
msa31161.2{327dNt_2603}	CTTAACCTTAC	GAGCCTGAGC	TTGAAACTAG	AGCTGATGAA	ACTGTTCTAG
msa31161.2{327d_18RS21}	CTTAACCTTAC	GAGCCTGAGC	TTGAAACTAG	AGCTGATGAA	ACTGTTCTAG
msa31161.2{327dNT_H36B}	CTTAACCTTAC	GAGCCTGAGC	TTGAAACTAG	AGCTGATGAA	ACTGTTCTAG
Consensus	*****	*****	*****	*****	*****
551					
msa31161.2{327dNt_2603}	AAAATGAAGA	AACTGTTGAT	GAGCACAAAA	CAAGTGTTCA	TCAAGCAATA
msa31161.2{327d_18RS21}	AAAATGAAGA	AACTGTTGAT	GAGCACAAAA	CAAGTGTTCA	TCAAGCAATA
msa31161.2{327dNT_H36B}	AAAATGAAGA	AACTGTTGAT	GAGCACAAAA	CAAGTGTTCA	TCAAGCAATA
Consensus	*****	*****	*****	*****	*****
601					
msa31161.2{327dNt_2603}	TCTTTTCGAG	AAGAGGGCTC	TCTGGTTATT	GCTAGTTTGG	ATGTAGATTT
msa31161.2{327d_18RS21}	TCTTTTCGAG	AAGAGGGCTC	TCTGGTTATT	GCTAGTTTGG	ATGTAGATTT
msa31161.2{327dNT_H36B}	TCTTTTCGAG	AAGAGGGCTC	TCTGGTTATT	GCTAGTTTGG	ATGTAGATTT
Consensus	*****	*****	*****	*****	*****
651					
msa31161.2{327dNt_2603}	GTCTCAACTA	GATGTTCAAA	TAGGAAAAAC	CAGTCATCTG	CCAGCTTATG
msa31161.2{327d_18RS21}	GTCTCAACTA	GATGTTCAAA	TAGGAAAAAC	CAGTCATCTG	CCAGCTTATG
msa31161.2{327dNT_H36B}	GTCTCAACTA	GATGTTCAAA	TAGGAAAAAC	CAGTCATCTG	CCAGCTTATG
Consensus	*****	*****	*****	*****	*****

Table 70: Comparative Sequences relating to SAG 1280

msa31161.2{327dNt_2603}	701	AAGAGTTATC	CTTACGACGT	AAATTTGAGA	TTCTAACATA	TTTTGACCAA
		AAGAGTTATC	CTTACGACGT	AAATTTGAGA	TTCTAACATA	TTTTGACCAA
		AAGAGTTATC	CTTACGACGT	AAATTTGAGA	TTCTAACATA	TTTTGACCAA
	Consensus	*****	*****	*****	*****	*****
msa31161.2{327d_18RS21}	751	ATTCGAAATG	AACGTTCCAA	AGTCCCAAGT	TTTAGACGAG	GTGATTTTGA
		ATTCGAAATG	AACGTTCCAA	AGTCCCAAGT	TTTAGACGAG	GTGATTTTGA
		ATTCGAAATG	AACGTTCCAA	AGTCCCAAGT	TTTAGACGAG	GTGATTTTGA
	Consensus	*****	*****	*****	*****	*****
msa31161.2{327dNT_H36B}	801	CACAGAGATG	GAAATGACAC	CAGTCTTTGA	TGGCGAGGAA	TTACTTACTT
		CACAGAGATG	GAAATGACAC	CAGTCTTTGA	TGGCGAGGAA	TTACTTACTT
		CACAGAGATG	GAAATGACAC	CAGTCTTTGA	TGGCGAGGAA	TTACTTACTT
	Consensus	*****	*****	*****	*****	*****
msa31161.2{327dNt_2603}	851	ATCTCGAAGC	TGATGGCAGT	CCCTATGAGC	TGAAACGAAC	GCTGACTACA
		ATCTCGAAGC	TGATGGCAGT	CCCTATGAGC	TGAAACGAAC	GCTGACTACA
		ATCTCGAAGC	TGATGGCAGT	CCCTATGAGC	TGAAACGAAC	GCTGACTACA
	Consensus	*****	*****	*****	*****	*****
msa31161.2{327d_18RS21}	901	GTCGAAGAAA	AGGAATTAGA	AAAAATTGGA	CAAGCCATTA	GGATAGAAAA
		GTCGAAGAAA	AGGAATTAGA	AAAAATTGGA	CAAGCCATTA	GGATAGAAAA
		GTCGAAGAAA	AGGAATTAGA	AAAAATTGGA	CAAGCCATTA	GGATAGAAAA
	Consensus	*****	*****	*****	*****	*****
msa31161.2{327dNT_H36B}	951	TCAAGAAAAA	TTGACTCAGC	TAGGgATTGa	TTTATCTCAG	TTTGACCCAG
		TCAAGAAAAA	TTGACTCAGC	TAGGgATTGa	TTTATCTCAG	TTTGACCCAG
		TCAAGAAAAA	TTGACTCAGC	TAGGgATTGr	TTTATCTCAG	TTTGACCCAG
	Consensus	*****	*****	***-***	*****	*****
msa31161.2{327dNt_2603}	1001	ACCGAGTCGG	TATTTTATTG	gATGCAGCAG	GTCGTtTTCG	TTTAaAaAAT
		ACCGAGTCGG	TATTTTATTG	gATGCAGCAG	GTCGTtTTCG	TTTAaAaAAT
		ACCGAGTCGG	TATTTTATTG	kATGCAGCAG	GTCGTyyTCG	TTTAwAwAAT
	Consensus	*****	*****	-*****	*****	*****
msa31161.2{327d_18RS21}	1051	GCAGACCTTG	CTTtACTAGG	TGGTTATCCC	AAAGCCTCGG	TAACTCAACT
		GCAGACCTTG	CTTtACTAGG	TGGTTATCCC	AAAGCCTCGG	TAACTCAACT
		GCAGACCTTG	CTTtACTAGG	TGGTTATCCC	AAAGCCTCGG	TAACTCAACT
	Consensus	*****	***-*****	*****	*****	*****
msa31161.2{327dNT_H36B}	1101	AGCCCTTGCG	ACAGAACTAC	TCCAAATGGG	ACTAAGTCAT	GAAAAGGTTG
		AGCCCTTGCG	ACAGAACTAC	TCCAAATGGG	ACTAAGTCAT	GAAAAGGTTG
		AGCCCTTGCG	ACAGAACTAC	TCCAAATGGG	ACTAAGTCAT	GAAAAGGTTG
	Consensus	*****	*****	*****	*****	*****
msa31161.2{327dNt_2603}	1151	AATTTTCTT	TGGTAGCCAG	CTTTCCATTG	AAGAGCTGCG	ACAAGTTGCC
		AATTTTCTT	TGGTAGCCAG	CTTTCCATTG	AAGAGCTGCG	ACAAGTTGCC
		AATTTTCTT	TGGTAGCCAG	CTTTCCATTG	AAGAGCTGCG	ACAAGTTGCC
	Consensus	*****	*****	*****	*****	*****
msa31161.2{327d_18RS21}	1201	TACGCCTTTT	TAtACCAAGA	ACTCAGCAGA	GAAGATGCGG	AGCAATTTGA
		TACGCCTTTT	TAcACCAAGA	ACTCAGCAGA	GAAGATGCGG	AGCAATTTGA
		TACGCCTTTT	TAcACCAAGA	ACTCAGCAGA	GAAGATGCGG	AGCAATTTGA
	Consensus	*****	**-*****	*****	*****	*****
msa31161.2{327dNT_H36B}	1251	AAAAGATAAA	GGTAATCAGC	CAGATTTAAC	TCTCAGAGAT	TGGAAAAGCA
		AAAAGATAAA	GGTAATCAGC	CAGATTTAAC	TCTCAGAGAT	TGGAAAAGCA
		AAAAGATAAA	GGTAATCAGC	CAGATTTAAC	TCTCAGAGAT	TGGAAAAGCA
	Consensus	*****	*****	*****	*****	*****
msa31161.2{327dNt_2603}	1301	AGCTAGAGAA	AGCTGAGGGA	AAAGAAGTAG	TTGATGAAGA	ATTCGCGGAA
		AGCTAGAGAA	AGCTGAGGGA	AAAGAAGTAG	TTGATGAAGA	ATTCGCGGAA
		AGCTAGAGAA	AGCTGAGGGA	AAAGAAGTAG	TTGATGAAGA	ATTCGCGGAA
	Consensus	*****	*****	*****	*****	*****
msa31161.2{327d_18RS21}	1351	AATCCACTGG	TTCAGAGAGT	ATTGGACACT	TATCCTCTGG	GGTCATTGGT
		AATCCACTGG	TTCAGAGAGT	ATTGGACACT	TATCCTCTGG	GGTCATTGGT
		AATCCACTGG	TTCAGAGAGT	ATTGGACACT	TATCCTCTGG	GGTCATTGGT
	Consensus	*****	*****	*****	*****	*****
msa31161.2{327dNT_H36B}	1400	AATCCACTGG	TTCAGAGAGT	ATTGGACACT	TATCCTCTGG	GGTCATTGGT
		AATCCACTGG	TTCAGAGAGT	ATTGGACACT	TATCCTCTGG	GGTCATTGGT
		AATCCACTGG	TTCAGAGAGT	ATTGGACACT	TATCCTCTGG	GGTCATTGGT
	Consensus	*****	*****	*****	*****	*****

Table 70: Comparative Sequences relating to SAG 1280

msa31161.2{327dNt_2603}	1401	TTCCTATAAG	GGACAGGACT	TTGAGGTCAT	GTCGGTCAGC	1450	GATGCTCGAT
		TTCCTATAAG	GGACAGGACT	TTGAGGTCAT	GTCGGTCAGC		GATGCTCGAT
		TTCCTATAAG	GGACAGGACT	TTGAGGTCAT	GTCGGTCAGC		GATGCTCGAT
	Consensus	*****	*****	*****	*****		*****
msa31161.2{327dNt_2603}	1451	TGAACGGTTT	GATTTCGGATT	GAGTTAGTCA	ATGACTTTTC	1500	GGATATCATT
		TGAACGGTTT	GATTTCGGATT	GAGTTAGTCA	ATGACTTTTC		GGATATCATT
		TGAACGGTTT	GATTTCGGATT	GAGTTAGTCA	ATGACTTTTC		GGATATCATT
	Consensus	*****	*****	*****	*****		*****
msa31161.2{327dNt_2603}	1501	GAACAAAATC	CAGTTCCTTTA	TGTGAGGACC	TGGGAAGAAG	1550	TCAGTCAGGC
		GAACAAAATC	CAGTTCCTTTA	TGTGAGGACC	TGGGAAGAAG		TCAGTCAGGC
		GAACAAAATC	CAGTTCCTTTA	TGTGAGGACC	TGGGAAGAAG		TCAGTCAGGC
	Consensus	*****	*****	*****	*****		*****
msa31161.2{327dNt_2603}	1551	ACTTCATCAG	CCAAAGGCAG	AACCACAAAC	AGAGTTAGAA	1600	GAAGCGGACC
		ACTTCATCAG	CCAAAGGCAG	AACCACAAAC	AGAGTTAGAA		GAAGCGGACC
		ACTTCATCAG	CCAAAGGCAG	AACCACAAAC	AGAGTTAGAA		GAAGCGGACC
	Consensus	*****	*****	*****	*****		*****
msa31161.2{327dNt_2603}	1601	AAGAATTAAA	CCTATTCTCA	TTTCTGGAAG	AGGAGCAGT	1650	TCAGAGTATT
		AAGAATTAAA	CCTATTCTCA	TTTCTGGAAG	AGGAGCAGT		TCAGAGTATT
		AAGAATTAAA	CCTATTCTCA	TTTCTGGAAG	AGGAGCAGT		TCAGAGTATT
	Consensus	*****	*****	*****	*****		*****
msa31161.2{327dNt_2603}	1651	GGACTATTGG	AACCAGATGA	TTCAGAAAAT	GGTCATAACG	1700	ATACTGATCT
		GGACTATTGG	AACCAGATGA	TTCAGAAAAT	GGTCATAACG		ATACTGATCT
		GGACTATTGG	AACCAGATGA	TTCAGAAAAT	GGTCATAACG		ATACTGATCT
	Consensus	*****	*****	*****	*****		*****
msa31161.2{327dNt_2603}	1701	TGAAGAAACA	GATAATCAAA	TTCCTGAAGA	GGAAGTCGTC	1750	GAAACAATTC
		TGAAGAAACA	GATAATCAAA	TTCCTGAAGA	GGAAGTCGTC		GAAACAATTC
		TGAAGAAACA	GATAATCAAA	TTCCTGAAGA	GGAAGTCGTC		GAAACAATTC
	Consensus	*****	*****	*****	*****		*****
msa31161.2{327dNt_2603}	1751	CAGAGATTCC	AGTAACGGAC	TTTTATTTTC	CAGAAGATTT	1800	GACGGACTTT
		CAGAGATTCC	AGTAACGGAC	TTTTATTTTC	CAGAAGATTT		GACGGACTTT
		CAGAGATTCC	AGTAACGGAC	TTTTATTTTC	CAGAAGATTT		GACGGACTTT
	Consensus	*****	*****	*****	*****		*****
msa31161.2{327dNt_2603}	1801	TATCCTAAGA	CTGCTAGAGA	TAAGGTTGAG	ACAAACATTG	1850	TGGCCATTCT
		TATCCTAAGA	CTGCTAGAGA	TAAGGTTGAG	ACAAACATTG		TGGCCATTCT
		TATCCTAAGA	CTGCTAGAGA	TAAGGTTGAG	ACAAACATTG		TGGCCATTCT
	Consensus	*****	*****	*****	*****		*****
msa31161.2{327dNt_2603}	1851	TTTGGTAAAA	AATCTAGAAG	TAGAGCACCG	CAATGCTTCA	1900	CCAAGTGAAC
		TTTGGTAAAA	AATCTAGAAG	TAGAGCACCG	CAATGCTTCA		CCAAGTGAAC
		TTTGGTAAAA	AATCTAGAAG	TAGAGCACCG	CAATGCTTCA		CCAAGTGAAC
	Consensus	*****	*****	*****	*****		*****
msa31161.2{327dNt_2603}	1901	AAGAACTCCT	TGCCAAGTAT	GTAGGCTGGG	GTGGACTAGC	1950	CAATGAATTT
		AAGAACTCCT	TGCCAAGTAT	GTAGGCTGGG	GTGGACTAGC		CAATGAATTT
		AAGAACTCCT	TGCCAAGTAT	GTAGGCTGGG	GTGGACTAGC		CAATGAATTT
	Consensus	*****	*****	*****	*****		*****
msa31161.2{327dNt_2603}	1951	TTTGATGACT	ATAATCCAAA	ATTTTCTAAG	GAACGAGAAG	2000	AACTGAAGAG
		TTTGATGACT	ATAATCCAAA	ATTTTCTAAG	GAACGAGAAG		AACTGAAGAG
		TTTGATGACT	ATAATCCAAA	ATTTTCTAAG	GAACGAGAAG		AACTGAAGAG
	Consensus	*****	*****	*****	*****		*****
msa31161.2{327dNt_2603}	2001	CCTAGTCACA	GATAAAGAGT	ATTTCGGATAT	GAAACAGTCC	2050	TCCCTGACAG
		CCTAGTCACA	GATAAAGAGT	ATTTCGGATAT	GAAACAGTCC		TCCCTGACAG
		CCTAGTCACA	GATAAAGAGT	ATTTCGGATAT	GAAACAGTCC		TCCCTGACAG
	Consensus	*****	*****	*****	*****		*****
msa31161.2{327dNt_2603}	2051	CCTATTACAC	AGACCCATCC	CTGATCCGTC	AGATGTGGGA	2100	TAAGTTGGAA
		CCTATTACAC	AGACCCATCC	CTGATCCGTC	AGATGTGGGA		TAAGTTGGAA
		CCTATTACAC	AGACCCATCC	CTGATCCGTC	AGATGTGGGA		TAAGTTGGAA
	Consensus	*****	*****	*****	*****		*****

Table 70: Comparative Sequences relating to SAG 1280

Consensus	*****	*****	*****	*****	*****
msa31161.2{327dNt_2603}	2101				2150
msa31161.2{327d_18RS21}	AGAGATGGCT	TTACAGGTGG	CAAAATCCTA	GATCCTTCCA	TGGGAACAGG
msa31161.2{327dNT_H36B}	AGAGATGGCT	TTACAGGTGG	CAAAATCCTA	GATCCTTCCA	TGGGAACAGG
Consensus	*****	*****	*****	*****	*****
msa31161.2{327dNt_2603}	2151				2200
msa31161.2{327d_18RS21}	GAATTTCTTT	GCGGCTATGC	CAAAACACTT	AAGAGAAAAG	AGTGAGTTGT
msa31161.2{327dNT_H36B}	GAATTTCTTT	GCGGCTATGC	CAAAACACTT	AAGAGAAAAG	AGTGAGTTGT
Consensus	*****	*****	*****	*****	*****
msa31161.2{327dNt_2603}	2201				2250
msa31161.2{327d_18RS21}	ATGGCGTAGA	GTTAGATACT	ATTACAGGAG	CTATTGCCAA	ACACCTTCAT
msa31161.2{327dNT_H36B}	ATGGCGTAGA	GTTAGATACT	ATTACAGGAG	CTATTGCCAA	ACACCTTCAT
Consensus	*****	*****	*****	*****	*****
msa31161.2{327dNt_2603}	2251				2300
msa31161.2{327d_18RS21}	CCCAATAGTC	ATATTGAAAT	TAAGGGATT	GAGACGGTGG	CTTTTAACGA
msa31161.2{327dNT_H36B}	CCCAATAGTC	ATATTGAAAT	TAAGGGATT	GAGACGGTGG	CTTTTAACGA
Consensus	*****	*****	*****	*****	*****
msa31161.2{327dNt_2603}	2301				2350
msa31161.2{327d_18RS21}	CAATAGTTTT	GATTTGGTGA	TTTCAAATGT	GCCCTTTGCC	AATATACGAA
msa31161.2{327dNT_H36B}	CAATAGTTTT	GATTTGGTGA	TTTCAAATGT	GCCCTTTGCC	AATATACGAA
Consensus	*****	*****	*****	*****	*****
msa31161.2{327dNt_2603}	2351				2400
msa31161.2{327d_18RS21}	TTGCGGATAA	TAGGTACGAT	AGGCCTTACA	TGATTCATGA	CTACTTTGTC
msa31161.2{327dNT_H36B}	TTGCGGATAA	TAGGTACGAT	AGGCCTTACA	TGATTCATGA	CTACTTTGTC
Consensus	*****	*****	*****	*****	*****
msa31161.2{327dNt_2603}	2401				2450
msa31161.2{327d_18RS21}	AAAAAGTCAC	TTGATTTGCT	TCATGATGGT	GGACAAGTAG	CGATTATCTC
msa31161.2{327dNT_H36B}	AAAAAGTCAC	TTGATTTGCT	TCATGATGGT	GGACAAGTAG	CGATTATCTC
Consensus	*****	*****	*****	*****	*****
msa31161.2{327dNt_2603}	2451				2500
msa31161.2{327d_18RS21}	TTCCACAGGA	ACTATGGATA	AGCGAACAGA	AAACATCTTA	CAAGATATTC
msa31161.2{327dNT_H36B}	TTCCACAGGA	ACTATGGATA	AGCGAACAGA	AAACATCTTA	CAAGATATTC
Consensus	*****	*****	*****	*****	*****
msa31161.2{327dNt_2603}	2501				2550
msa31161.2{327d_18RS21}	GTGAGACAAC	TGAATTTCTT	GGTGGGGTTC	GACTGCCTGA	CTCTGCCTTT
msa31161.2{327dNT_H36B}	GTGAGACAAC	TGAATTTCTT	GGTGGGGTTC	GACTGCCTGA	CTCTGCCTTT
Consensus	*****	*****	*****	*****	*****
msa31161.2{327dNt_2603}	2551				2600
msa31161.2{327d_18RS21}	AAGGCCATTG	CAGGAACGAG	TGTCACAACG	GATATGTTAT	TCTTCCAGAA
msa31161.2{327dNT_H36B}	AAGGCCATTG	CAGGAACGAG	TGTCACAACG	GATATGTTAT	TCTTCCAGAA
Consensus	*****	*****	*****	*****	*****
msa31161.2{327dNt_2603}	2601				2650
msa31161.2{327d_18RS21}	ACACTTAGAC	AAGGGATATG	TGGCAGACGA	TTTAGCCTTT	TCAGGTTCCA
msa31161.2{327dNT_H36B}	ACACTTAGAC	AAGGGATATG	TGGCAGACGA	TTTAGCCTTT	TCAGGTTCCA
Consensus	*****	*****	*****	*****	*****
msa31161.2{327dNt_2603}	2651				2700
msa31161.2{327d_18RS21}	TTCGCTATGA	CAAGGATAGT	CGCATTTGGC	TCAATCCCTA	TTTTGATGGA
msa31161.2{327dNT_H36B}	TTCGCTATGA	CAAGGATAGT	CGCATTTGGC	TCAATCCCTA	TTTTGATGGA
Consensus	*****	*****	*****	*****	*****
msa31161.2{327dNt_2603}	2701				2750
msa31161.2{327d_18RS21}	GAATACAATA	GCCAGGTGCT	AGGAACCTAC	GAGGTCAGGA	ATTTTAACGG
msa31161.2{327dNT_H36B}	GAATACAATA	GCCAGGTGCT	AGGAACCTAC	GAGGTCAGGA	ATTTTAACGG
Consensus	*****	*****	*****	*****	*****
msa31161.2{327dNt_2603}	2751				2800
msa31161.2{327d_18RS21}	AGGAACACTT	TCTGTTAAGG	GGACTAGTGA	TGACTTGATT	GCAAGTGTTG

Table 70: Comparative Sequences relating to SAG 1280

msa31161.2{327dNT_H36B}	AGGAACACTT	TCTGTTAAGG	GGACTAGTGA	TGACTTGATT	GCAAGTGTGG		
Consensus	*****	*****	*****	*****	*****		
msa31161.2{327dNt_2603}	2801	AAACAGCTCT	AAATCACGTT	AAGGCCCCAA	GAGAGATTGA	2850	TAGAAATGAG
msa31161.2{327d_18RS21}	AAACAGCTCT	AAATCACGTT	AAGGCCCCAA	GAGAGATTGA	TAGAAATGAG		
msa31161.2{327dNT_H36B}	AAACAGCTCT	AAATCACGTT	AAGGCCCCAA	GAGAGATTGA	TAGAAATGAG		
Consensus	*****	*****	*****	*****	*****		
msa31161.2{327dNt_2603}	2851	GTCATCATT	ACCCAGATGT	GTTGACCAA	CAAGTCAATG	2900	ATACCTCCAT
msa31161.2{327d_18RS21}	GTCATCATT	ACCCAGATGT	GTTGACCAA	CAAGTCAATG	ATACCTCCAT		
msa31161.2{327dNT_H36B}	GTCATCATT	ACCCAGATGT	GTTGACCAA	CAAGTCAATG	ATACCTCCAT		
Consensus	*****	*****	*****	*****	*****		
msa31161.2{327dNt_2603}	2901	TCCAGCTGAA	ATGAGGGAAA	ATCTAGGTCA	GTACAGTTTT	2950	GGTTATCAGG
msa31161.2{327d_18RS21}	TCCAGCTGAA	ATGAGGGAAA	ATCTAGGTCA	GTACAGTTTT	GGTTATCAGG		
msa31161.2{327dNT_H36B}	TCCAGCTGAA	ATGAGGGAAA	ATCTAGGTCA	GTACAGTTTT	GGTTATCAGG		
Consensus	*****	*****	*****	*****	*****		
msa31161.2{327dNt_2603}	2951	GGTCTACAGT	TTACTATCGA	GATAACAAAG	GCATTGAGT	3000	CGGAACCAAG
msa31161.2{327d_18RS21}	GGTCTACAGT	TTACTATCGA	GATAACAAAG	GCATTGAGT	CGGAACCAAG		
msa31161.2{327dNT_H36B}	GGTCTACAGT	TTACTATCGA	GATAACAAAG	GCATTGAGT	CGGAACCAAG		
Consensus	*****	*****	*****	*****	*****		
msa31161.2{327dNt_2603}	3001	ACGGAAGAAA	TCAGTTACTA	TGTCGATGAA	GAG	3033	GAG
msa31161.2{327d_18RS21}	ACGGAAGAAA	TCAGTTACTA	TGTCGATGAA	GAG			
msa31161.2{327dNT_H36B}	ACGGAAGAAA	TCAGTTACTA	TGTCGATGAA	GAG			
Consensus	*****	*****	*****	***			

SEQ ID. NO. 7004

STRAIN H36B frame: 1

GGKMNQEVLLQMMRATI PRDRALLEAFLLYYQAEHFDEEWDSL I HQFMTNRQEINKSVQVL
HFETDVSAFVQASPYDTAHDLLTYTQVFGQSGQLDKLSPSEKNLVIEVALFNLATRFQ
LLDSNGHYQTISPDSLLQSRGANLVNVRVANNLADRISRDIEQFLTYEPELETRADE
TVLENEETVDEHKTSVHQAI SFREEGSLVIA SLDVDLSQLDVQIGKTSHLPAYEELSLRR
KFEILTYFDQIRNERSKVP SFRRGDFDTEMEMTPVFDGEELLTYLEADGSPYELKRTLTT
VEEKELEKIGQAIRIENQEKLTLXIXLSQFDPDRVGILLXAAGRXLXNADLASLGGYP
KASVTQLALATELLQMGLSHEKVEFFFGSLSIEELRQVAYAFHQLSREDAEQFEKDK
GNQPDLTLDWKSLEKAEGKEVVDEEFAENPLVQRVLDITYPLGSLVSYKGQDFEVMVS
DARLNGLI RIELVND FSDI IEQNPVLYVRTWEEVSQALHQPKEPQTELEADQELNLF
FLEELVQSIGLLEPDDSENGHNDTLEETDNQI PEEEVVETI PEI PVTDFYFPEDLTDF
YPKTARDKVETNI VAI RLKVNLEVEHRNASPSEQELLAKYVGWGLANEFFDDYNPKFSK
EREELKSLVTDKEYSDMKQSSLTAYYTDPSLIRQMWDKLERDGTGGKILDPMSGTGNFF
AAMPKHLREKSELYGVELDTITGAI AKHLHPNSHIEIKGFETVAFNDNSFDLVISNVPFA
NIRIADNRYDRPYMIHDYFVKSLDLLHDGGQVAI ISSTGTMDKRTENILQDIRETTEFL
GGVRLPDSAFKAIAGTSVTTDMLFFQKHLDKGYVADDLAFSGSIRYDKDSRIWLNPFYFDG
EYNSQVLGTIYEVNRFNGGTL SVKGTSDDLIASVETALNHVKAPREIDRNEVI INPDVLTK
QVNDTSIPAEMRENLGQYSFGYQGSTVYYRDNKGIRVGTKTEEISYYVDEE

SEQ ID. NO. 7005

STRAIN 18RS21 frame: 1

XGKMNQEVLLQMMRATI PRDRALLEAFLLYYQAEHFDEEWDSL I HQFMTNRQEINKSVQVL
HFETDVSAFVQASPYDTAHDLLTYTQVFGQSGQLDKLSPSEKNLVIEVALFNLATRFQ
LLDSNGHYQTISPDSLLQSRGANLVNVRVANNLADRISRDIEQFLTYEPELETRADE
TVLENEETVDEHKTSVHQAI SFREEGSLVIA SLDVDLSQLDVQIGKTSHLPAYEELSLRR
KFEILTYFDQIRNERSKVP SFRRGDFDTEMEMTPVFDGEELLTYLEADGSPYELKRTLTT
VEEKELEKIGQAIRIENQEKLTLGIDLSQFDPDRVGILLDAAGRFRLLKNADLALLGGYP
KASVTQLALATELLQMGLSHEKVEFFFGSLSIEELRQVAYAFHQLSREDAEQFEKDK
GNQPDLTLDWKSLEKAEGKEVVDEEFAENPLVQRVLDITYPLGSLVSYKGQDFEVMVS
DARLNGLI RIELVND FSDI IEQNPVLYVRTWEEVSQALHQPKEPQTELEADQELNLF
FLEELVQSIGLLEPDDSENGHNDTLEETDNQI PEEEVVETI PEI PVTDFYFPEDLTDF
YPKTARDKVETNI VAI RLKVNLEVEHRNASPSEQELLAKYVGWGLANEFFDDYNPKFSK
EREELKSLVTDKEYSDMKQSSLTAYYTDPSLIRQMWDKLERDGTGGKILDPMSGTGNFF
AAMPKHLREKSELYGVELDTITGAI AKHLHPNSHIEIKGFETVAFNDNSFDLVISNVPFA
NIRIADNRYDRPYMIHDYFVKSLDLLHDGGQVAI ISSTGTMDKRTENILQDIRETTEFL
GGVRLPDSAFKAIAGTSVTTDMLFFQKHLDKGYVADDLAFSGSIRYDKDSRIWLNPFYFDG
EYNSQVLGTIYEVNRFNGGTL SVKGTSDDLIASVETALNHVKAPREIDRNEVI INPDVLTK
QVNDTSIPAEMRENLGQYSFGYQGSTVYYRDNKGIRVGTKTEEISYYVDEE

SEQ ID. NO. 7006

STRAIN 2603 frame: 1

GGKMNQEVLLQMMRATI PRDRALLEAFLLYYQAEHFDEEWDSL I HQFMTNRQEINKSVQVL
HFETDVSAFVQASPYDTAHDLLTYTQVFGQSGQLDKLSPSEKNLVIEVALFNLATRFQ
LLDSNGHYQTISPDSLLQSRGANLVNVRVANNLADRISRDIEQFLTYEPELETRADE
TVLENEETVDEHKTSVHQAI SFREEGSLVIA SLDVDLSQLDVQIGKTSHLPAYEELSLRR
KFEILTYFDQIRNERSKVP SFRRGDFDTEMEMTPVFDGEELLTYLEADGSPYELKRTLTT
VEEKELEKIGQAIRIENQEKLTLGIDLSQFDPDRVGILLDAAGRFRLLKNADLALLGGYP
KASVTQLALATELLQMGLSHEKVEFFFGSLSIEELRQVAYAFHQLSREDAEQFEKDK
GNQPDLTLDWKSLEKAEGKEVVDEEFAENPLVQRVLDITYPLGSLVSYKGQDFEVMVS

Table 70: Comparative Sequences relating to SAG 1280

DARLNGLIIRIELVNDFSDIIEQNPLVLYVRTWEEVSQALHQPKEPQTELEADQELNLF
 FLEEEPVQSIGLLEPDDSENGHNDTDLEETDNQIPPEEVVETIPEIPVTDIFYFPEDLTDF
 YPKTARDKVETNIVAIRLVKNLEVEHRNASPSEQELLAKYVGWGLANEFFDDYNPKFSK
 EREELKSLVTDKEYSDMKQSSLTAYYTDPSLIRQMWDKLERDGTGGKILDPSMGTGNFF
 AAMPKHLREKSELYGVELDTITGAIKHLHPNSHIEIKGFETVAFNDNSFDLVISNVPFA
 NIRIADNRYDRPYMIHDYFVKKSLDLLHDGGQVAIISSTGTMDKRTENILQDIRETTEFL
 GGVRLPDSAFKAIAGTSVTDMLEFFQKHLKGYVADDLAFSGSIRYDKDSRIWLNPFYFDG
 EYNSQVLGTYEVRNFNGGTLVKGTSDDLIASVETALNHVKAPREIDRNEVIINPDVLT
 QVNDTSIPAEMRENLGQYSFGYQGSTVYYRDNKGIRVGTKEEISYYVDEE

PRETTY of: /biotmp/msa23816.2{*} June 20, 2002 11:04 ..

msa23816.2{327dNT_H36B}	1	50
msa23816.2{327dnt_2603}	gGKMNQEVLL QMMRATIPRD RALLEAFLLY QAHEFDEEWD SLIHQFMTNR	
msa23816.2{327d_18RS21}	gGKMNQEVLL QMMRATIPRD RALLEAFLLY QAHEFDEEWD SLIHQFMTNR	
Consensus	*****	
msa23816.2{327dNT_H36B}	51	100
msa23816.2{327dnt_2603}	QEINKSVQVL HFETDVSAFV QASPYDTAHD LLTYTQVFGQ SGLQKLDKLS	
msa23816.2{327d_18RS21}	QEINKSVQVL HFETDVSAFV QASPYDTAHD LLTYTQVFGQ SGLQKLDKLS	
Consensus	*****	
msa23816.2{327dNT_H36B}	101	150
msa23816.2{327dnt_2603}	PSEKNLVIEV ALFNLATRFQ LLDSNGHYQT ISPDSLLOKS RGANLVNVYR	
msa23816.2{327d_18RS21}	PSEKNLVIEV ALFNLATRFQ LLDSNGHYQT ISPDSLLOKS RGANLVNVYR	
Consensus	*****	
msa23816.2{327dNT_H36B}	151	200
msa23816.2{327dnt_2603}	VANNLADRIS RDIEQFLTY EPELETRADE TVLENEETVD EHKTSVHQAI	
msa23816.2{327d_18RS21}	VANNLADRIS RDIEQFLTY EPELETRADE TVLENEETVD EHKTSVHQAI	
Consensus	*****	
msa23816.2{327dNT_H36B}	201	250
msa23816.2{327dnt_2603}	SFREEGSLVI ASLDVDLSQL DVQIGKTSHL PAYEELSLRR KFEILTYFDQ	
msa23816.2{327d_18RS21}	SFREEGSLVI ASLDVDLSQL DVQIGKTSHL PAYEELSLRR KFEILTYFDQ	
Consensus	*****	
msa23816.2{327dNT_H36B}	251	300
msa23816.2{327dnt_2603}	IRNERSKVPS FRRGDFDTEM EMTVPVFDGEE LLTYLEADGS PYELKRTLTT	
msa23816.2{327d_18RS21}	IRNERSKVPS FRRGDFDTEM EMTVPVFDGEE LLTYLEADGS PYELKRTLTT	
Consensus	*****	
msa23816.2{327dNT_H36B}	301	350
msa23816.2{327dnt_2603}	VEEKELEKIG QAIRIENQEK LTQLxIxLSQ FDPDRVGILL xAAGRRLxN	
msa23816.2{327d_18RS21}	VEEKELEKIG QAIRIENQEK LTQLgIdLSQ FDPDRVGILL dAAGRfRLkN	
Consensus	*****	
msa23816.2{327dNT_H36B}	351	400
msa23816.2{327dnt_2603}	ADLAsLGGYP KASVTQLALA TELLQMGLSH EKVEFFFGSQ LSIEELRQVA	
msa23816.2{327d_18RS21}	ADLAlLGGYP KASVTQLALA TELLQMGLSH EKVEFFFGSQ LSIEELRQVA	
Consensus	*****	
msa23816.2{327dNT_H36B}	401	450
msa23816.2{327dnt_2603}	YAFhQELSR EDAAEQFEKDK GNQPDLTLD WSKLEKAEG KEVVDEEFAE	
msa23816.2{327d_18RS21}	YAFlyQELSR EDAAEQFEKDK GNQPDLTLD WSKLEKAEG KEVVDEEFAE	
Consensus	*****	
msa23816.2{327dNT_H36B}	451	500
msa23816.2{327dnt_2603}	NPLVQVRVLD YPLGSLVSYK QODFEVMSVS DARLNGLIIRI ELVNDFSDI	
msa23816.2{327d_18RS21}	NPLVQVRVLD YPLGSLVSYK QODFEVMSVS DARLNGLIIRI ELVNDFSDI	
Consensus	*****	
msa23816.2{327dNT_H36B}	501	550
msa23816.2{327dnt_2603}	EQNPVLYVRT WEEVSQALHQ PKAEPQTELE EADQELNLF FLEEEpVQSI	
msa23816.2{327d_18RS21}	EQNPVLYVRT WEEVSQALHQ PKAEPQTELE EADQELNLF FLEEEpVQSI	
Consensus	*****	
msa23816.2{327dNT_H36B}	551	600
msa23816.2{327dnt_2603}	GLLEPDDSEN GHNDTDLEET DNQIPPEEVV ETIPEIPVTD FYFPEDLTDF	
msa23816.2{327d_18RS21}	GLLEPDDSEN GHNDTDLEET DNQIPPEEVV ETIPEIPVTD FYFPEDLTDF	
Consensus	*****	

Table 70: Comparative Sequences relating to SAG 1280

msa23816.2{327dNT_H36B}	601				650
	YPKTARDKVE	TNIVAIRLVK	NLEVEHRNAS	PSEQELLAKY	VGWGGLANEF
	msa23816.2{327dNt_2603}	YPKTARDKVE	TNIVAIRLVK	NLEVEHRNAS	PSEQELLAKY
	msa23816.2{327d_18RS21}	YPKTARDKVE	TNIVAIRLVK	NLEVEHRNAS	PSEQELLAKY
Consensus	*****	*****	*****	*****	*****
msa23816.2{327dNT_H36B}	651				700
	FDDYNPKFSK	EREELKSLVT	DKEYSDMKQS	SLTAYYTDPS	LIRQMWDKLE
	msa23816.2{327dNt_2603}	FDDYNPKFSK	EREELKSLVT	DKEYSDMKQS	SLTAYYTDPS
	msa23816.2{327d_18RS21}	FDDYNPKFSK	EREELKSLVT	DKEYSDMKQS	SLTAYYTDPS
Consensus	*****	*****	*****	*****	*****
msa23816.2{327dNT_H36B}	701				750
	RDGFTGGKIL	DPSMGTGNFF	AAMPKHLREK	SELYGVELDT	ITGAIAKHLH
	msa23816.2{327dNt_2603}	RDGFTGGKIL	DPSMGTGNFF	AAMPKHLREK	SELYGVELDT
	msa23816.2{327d_18RS21}	RDGFTGGKIL	DPSMGTGNFF	AAMPKHLREK	SELYGVELDT
Consensus	*****	*****	*****	*****	*****
msa23816.2{327dNT_H36B}	751				800
	PNSHIEIKGF	ETVAFNDNSF	DLVISNVPFA	NIRIADNRYD	RPYMIHDYFV
	msa23816.2{327dNt_2603}	PNSHIEIKGF	ETVAFNDNSF	DLVISNVPFA	NIRIADNRYD
	msa23816.2{327d_18RS21}	PNSHIEIKGF	ETVAFNDNSF	DLVISNVPFA	NIRIADNRYD
Consensus	*****	*****	*****	*****	*****
msa23816.2{327dNT_H36B}	801				850
	KKSLDLLHDG	GQVAIISSTG	TMDKRTENIL	QDIRETTEFL	GGVRLPDSAF
	msa23816.2{327dNt_2603}	KKSLDLLHDG	GQVAIISSTG	TMDKRTENIL	QDIRETTEFL
	msa23816.2{327d_18RS21}	KKSLDLLHDG	GQVAIISSTG	TMDKRTENIL	QDIRETTEFL
Consensus	*****	*****	*****	*****	*****
msa23816.2{327dNT_H36B}	851				900
	KAIAGTSVTT	DMLFFQKHL	KGYVADDLAF	SGSIRYDKDS	RIWLNPFYFDG
	msa23816.2{327dNt_2603}	KAIAGTSVTT	DMLFFQKHL	KGYVADDLAF	SGSIRYDKDS
	msa23816.2{327d_18RS21}	KAIAGTSVTT	DMLFFQKHL	KGYVADDLAF	SGSIRYDKDS
Consensus	*****	*****	*****	*****	*****
msa23816.2{327dNT_H36B}	901				950
	EYNSQVLGTY	EVRFNFGGTL	SVKGTSDDLI	ASVETALNHV	KAPREIDRNE
	msa23816.2{327dNt_2603}	EYNSQVLGTY	EVRFNFGGTL	SVKGTSDDLI	ASVETALNHV
	msa23816.2{327d_18RS21}	EYNSQVLGTY	EVRFNFGGTL	SVKGTSDDLI	ASVETALNHV
Consensus	*****	*****	*****	*****	*****
msa23816.2{327dNT_H36B}	951				1000
	VIINPDVLTK	QVNDTSIPAE	MRENLGQYSF	GYQGSTVYYR	DNKGIRVGTK
	msa23816.2{327dNt_2603}	VIINPDVLTK	QVNDTSIPAE	MRENLGQYSF	GYQGSTVYYR
	msa23816.2{327d_18RS21}	VIINPDVLTK	QVNDTSIPAE	MRENLGQYSF	GYQGSTVYYR
Consensus	*****	*****	*****	*****	*****
msa23816.2{327dNT_H36B}	1001	1011			
	TEEISYYVDE	E			
	msa23816.2{327dNt_2603}	TEEISYYVDE	E		
	msa23816.2{327d_18RS21}	TEEISYYVDE	E		
Consensus	*****	*			

Table 71: Comparative Sequences relating to SAG1333

SEQ ID NO. 7101

STRAIN 2603

ATGAAAAAGAAAATTATTTTGAAAAGTAGTGTCTTGGTTTAGTCGCTGGGACTTCTATT
 ATGTTCTCAAGCGTGTTCGCGGACCAAGTCGGTGTCCAAGTTATAGGCGTCAATGACTTT
 CATGGTGCACTTGACAATACTGGAACAGCAAATATGCCTGATGGAAAAGTTGCTAATGCT
 GGTACTGCTGCTCAATTAGATGCTTATATGGATGACGCTCAAAAAGATTTCAAACAACT
 AACCTAATGGTGAAGCATTAGGGTTCAAGCAGGCGATATGGTTGGAGCAAGTCCAGCC
 AACTCTGGGCTTCTTCAAGATGAACCAACTGTCAAAAATTTTAATGCAATGAATGTTGAG
 TATGGCACATTGGGTAACCATGAATTTGATGAAGGGTTGGCAGAATATAATCGTATCGTT
 ACTGGTAAAGCCCCTGCTCCAGATTCTAATATTAATAATATTACGAAATCATACCCACAT
 GAAGCTGCAAAACAAGAAATTTAGTGGCAAATGTTATTGATAAAGTTAACAAACAAATTT
 CCTTACAATTGGAAGCCTTACGCTATTAAAAATATTCCTGTAAATAACAAAAGTGTGAAC
 GTTGGCTTTATCGGGATTGTCAACAAAGACATCCCAAACCTTGTCTTACGTAAAAATTAT
 GAACAATATGAATTTTAGATGAAGCTGAAACAATCGTTAAATACGCCAAAGAAATTACAA
 GCTAAAAATGTCAAAGCTATTGTAGTTCTCGCACATGTACCTGCAACAAGTAAAAATGAT
 ATTGCTGAAGGTGAAGCAGCAGAAATGATGAAAAAAGTCAATCAACTCTTCCCTGAAAAAT
 AGCGTAGATATTGTCTTTGCTGGACACAATCATCAATATACAAATGGTCTTGTGTTGGTAAA
 ACTCGTATTGTACAAGCGCTCTCTCAAGGAAAAGCCTATGCTGATGTACGTGGTGTCTTA
 GATACTGATACACAAGATTTCAATTGAGACCCCTTCAGCTAAAGTAATTGCAGTTGCTCCT
 GGTAAAAAACAAGGTAGTGCCGATATTCAAGCCATTGTTGACCAAGCTAATACTATCGTT
 AAACAAGTAACAGAAGCTAAAAATTTGGTACTGCCGAGGTAAAGTGTATGATTACGCGTTCT
 GTTGTATCAAGATAATGTTAGTCCGGTAGGCAGCCTCATCACAGAGGCTCAACTAGCAATTT
 GCTCGAAAAAGCTGGCCAGATATCGATTTTGGCATGACAAATAATGGTGGCAATTCGTGCT
 GACTTACTCATCAAACCAGATGGAACAATCACCTGGGGAGCTGCACAAGCAGTTCAACCT
 TTTGGTAATATCTTACAAGTCGTGCAAAATTTAGTGGTAGAGATCTTTATAAAGCACTCAAC
 GAACAATACGACCAAAAAACAAATTTCTTCCCTTCAAATAGCTGGTCTGCGATACACTTAC
 ACAGATAATAAAGAGGGCGGGGAAGAAACACCATTTAAAGTTGTAAAAGCTTATAAATCA
 AATGGTGAGGAAATCAATCCTGATGCAAAATACAAATTAGTTATCAATGACTTTTATTTC
 GGTGGTGGTGATGGCTTTGCAAGCTTTCAGAAATGCCAAACTTTCTAGGAGCCATTAACCCC
 GATACAGAGGTATTTATGGCCTATATCACTGATTTAGAAAAAGCTGGTAAAAAAGTGAGC
 GTTCCAAATAATAAACCTAAAAATCTATGTCACTATGAAGATGGTTAATGAACTATTACA
 CAAAATGATGGTACACATAGCATTATTAAGAACTTTATTTAGATCGACAAGGAAATATT
 GTAGCACAAGAGATTGTATCAGACACTTTAAACCAACAAATCAAAATCTACAAAAATC
 AACCTGTAACTACAATTCACAAAAACAAATTTACACCAATTTACAGCTATTAAACCCTATG
 AGAAATTATGGCAAAACCATCAAACCTCACTACTGTAAAATCAAAACAATTACCAAAAAACA
 AACTCTGAATATGGACAATCATTCCTTATGTCTGTCTTTGGTGTGGACTTATAGGAATT
 GCTTTAAATACAAAGAAAAACATATGAAA

SEQ ID NO. 7102

STRAIN 090

AAGTCGGTGTCCAAGTTATAGGCGTCAATGACTTTTCATGGTGCACTTGAC
 AATACTGGAACAGCAAATATGCCTGACGGAAGTTACTAATGCTGGCAC
 TGCTGCTCAATTAGATGCTTATATGGATGATGCTCAAAAAGATTTCAAAC
 AAATAACCCCTAATGGTGAAAGCAATTAGAGTTCAAGCTGGTGATATGGTT
 GGAGCAAGTCCAGCTAACTCAGGGCTTCTTCAAGATGAACCAACCGTTAA
 AACATTTAATGCAATGAATGTTGAGTATGGCACATTAGGTAACCATGAAT
 TTGATGAAGGTTTGGCAGAATACAAATCGTATCGTTACTGGAAAGGCCCT
 GCTCCAGATTCTAATATAAATAATATTACGAAATCATACCCACACGAAGC
 TGCAAAACAAGAAATTTAGTGGCAAACGTTATTGATAAAGTTAACAAAC
 AAATCCCTTACAATTTGGAACCTTACGCTATTAAAAATATTCCTGTAAAT
 AACAAAAGTGTGAACGTTGGCTTTATCGGAATCGTTACCAAAGACATCCC
 AAACCTTGTCTTACGTAAAAATTATGAACAATATGAATTTTATAGATGAAG
 CTGAAACAATCGTTTAAATACGCCAAAGAAATTACAAGCTAAAAATGTCAAG
 GCTATTGTAGTCCCTGCTCATGTACCTGCAACAAGCAAGGATGATATTGC
 TGAAGGTGAAGCAGCAGAAATGATGAAAAAAGTCAATCAACTCTTCCCTG
 AAAATAGCCTAGATATTGTCTTTGCTGGACACAATCATCAATATACAAAT
 GGTCTTGTGGTAAAACTCGCATTGTACAAGCGCTCTCTCAAGGAAAAGC
 CTATGCTGACGTACGTGGTGTCTAGATACGTGATACACAAGATTTTCAATTG
 AAACCCCTTCAAGCTAAAGTAGTTGCAGTTGCTCCTGGTAAAAAACAAGGT
 AGTGCCGATATTCAAGCCATTGTTGACCAAGCTAATACTATCGTTAAACA
 AGTAACAGAAGCTAAATTTGGTACTGCCGAGGTAAGTGGCATGATTACGC
 GTTCTGTTGATCAAGATAATGTTAGTCCAGTAGGCAGCCTCATCACAGAG
 GCTCAACTAGCAATTGCTCGAAAAAGCTGGCCAGATATCGATTTTGCCAT
 GACAAATAATGGTGGCATTCTGTGCTGACTTACTCATCAAACCAGATGGAA
 CAATCACCTGGGGAGCTGCACAAGCAGTTCAACCTTTTGGTAATATCTTA
 CAAGTCGTGCAAAATTACTGGTAGAGATCTTTATAAAGCACTCAACGAACA
 ATACGACCAAAAACAAATTTCTTCTTCAAATAGCTGGTCTGCGATACA
 CTTACACAGATAATAAAGAGGGCGGAGAAGAAACACCATTTAAAGTTGTA
 AAAGCTTATAAATCAAATGGTGAAGAAATCAATCCTGATGCAAAATACAA
 ATTAGTTATCAATGACTTTTATTTCGGTGGTGGTGGTGGCTTTGCAAGCT
 TCAGAAATGCCAACTTCTAGGAGCCATTAATCCCAGATACAGAGGTATTT
 ATGGCCTATATCACTGATTTAGAAAAAGCTGGTAAAAAAGTGAGCGTTCC
 AAATAATAAACCTAAATCTATGTCACTATGAAGATGGTTAATGAACTA
 TTACACAAAATGATGGTACACATAGCATTATTAAGAACTTTATTTAGAT
 CGACAAGGAAATATTGTAGCACAAGAGATTGTATCAGACACTTTAAACCA
 AACAAAATCAAAATCTACAAAAATCAACCTGTAACTACAATTCACAAAA
 AACAAATTACACCAATTTACAGCTATTAAACCCTATGAGAAATTATGGCAAA
 CCATCAAACCTCACTACTGTAAAATCAAAACAA

SEQ ID NO. 7103

STRAIN A909

GCGTCAATGACTTTTCATGGTGCACTTGACAATACTGGAACAGCAAATATG
 CTTGACGGAAGTTACTAATGCTGGCACTGCTGCTCAATTAGATGCTTA

Table 71: Comparative Sequences relating to SAG1333

TATGGATGATGCTCAAAAAGATTTCAAACAACTAACCTAATGGTGAAA
 GCATTAGAGTTCAAGCTGGTGATATGGTTGGAGCAAGTCCAGCTAACTCA
 GGGCTTCTTCAAGATGAACCAACCGTTAAACATTTAATGCAATGAATGT
 TGAGTATGGCACATTAGGTAACCATGAATTTGATGAAGGTTTGGCAGAAT
 ACAATCGTATCGTTACTGGAAAGGCCCTGCTCCaGaTTCTAATATAAAT
 AATATTACGAAATCATACCCACACGAAGCTGCAAAACAAGAAATTTGTAGT
 GGCAAACGTTATTGATAAAGTTAAACAAACAAATCCCTTACAATTGGAAAC
 CTTACACTATTAAAAATATTCTGTAAATAACAAAAGTGTGAACGTTGGC
 TTTATCGGAATCGTTACCAAAGACATCCCAAACCTTGTCTTACGTAAAAA
 TTATGAACAATATGAATTTTATAGATGAAGCTGAAACAATCGTTAAATACG
 CCAAAGAATTACAAGCTAAAAATGTCAAGGCTATTGTAGTCTTTGCTCAT
 GTACCTGCAACAAGCAAGGATGATATTGCTGAAGGTGAAGCAGCAGAAAT
 GATGAAAAAAGTCAATCAACTCTTCCCTGAAAATAGCGTAGATATTGTCT
 TTGCTGGACACAATCATCAATATACAAATGGTCTTGTGGTAAAACTCGT
 ATTGTACAAGCGCTCTCTCAAGGAAAAGCCTATGCTGATGTACGTGGTGT
 CCTAGATACTGATACACAAGATTTTATTGAAACCCCTTCAGCTAAAGTAA
 TTGCAGTTGCTCCTGGTAAAAAACAGGTAGTGCCGATATTCAAGCCATT
 GTTGACCAAGCTAATACTATCGTTAAACAAGTAACAGAAGCTAAAAATGG
 TACTGCCGAGGTAAGTGGCATGATTACGCGTTCTGTTGATCAAGATAATG
 TTAGTCCGGTAGGCAGCCTCATCACAGAGGCTCAACTAGCAATTGCTCGA
 AAAAGCTGGCCAGATATCGATTTTGGCATGACAAATAATGGTGGCATTCTG
 TGCTGACTTACTCATCAAACAGATGGAACAATCACCTGGGGAGCTGCAC
 AAGCAGTTCAACCTTTTGGTAATATCTTACAAGTCGTGAAATTAAGTGT
 AGAGATCTTTATAAAGCACTCAACGAACAATACGACCAAAAAACAAATTT
 CTTCCTTCAAATAGCTGGTCTGCGATACACTTACACAGATAATAAAGAGG
 GCGGGAAGAAACACCATTTAAAGTTGTAAAGCTTATAAATCAAATGGT
 GAGGAAATCAATCCTGATGCAAAATACAAATTAGTTATCAATGACTTTT
 ATTCCGGTGGTGGTGTGCTTTGCAAGCTTCAGAAATGCCAACTTCTAG
 GAGCCATTAAATCCCGATACAGAGGTATTTATGGCCTATATCACTGATTTA
 GAAAAAGCTGGTAAAAAAGTGAGCGTTCCAAATAATAAACCTAAAAATCTA
 TGTCACTATGAAGATGGTTAATGAACTATTACACAAAATGATGGTACAT
 ATAGCATTATTAAAGAACTTTATTTAGATCGACAAGGAAATATTGTAGCA
 CAAGAGATTGTATCAGACACTTTAAACCAAACAAAATCAAATCTACAAA
 AATCAACCCTGTAACATAATTACAAAAACAATTACACCAATTTACAG
 CTATTAAACCCTATGAGAAATTATGGCAAACCATCAAACCTCACTACTGTA
 AAATCAAAACAA

SEQ ID NO. 7104

STRAIN H36B

CCAAGTCGGTGTCCAAGTTATAGGCGTCAATGACTTTTATGGTGCACTTG
 ACAATACTGGAACAGCAAATATGCCTGACGGAAGTTACTAATGCTGGC
 ACTGCTGCTCAATTAGATGCTTATATGGATGATGCTCAAAAAGATTTCAA
 ACAAACTAACCCTAATGGTGAAAGCATTAGAGTTCAAGCTGGTGATATGG
 TTGGAGCAAGTCCAGCTAACTCAGGGCTTCTTCAAGATGAACCAACCGTT
 AAAACATTTAATGCAATGAATGTTGAGTATGGCACATTAGGTAACCATGA
 ATTTGATGAAGGTTTGGCAGAATACAATCGTATCGTTACTGGAAAGGCC
 CTGCTCCAGATTCTAATATAAATAATATTACGAAATCATACCCACACGAA
 GCTGCAAAACAAGAAATTTAGTGGCAAACGTTATTGATAAAGTTAACAA
 ACAATCCCTTACAATTGGAAACCTTACACTATTAAAAATATTCTGTAA
 ATAACAAAAGTGTGAACGTTGGCTTTATCGGAATCGTTACCAAAGACATC
 CCAAACCTTGTCTTACGTAAAAAATTATGAACAATATGAATTTTATAGATGA
 AGCTGAAACAATCGTTAAATACGCCAAAGAATTACAAGCTAAAAATGTCA
 AGGCTATTGTAGTCTTGTCTCATGTACCTGCAACAAGCAAGGATGATATT
 GCTGAAGGTGAAGCAGCAGAAATGATGAAAAAAGTCAATCAACTCTTCCC
 TGAAAAATAGCGTAGATATTGTCTTTGCTGGACACAATCATCAATATACAA
 ATGGTCTTGTGGTAAAACTCGTATTGTACAAGCGCTCTCTCAAGGAAAA
 GCCTATGCTGATGTACGTGGTGTCTAGATACTGATACACAAGATTTTCT
 TGAAACCCCTTCAGCTAAAGTAATTGCAGTTGCTCTTGGTAAAAAACAG
 GTAGTGCCGATATTCAAGCCATTGTTGACCAAGCTAATACTATCGTTAAA
 CAAGTAACAGAAGCTAAATTTGGTACTGCCGAGGTAAGTGGCATGATTAC
 GCGTTCTGTTGATCAAGATAATGTTAGTCCGGTAGGCAGCCTCATCACAG
 AGGCTCAACTAGCAATTGCTCGAAAAGCTGGCCAGATATCGATTTTGGC
 ATGACAAATAATGGTGGCATTCTGCTGACTTACTCATCAAACAGATGG
 AACAATCACCTGGGGAGCTGCACAAGCAGTTCAACCTTTTGGTAATATCT
 TACAAGTCGTGAAATTAAGTGGTAGAGATCTTTATAAAGCACTCAACGAA
 CAATACGACCAAAAAACAAATTTCTTCTTCAAATAGCTGGTCTGCGATA
 CACTTACACAGATAATAAAGAGGGCGGGGAAGAAACACCATTTAAAGTTG
 TAAAAGCTTATAAATCAAATGGTGAGGAAATCAATCCTGATGCAAAATAC
 AAATTAGTTATCAATGACTTTTATTTCGGTGGTGGTGTGCTTTGCAAG
 CTTTCAAGAAATGCCAACTTCTAGGAGCCATTAAATCCCGATACAGAGGTAT
 TTATGGCCTATATCACTGATTTAGAAAAAGCTGGTAAAAAAGTGAGCGTT
 CCAAATAATAAACCTAAATCTATGTCACTATGAAGATGGTTAATGAAAC
 TATTACACAAAATGATGGTACATATAGCATTATTAGAAACTTTATTAG
 ATCGACAAGGAAATATTGTAGCACAAGAGATTGTATCAGACACTTTAAAC
 CAAACAAAATCAAATCTACAAAAATCAACCCTGTAACATAAATTCACAA
 AAAACAATTACACCAATTTACAGCTATTAACCCTATGAGAAATTATGGCA
 AACCATCAAACCTCACTACTGTAAATCAAA

SEQ ID NO. 7105

STRAIN 18RS21

GACCAAGTCGGTGTCCAAGTTATAGGCGTCAATGACTTTT
 ATGGTGCACCTTGACAATACTGGAACAGCAAATATGCCTGACGGAAGTT
 AnTAATGCTGGCACTGCTGCTCAATTAGATGCTTATATGGATGATGCTCA

Table 71: Comparative Sequences relating to SAG1333

AAAAGATTTCAAACAACTAACCCTAATGGTGAAAGCATTAGAGTTCAAG
 CTGGTGATATGGTTGGAGCAAGTCCAGCTAACTCAGGGCTTCTTCAAGAT
 GAACCAACCGTTAAACATTTAATGCAATGAATGTTGAGTATGGCACATT
 AGGTAACCATGAATTTGATGAAGGTTTGGCAGAATACAATCGTATCGTTA
 CTGGAAAGGCCCTGCTCCAGATTCTAATATAAATAATATTACGAAATCA
 TACCCACACGAAGCTGCAAAACAAGAAATTGTAGTGGCAAACGTTATTGA
 TAAAGTTAAACAAACAAATCCCTTACAATTGGAAACCTTACACTATTAAAA
 ATATTCTGTAAATAACAAAAGTGTGAACGTTGGCTTTATCGGAATCGTT
 ACCAAAGACATCCCAAACCTTGTCTTACGTAAAAATTATGAACAATATGA
 ATTTTGTAGATGAAGCTGAAACAATCGTTAAATACGCCAAAGAATTACAAG
 CTAAAAATGTCAAGGCTATTGTAGTCCCTTGCTCATGTACCTGCAACAAGC
 AAGGATGATATTGCTGAAGGTGAAGCAGCAGAAATGATGAAAAAGTCAA
 TCAACTCTTCCCTGAAAATAGCGTAGATATTGTCTTTGCTGGACACAATC
 ATCAATATACAAATGGTCTTGTGGTAAAACTCGTATTGTACAAGCGCTC
 TCTCAAGGAAAAGCCTATGCTGATGTACGTGGTGTCTTAGATACTGATAC
 ACAAGATTTTATTGAAACCCCTTACGCTAAAGTAATTGCAGTTGCTCCTG
 GTAAAAAACAAGGTAGTCCGATATTCAAGCCATTGTTGACCAAGCTAAT
 ACTATCGTTAAACAAGTAACAGAAGCTAAAATTGGTACTGCCGAGGTAAG
 TGGCATGATTACGCGTTCTGTTGATCAAGATAATGTTAGTCCGGTAGGCA
 GCCTCATCACAGAGGCTCAACTAGCAATTGCTCGAAAAAGCTGGCCAGAT
 ATCGATTTTGCCATGACAAATAATGGTGGCATTCTGTGCTGACTTACTCAT
 CAAACCAAGATGGAACAATCACCTGGGGAGCTGCACAAGCAGTTCAACCTT
 TTGGTAATATCTTACAAGTCGTGCAAAATTAAGTGGTAGAGATCTTTATAAA
 GCACTCAACGAACAATACGACCAAAAACAAAATTTCTTCTTCAAATAGC
 TGGTCTGCGATACACTTACACAGATAATAAAGAGGGCGGGGAAGAAACAC
 CATTTAAAGTTGTAAAAGCTTATAAATCAAATGGTGAGGAAATCAATCCT
 GATGCAAAATACAAATTAGTTATCAATGACTTTTTATTTCGGTGGTGGTGA
 TGGCTTTGCAAGCTTCAGAAATGCCAACTTCTAGGAGCCATTAAATCCCG
 ATACAGAGGTATTTATGGCCTATATCACTGATTTAGAAAAAGCTGGTAAA
 AAAGTGAGCGTTCCAAATAATAAACCTAAAATCTATGTCACTATGAAGAT
 GGTAAATGAAACTATTACACAAAATGATGGTACATATAGCATTATTAAGA
 AACTTTATTTAGATCGACAAGGAAATATTGTAGCACAAGAGATTGTATCA
 GACACTTTAAACCAAAACAAAATCAAATCTACAAAAATCAACCCTGTAAC
 TACAATTCACAAAAACAATTACACCAATTTACAGCTATTAACCTATGA
 GAAATTATGGCAAACCATCAAACCTCACTACTGTAAAATCAAAA

SEQ ID NO. 7106

STRAIN M732

ACCAAGTCGGTGTCCAAGTTATAGGCGTCAATGACTTTTATGGTGCACTT
 GACAATACTGGAACAGCAAAATATGCCTGACGGAAGTTACTAATGCTGG
 CACTGCTGCTCAATTAGATGCTTATATGGATGATGCTCAAAAAGATTTCA
 AACAACTAACCCTAATGGTGAAAGCATTAGAGTTCAAGCTGGTGATATG
 GTTGGAGCAAGTCCAGCTAACTCAGGGCTTCTTCAAGATGAACCAACCGT
 TAAAACATTTAATGCAATGAATGTTGAGTATGGCACATTAGGTAACCATG
 AATTTGATGAAGGTTTGGCAGAATACAATCGTATCGTTACTGGAAGGCC
 CCTGCTCCAGATTCTAATATAAATAATATTACGAAATCATACCCACACGA
 AGCTGCAAAACAAGAAATTTGTAGTGGCAAACGTTATTGATAAAGTTAACA
 AACAAATCCCTTACAATTGGAAACCTTACACTATTAATAAATATTCTGTGA
 AATAACAAAAGTGTGAACGTTGGCTTTATCGGAATCGTTACCAAAGACAT
 CCCAAACCTTGTCTTACGTAAAAATTATGAACAATATGAATTTTATAGATG
 AAGCTGAAACAATCGTTAAATACGCCAAAGAATTACAAGCTAAAAATGTC
 AAGGCTATTGTAGTCTTGTCTCATGTACCTGCAACAAGCAAGGATGATAT
 TGCTGAAGGTGAAGCAGCAGAAATGATGAAAAAGTCAATCAACTCTTCC
 CTGAAAATAGCGTAGATATTGTCTTTGCTGGACACAATCATCAATATACA
 AATGGTCTTGTGGTAAAACTCGTATTGTACAAGCGCTCTCTCAAGGAAA
 AGCCTATGCTGATGTACGTGGTGTCTTAGATACTGATACACAAGATTTCA
 TTGAAACCCCTTCAAGCTAAAGTAATTGCAGTTGCTCCTGGTAAAAAACA
 GGTAGTGCCGATATTCAAGCCATTGTTGACCAAGCTAATACTATCGTTAA
 ACAAGTAACAGAAGCTAAAATTGGTACTGCCGAGGTAAGTGGCATGATTA
 CGCGTTCTGTTGATCAAGATAATGTTAGTCCGGTAGGCAGCCTCATCACA
 GAGGCTCAACTAGCAATTGCTCGAAAAAGCTGGCCAGATATCGATTTTGC
 CATGACAAATAATGGTGGCATTCTGTGCTGACTTACTCATCAAACAGATG
 GAACAATCACCTGGGGAGCTGCACAAGCAGTTCAACCTTTTGGTAATATC
 TTACAAGTCGTGCAAAATTAAGTGGTAGAGATCTTTATAAAGCACTCAACGA
 ACAATACGACCAAAAACAAAATTTCTTCTTCAAATAGCTGGTCTGCGAT
 ACCTTACACAGATAATAAAGAGGGCGGGGAAGAAACACCATTTAAAGTT
 GTAAAAGCTTATAAATCAAATGGTGAGGAAATCAATCCTGATGCAAAATA
 CAAATTAGTTATCAATGACTTTTTATTTCGGTGGTGGTGGTGGCTTTGCAA
 GCTTCAGAAAATGCCAACTTCTAGGAGCCATTAAATCCGATACAGAGGTA
 TTTATGGCCTATATCACTGATTTAGAAAAAGCTGGTAAAAAAGTGAGCAT
 TCCAAATAATAAACCTAAAATCTATGTCACTATGAAGATGGTTAATGAAA
 CTATTACACAAAATGATGGTACATATAGCATTATTAAGAACTTTATTTA
 GATCGACAAGGAAATATTGTAGCACAAGAGATTGTATCAGACACTTTAAA
 CCAACAAAATCAAATCTACAAAAATCAACCCTGTAACCTACAATTCACA
 AAAACAATTACACCAATTTACAGCTATTAACCTATGAGAAATTATGGC
 AAACCATCAAACCTCACTACTGTAAAATCAAAACAA

SEQ ID NO. 7107

STRAIN COH1

ACCAAGTCGGTGTCCAAGTTATAGGCGTCAATGACTTTTATGGTGCACTT
 GACAATACTGGAACAGCAAAATATGCCTGACGGAAGTTACTAATGCTGG
 CACTGCTGCTCAATTAGATGCTTATATGGATGATGCTCAAAAAGATTTCA
 AACAACTAACCCTAATGGTGAAAGCATTAGAGTTCAAGCTGGTGATATG

Table 71: Comparative Sequences relating to SAG1333

GTTGGAGCAAGTCCAGCTAACTCAGGGCTTCTTCAAGATGAACCAACCGT
 TAAAACATTTAATGCAATGAATGTTGAGTATGGCACATTAGGTAACCATG
 AATTTGATGAAGGTTTGGCAGAATACAATCGTATCGTTACTGGAAAGGCC
 CCTGCTCCAGATTCTAATATAAATAATATTACGAAATCATACCCACACGA
 AGCTGCAAAACAAGAAATTGTAGTGGCAAACGTTATTGATAAAGTTAACA
 AACAAATCCCTTACAATTGGAAACCTTACACTATTAAAAATATTCTGTGA
 AATAACAAAAGTGTGAACGTTGGCTTTATCGGAATCGTTACCAAAGACAT
 CCCAAACCTTGTCTTACGTAAAAATTATGAACAATATGAATTTTAGATG
 AAGCTGAAACAATCGTTAAATACGCCAAAGAATTACAAGCTAAAAATGTC
 AAGGCTATTGTAGTCCTTGCTCATGTACCTGCAACAAGCAAGGATGATAT
 TGCTGAAGGTGAAGCAGCAGAAATGATGAAAAAGTCAATCAACTCTTCC
 CTGAAAATAGCGTAGATATTGTCTTTGCTGGACACAATCATCAATATACA
 AATGGTCTTGTGGTAAAACTCGTATTGTACAAGCGCTCTCTCAAGGAAA
 AGCCTATGCTGATGTACGTGGTGTCTAGATACTGATACACAAGATTTCA
 TTGAAACCCCTTCAGCTAAAGTAATTGCAGTTGCTCCTGGTAAAAAACA
 GGTAAGTCCCGATATTCAAGCCATTGTGACCAAGCTAATACTATCGTTAA
 ACAAGTAACAGAAGCTAAAATTGGTACTGCCGAGGTAAGTGGCATGATTA
 CGCGTTCTGTTGATCAAGATAATGTTAGTCCGGTAGGCAGCCTCATCACA
 GAGGCTCAACTAGCAATTGCTCGAAAAAGCTGGCCAGATATCGATTTTGC
 CATGACAAATAATGGTGGCATTCTGTCTGACTTACTCATCAAACCAGATG
 GAACAATCACCTGGGGAGCTGCACAAGCAGTTCAACCTTTTGGTAATATC
 TTACAAGTCGTGCAAAATTACTGGTAGAGATCTTTATAAAGCACTCAACGA
 ACAATACGACCAAAAAACAAATTTCTTCTTCAAATAGCTGGTCTGCGAT
 ACACCTTACACAGATAATAAAGAGGGCGGGGAAGAAACACCATTTTAAAGTT
 GTAAAAGCTTATAAATCAAATGGTGAGGAAATCAATCCTGATGCAAAATA
 CAAATTAGTTATCAATGACTTTTTATTCTGGTGGTGGTGGTGGCTTTGCAA
 GCTTCAGAAATGCCAACTTCTAGGAGCCATTAAATCCCGATACAGAGGTA
 TTTATGGCCTATATCACTGATTTAGAAAAAGCTGGTAAAAAAGTGAGCAT
 TCCAAATAATAAACCTAAAATCTATGTCACTATGAAGATGGTTAATGAAA
 CTATTACACAAAATGATGGTACATATAGCATTATTAAGAACTTTATTTA
 GATCGACAAGGAAATATTGTAGCACAAGAGATTGTATCAGACACTTTAAA
 CCAACAAAATCAAATCTACAAAATCAACCCTGTAACCTACAATTCACA
 AAAAAACAATTACACCAATTTACAGCTATTAACCCCTATGAGAAATTATGGC
 AAACCATCAAACCTCACTACTGTAAAATCAAA

SEQ ID NO. 7108

STRAIN M781

CAAGTCGGTGTCCAAGTTATAGGCGTCAATGACTTTTCATGGTGCACCTTGA
 CAATACTGGAACAGCAAATATGCCTGACGGAAGTTACTAATGCTGGCA
 CTGCTGCTCAATTAGATGCTTATATGGATGATGCTCAAAAAGATTTCAAA
 CAACTAACCCCTAATGGTGAAAGCATTAGAGTTCAAGCTGGTGGTGGTGGT
 TGGAGCAAGTCCAGCTAACTCAGGGCTTCTTCAAGATGAACCAACCGTTA
 AAACATTTAATGCAATGAATGTTGAGTATGGCACATTAGGTAACCATGAA
 TTTGATGAAGGTTTGGCAGAATACAATCGTATCGTTACTGGAAAGGCCCC
 TGCTCCAGATTCTAATATAAATAATATTACGAAATCATACCCACACGAAG
 CTGCAAAACAAGAAATTGTAGTGGCAAACGTTATTGATAAAGTTAACAAA
 CAAATCCCTTACAATTGGAAACCTTACACTATTAAAAATATTCTGTAAA
 TAACAAAAGTGTGAACGTTGGCTTTATCGGAATCGTTACCAAAGACATCC
 CAAACCTTGTCTTACGTAAAAATTATGAACAATATGAATTTTAGATGAA
 GCTGAAACAATCGTTAAATACGCCAAAGAATTACAAGCTAAAAATGTCAA
 GGCTATTGTAGTCCTTGCTCATGTACCTGCAACAAGCAAGGATGATATTG
 CTGAAGGTGAAGCAGCAGAAATGATGAAAAAGTCAATCAACTCTTCCCT
 GAAAATAGCGTAGATATTGTCTTTGCTGGACACAATCATCAATATACAAA
 TGGTCTTGTGGTAAAACTCGTATTGTACAAGCGCTCTCTCAAGGAAAAG
 CCTATGCTGATGTACGTGGTGTCTAGATACTGATACACAAGATTTTCAAT
 GAAACCCCTTCAGCTAAAGTAATTGCAGTTGCTCCTGGTAAAAAACAGG
 TAGTGCCGATATTCAAGCCATTGTGACCAAGCTAATACTATCGTTAAAC
 AAGTAACAGAAGCTAAAATTGGTACTGCCGAGGTAAGTGGCATGATTACG
 CGTTCTGTTGATCAAGATAATGTTAGTCCGGTAGGCAGCCTCATCACAGA
 GGCTCAACTAGCAATTGCTCGAAAAAGCTGGCCAGATATCGATTTTGCCA
 TGACAAATAATGGTGGCATTCTGTCTGACTTACTCATCAAACCAGATGGA
 ACAATCACCTGGGGAGCTGCACAAGCAGTTCAACCTTTTGGTAATATCTT
 ACAAGTCGTGCAAAATTACTGGTAGAGATCTTTATAAAGCACTCAACGAAC
 AATACGACCAAAAAACAAATTTCTTCTTCAAATAGCTGGTCTGCGATAC
 ACTTACACAGATAATAAAGAGGGCGGGGAAGAAACACCATTTTAAAGTTGT
 AAAAGCTTATAAATCAAATGGTGAGGAAATCAATCCTGATGCAAAATACA
 AATTAGTTATCAATGACTTTTTATTCTGGTGGTGGTGGTGGTGGTGGTGGT
 TTCAGAAATGCCAACTTCTAGGAGCCATTAAATCCCGATACAGAGGTATT
 TATGGCCTATATCACTGATTTAGAAAAAGCTGGTAAAAAAGTGAGCATTC
 CAAATAATAAACCTAAAATCTATGTCACTATGAAGATGGTTAATGAAACT
 ATTACACAAAATGATGGTACATATAGCATTATTAAGAACTTTATTTAGA
 TCGACAAGGAAATATTGTAGCACAAGAGATTGTATCAGACACTTTAAACC
 AAACAAAATCAAATCTACAAAATCAACCCTGTAACCTACAATTCACAAA
 AAACAATTACACCAATTTACAGCTATTAACCCCTATGAGAAATTATGGCAA
 ACCATCAAACCTCACTACTGTAAAATCAAA

SEQ ID NO. 7109

STRAIN CJB110

GACCAAGTCGGTGTCCAAGTTATAGGCGTCAATGACTTTTCATGGTGC
 ACTTGACAATACTGGAACAGCAAATATGCCTGACGGAAGTTACTAATG
 CTGGCACTGCTGCTCAATTAGATGCTTATATGGATGATGCTCAAAAAGAT
 TTCAAACAACTAACCCCTAATGGTGAAAGCATTAGAGTTCAAGCTGGTGA
 TATGGTTGGAGCAAGTCCAGCTAACTCAGGGCTTCTTCAAGATGAACCAA

Table 71: Comparative Sequences relating to SAG1333

CCGTTAAAAACATTTAATGCAATGAATGTTGAGTATGGCACATTAGGTAAC
 CATGAATTTGATGAAGGTTTGGCAGAATACAATCGTATCGTTACTGGAAA
 GGCCCTGCTCCAGATTCTAATATAAATAATATTACGAAATCATACCCAC
 ACGAAGCTGCAAAAACAAGAAATTTAGTAGTGGCAAACGTTATTGATAAAGTT
 AACAAAACAAATCCCTTACAATTGGAAACCTTACGCTATTAAAAATATTCC
 TGTAAATAACAAAAGTGTGAACGTTGGCTTTATCGGAATCGTTACCAAAG
 ACATCCCAAACCTTGTCTTACGTAAAAATTATGAACAATATGAATTTTAA
 GATGAAGCTGAAACAATCGTTAAATACGCCAAAGAATTACAAGCTAAAAA
 TGTCAAGGCTATTGTAGTCCCTTGTCTCATGTACCTGCAACAAGCAAGGATG
 ATATTGCTGAAGGTGAAGCAGCAGAAATGATGAAAAAAGTCAATCAACTC
 TTCCCTGAAAATAGCGTAGATATTGTCTTTGCTGGACACAATCATCAATA
 TACAAATGGTCTTGTGGTAAACTCGCATTTGTACAAGCGCTCTCTCAAG
 GAAAAGCCTATGCTGACGTACGTGGTGTCTTAGATACTGATACACAAGAT
 TTCATTGAAACCCCTTCAAGCTAAAGTAGTTGCAGTTGCTCCTGGTAAAAA
 AACAGGTAGTGGCGATATTCAAGCCATTGTTGACCAAGCTAATACTATCG
 TTAACAAGTAACAGAGCTAAAATTGGTACTGCCGAGGTAAGTGGCATG
 ATTACGCGTTCTGTTGATCAAGATAATGTTAGTCCAGTAGGCAGCCTCAT
 CACAGAGGCTCACTAGCAATTGCTCGAAAAAGCTGGCCAGATATCGATT
 TTGCCATGACAAATAATGGTGGCATTTCGTGCTGACTTACTCATCAAACCA
 GATGGAACCAATCACCTGGGGAGCTGCACAAGCAGTTCAACCTTTTGGTAA
 TATCTTACAAGTCTGCGAAATTACTGGTAGAGATCTTTATAAAGCACTCA
 ACGAACCAATACGACCAAAAACAAAATTTCTTCTTCAAATAGCTGGTCTG
 CGATACACTTACACAGATAATAAAGAGGGCGGAGAAGAAACACCATTAA
 AGTTGTAAAAGCTTATAAATCAAATGGTGAAGAAATCAATCCTGATGCAA
 AATACAAATTAGTTATCAATGACTTTTTATTTCGGTGGTGGTGGTGGCTTT
 GCAAGCTTCAGAAATGCCAAACTTCTAGGAGCCATTAAATCCCGATACAGA
 GGTATTTATGGCCTATATCACTGATTTAGAAAAAGCTGGTAAAAAAGTGA
 GCGTTCCAAATAATAAACCTAAAATCTATGTCACTATGAAGATGGTTAAT
 GAAACTATTACACAAAATGATGGTACACATAGCATTTAATAAGAACTTTA
 TTTAGATCGACAAGGAAATATTGTAGCACAAGAGATTGTATCAGACACTT
 TAAACCAAACAAATCAAATCTACAAAATCAACCCTGTAACCTACAATT
 CACAAAAACAAATTACACCAATTTACAGCTATTAACCCTATGAGAAATTA
 TGGCAAACCATCAAACCTCACTACTGTAAAATCA

SEQ ID NO. 7110

STRAIN 1169NT

CAAGTCGGTGTCCAAGTTATAGGCGTCAATGACTTTTCATGGTGCACCTGA
 CAATACTGGAACAGCAAATATGCCTGATGGAAAAGTTGCTAATGCTGGTA
 CTGCTGCTCAATTAGATGCTTATATGGATGACGCTCAAAAAGATTTCAA
 CAACTAACCCCTAATGGTGAAGCATTAGGGTTCAAGCAGGCGATATGGT
 TGGAGCAAGTCCAGCCAACTCTGGGCTTCTTCAAGATGAACCAACTGTCA
 AAAATTTTAAATGCAATGAATGTTGAGTATGGCACATTGGGTAACCATGAA
 TTTGATGAAGGGTTGGCAGAATATAATCGTATCGTTACTGGTAAAGCCCC
 TGCTCCAGATTCTAATATTAATAATATTACGAAATCATACCCACATGAAG
 CTGCAAAACAAGAAATTTAGTAGTGGCAAATGTTATTGATAAAGTTAACAAA
 CAAATTCCTTACAATTGGAAGCCTTACGCTATTAAAAATATTCTGTAAA
 TAACAAAAGTGTGAACGTTGGCTTTATCGGGATTGTACCAAAGACATCC
 CAAACCTTGTCTTACGTAAAAATTATGAACAATATGAATTTTATAGATGAA
 GCTGAAACAATCGTTAAATACGCCAAAGAATTACAAGCTAAAAATGTCAA
 AGCTATTGTAGTCTCTCGCACATGTACCTGCAACAAGTAAAAATGATATTG
 CTGAAGGTGAAGCAGCAGAAATGATGAAAAAAGTCAATCAACTCTTCCCT
 GAAAAATAGCGTAGATATTGTCTTTGCTGGACACAATCATCAATATACAAA
 TGGTCTTGTGGTAAACTCGTATTGTACAAGCGCTCTCTCAAGGAAAAG
 CCTATGCTGATGTACGTGGTGTCTTAGATACTGATACACAAGATTTTCAAT
 GAGACCCCTTCAAGCTAAAGTAATTGCAGTTGCTCCTGGTAAAAAACAGG
 TAGTGGCGATATTCAAGCCATTGTTGACCAAGCTAATACTATCGTTAAAC
 AAGTAACAGAAGCTAAAATTGGTACTGCCGAGGTAAGTGTATGATTACG
 CGTTCTGTTGATCAAGATAATGTTAGTCCGGTAGGCAGCCTCATCACAGA
 GGCTCAACTAGCAATTGCTCGAAAAAGCTGGCCAGATATCGATTTTGCCA
 TGACAAATAATGGTGGCATTTCGTGCTGACTTACTCATCAAACAGATGGA
 ACAATCACCTGGGGAGCTGCACAAGCAGTTCAACCTTTTGGTAATATCTT
 ACAAGTCTGCGAAATTACTGGTAGAGATCTTTATAAAGCACTCAACGAAC
 AATACGACCAAAAACAAAATTTCTTCTTCAAATAGCTGGTCTGCGATAC
 ACTTACACAGATAATAAAGAGGGCGGGGAAGAAACACCATTAAAGTTGT
 AAAAGCTTATAAATCAAATGGTGAAGAAATCAATCCTGATGCAAAATACA
 AATTAGTTATCAATGACTTTTTATTTCGGTGGTGGTGGTGGCTTTGCAAGC
 TTCAGAAATGCCAAACTTCTAGGAGCCATTAAACCCGATACAGAGGTATT
 TATGGCCTATATCACTGATTTAGAAAAAGCTGGTAAAAAAGTGAAGCTTC
 CAAATAATAAACCTAAAATCTATGTCACTATGAAGATGGTTAATGAACT
 ATTACACAAAATGATGGTACACATAGCATTATTAAGAACTTTATTTAGA
 TCGACAAGGAAATATTGTAGCACAAGAGATTGTATCAGACACTTTAAACC
 AAACAAAATCAAATCTACAAAATCAACCCTGTAACCTACAATTACAAA
 AAACAATTACACCAATTTACAGCTATTAACCCTATGAGAAATTATGGCAA
 ACCATCAAACCTCACTACTGTAAAATCAAA

SEQ ID NO. 7111

STRAIN JM9130013

CGGTGTCCAAGTTATAGGCGTCAATGACTTTTCATGGTGCACCTTGACAATA
 CTGGAACAGCAAATATGCCTGACGGAAGTTACTAATGCTGGCACTGCT
 GCTCAATTAGATGCTTATATGGATGATGCTCAAAAAGATTTCAAACAAAC
 TAACCCTAATGGTGAAGCATTAGAGTTCAAGCTGGTGGTGGTGGTGGGAG
 CAAGTCCAGCTAACTCAGGGCTTCTTCAAGATGAACCAACCGTTAAACA
 TTTAATGCAATGAATGTTGAGTATGGCACATTAGGTAACCATGAATTTGA

Table 71: Comparative Sequences relating to SAG1333

TGAAGGTTTGGCAGAATACAATCGTATCGTTACTGGAAAGGCCCTGCTC
 CAGATTcTAATATAAATAATATTACGAAATCATACCCACACGAAGCTGCA
 AAACAAGAAATTGTAGTGGCAAACGTTATTGATAAAGTTAACAAACAAAT
 CCCTTACAATTGGAAACCTTACACTATTAAAAATATTCTGTAAATAACA
 AAAGTGTGAACGTTGGCTTTATCGGAATCGTTACCAAAGACATCCCAAAC
 CTTGTCTTACGTAAAAATTATGAACAATATGAATTTTATAGATGAAGCTGA
 AACAAATCGTTAAATACGCCAAAGAATTACAAGCTAAAAATGTCAAGGCTA
 TTGTAGTCCTTGCTCATGTACCTGCAACAAGCAAGGATGATATTGCTGAA
 GGTGAAGCAGCAGAAATGATGAAAAAGTCAATCAACTCTTCCCTGAAAA
 TAGCGTAGATATTGTCTTTGCTGGACACAATCATCAATATACAAATGGTC
 TTGTTGGTAAAACTCGTATTGTACAAGCGCTCTCTCAAGGAAAAAGCCTAT
 GCTGATGTACGTGGTGTCTAGATACTGATACACAAGATTTTATTGAAAC
 CCCTTCAGCTAAAGTAATTGCAGTTGCTCCTGGTAAAAAACAGGTAGTG
 CCGATATTCAAGCCATTGTTGACCAAGCTAATACTATCGTTAAACAAGTA
 ACAGAAGCTAAAATTGGTACTGCCGAGGTAAGTGGCATGATTACGCGTTC
 TGTGATCAAGATAATGTTAGTCCGGTAGGCAGCCTCATCACAGAGGCTC
 AACTAGCAATTGCTCGAAAAAGCTGGCCAGATATCGATTTTGCCATGACA
 AATAATGGTGGCATTCTGTGCTGACTTACTCATCAAACCAGATGGAACAAT
 CACCTGGGGAGCTGCACAAGCAGTTCAACCTTTTGGTAATATCTTACAAG
 TCGTCGAAATTACTGGTAGAGATCTTTATAAAGCACTCAACGAACAATAC
 GACCAAAAAACAAAATTTCTTCTTCAAATAGCTGGTCTGCGATACACTTA
 CACAGATAATAAAGAGGGCGGGGAAGAAACACCATTTAAAGTTGTAAAG
 CTTATAAATCAAATGGTGGAGAAATCAATCCTGATGCAAAATACAAATTA
 GTTATCAATGACTTTTTATTTCGGTGGTGGTGGTGGCTTTGCAAGCTTCAG
 AAATGCCAAACTTCTAGGAGCCATTAAATCCCGATACAGAGGTATTTATGG
 CCTATATCACTGATTTAGAAAAAGCTGGTAAAAAGTGGAGCGTTCCAAAT
 AATAAACCTAAAATCTATGTCACTATGAAGATGGTTAATGAAACTATTAC
 ACAAATGATGGTACATATAGCAATTATTGAGAACTTTATTTAGATCGAC
 AAGGAAATATTGTAGCACAAGAGATTGTATCAGACACTTTAAACCAAACA
 AAATCAAATCTACAAAAATCAACCCTGTAACCTACAATTCACAAAAACA
 ATTACACCAATTTACAGCTATTAAACCCTATGAGAAATTATGGCAAACCAT
 CAACTCCACTACTGTAAATCAAAA

PRETTY of: /biotmp/msa237456.2{*} May 14, 2003 03:20 ..

	1				50
msa237456.2{328_1169NT}	-----	-----	-----	-----	-----
msa237456.2{328_2603}	atgaaaaaga	aaattattht	gaaaagtagt	gttcttggtt	tagtcgctgg
msa237456.2{328_18RS21}	-----	-----	-----	-----	-----
msa237456.2{328_H36B}	-----	-----	-----	-----	-----
msa237456.2{328_COH1}	-----	-----	-----	-----	-----
msa237456.2{328_M732}	-----	-----	-----	-----	-----
msa237456.2{328_M781}	-----	-----	-----	-----	-----
msa237456.2{328_JM9130013}	-----	-----	-----	-----	-----
msa237456.2{328_A909}	-----	-----	-----	-----	-----
msa237456.2{328_090}	-----	-----	-----	-----	-----
msa237456.2{328_CJB110}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	51				100
msa237456.2{328_1169NT}	-----	-----	-----	----caagtc	ggtgtccaag
msa237456.2{328_2603}	gacttctatt	atgttctcaa	gcgtgttcgc	gGACcaagtc	ggtgtccaag
msa237456.2{328_18RS21}	-----	-----	-----	~GACcaagtc	ggtgtccaag
msa237456.2{328_H36B}	-----	-----	-----	~Ccaagtc	ggtgtccaag
msa237456.2{328_COH1}	-----	-----	-----	~ACcaagtc	ggtgtccaag
msa237456.2{328_M732}	-----	-----	-----	~ACcaagtc	ggtgtccaag
msa237456.2{328_M781}	-----	-----	-----	----caagtc	ggtgtccaag
msa237456.2{328_JM9130013}	-----	-----	-----	-----c	ggtgtccaag
msa237456.2{328_A909}	-----	-----	-----	-----	-----
msa237456.2{328_090}	-----	-----	-----	----aagtc	ggtgtccaag
msa237456.2{328_CJB110}	-----	-----	-----	~GACcaagtc	ggtgtccaag
Consensus	*****	*****	*****	****-	-----
	101				150
msa237456.2{328_1169NT}	ttatagGCGT	CAATGACTTT	CATGGTGCAC	TTGACAATAC	TGGAACAGCA
msa237456.2{328_2603}	ttatagGCGT	CAATGACTTT	CATGGTGCAC	TTGACAATAC	TGGAACAGCA
msa237456.2{328_18RS21}	ttatagGCGT	CAATGACTTT	CATGGTGCAC	TTGACAATAC	TGGAACAGCA
msa237456.2{328_H36B}	ttatagGCGT	CAATGACTTT	CATGGTGCAC	TTGACAATAC	TGGAACAGCA
msa237456.2{328_COH1}	ttatagGCGT	CAATGACTTT	CATGGTGCAC	TTGACAATAC	TGGAACAGCA
msa237456.2{328_M732}	ttatagGCGT	CAATGACTTT	CATGGTGCAC	TTGACAATAC	TGGAACAGCA
msa237456.2{328_M781}	ttatagGCGT	CAATGACTTT	CATGGTGCAC	TTGACAATAC	TGGAACAGCA
msa237456.2{328_JM9130013}	ttatagGCGT	CAATGACTTT	CATGGTGCAC	TTGACAATAC	TGGAACAGCA
msa237456.2{328_A909}	-----GCGT	CAATGACTTT	CATGGTGCAC	TTGACAATAC	TGGAACAGCA
msa237456.2{328_090}	ttatagGCGT	CAATGACTTT	CATGGTGCAC	TTGACAATAC	TGGAACAGCA
msa237456.2{328_CJB110}	ttatagGCGT	CAATGACTTT	CATGGTGCAC	TTGACAATAC	TGGAACAGCA
Consensus	-----****	*****	*****	*****	*****
	151				200
msa237456.2{328_1169NT}	AATATGCCTG	AtGGAAAAGT	TgcTAATGCT	GGtACTGCTG	CTCAATTAGA
msa237456.2{328_2603}	AATATGCCTG	AtGGAAAAGT	TgcTAATGCT	GGtACTGCTG	CTCAATTAGA
msa237456.2{328_18RS21}	AATATGCCTG	AcGGAAAAGT	TanTAATGCT	GGcACTGCTG	CTCAATTAGA
msa237456.2{328_H36B}	AATATGCCTG	AcGGAAAAGT	TacTAATGCT	GGcACTGCTG	CTCAATTAGA
msa237456.2{328_COH1}	AATATGCCTG	AcGGAAAAGT	TacTAATGCT	GGcACTGCTG	CTCAATTAGA

Table 71: Comparative Sequences relating to SAG1333

msa237456.2{328_M732}	AATATGCCTG	AcGGAAAAGT	TacTAATGCT	GGcACTGCTG	CTCAATTAGA
msa237456.2{328_M781}	AATATGCCTG	AcGGAAAAGT	TacTAATGCT	GGcACTGCTG	CTCAATTAGA
msa237456.2{328_JM9130013}	AATATGCCTG	AcGGAAAAGT	TacTAATGCT	GGcACTGCTG	CTCAATTAGA
msa237456.2{328_A909}	AATATGCCTG	AcGGAAAAGT	TacTAATGCT	GGcACTGCTG	CTCAATTAGA
msa237456.2{328_090}	AATATGCCTG	AcGGAAAAGT	TacTAATGCT	GGcACTGCTG	CTCAATTAGA
msa237456.2{328_CJB110}	AATATGCCTG	AcGGAAAAGT	TacTAATGCT	GGcACTGCTG	CTCAATTAGA
Consensus	*****	*-*****	*-*****	**-*****	*****
msa237456.2{328_1169NT}	TGCTTATATG	GATGAcGCTC	AAAAAGATTT	CAAACAAACT	AACCCTAATG
msa237456.2{328_2603}	TGCTTATATG	GATGAcGCTC	AAAAAGATTT	CAAACAAACT	AACCCTAATG
msa237456.2{328_18RS21}	TGCTTATATG	GATGAcGCTC	AAAAAGATTT	CAAACAAACT	AACCCTAATG
msa237456.2{328_H36B}	TGCTTATATG	GATGAcGCTC	AAAAAGATTT	CAAACAAACT	AACCCTAATG
msa237456.2{328_COH1}	TGCTTATATG	GATGAcGCTC	AAAAAGATTT	CAAACAAACT	AACCCTAATG
msa237456.2{328_M732}	TGCTTATATG	GATGAcGCTC	AAAAAGATTT	CAAACAAACT	AACCCTAATG
msa237456.2{328_M781}	TGCTTATATG	GATGAcGCTC	AAAAAGATTT	CAAACAAACT	AACCCTAATG
msa237456.2{328_JM9130013}	TGCTTATATG	GATGAcGCTC	AAAAAGATTT	CAAACAAACT	AACCCTAATG
msa237456.2{328_A909}	TGCTTATATG	GATGAcGCTC	AAAAAGATTT	CAAACAAACT	AACCCTAATG
msa237456.2{328_090}	TGCTTATATG	GATGAcGCTC	AAAAAGATTT	CAAACAAACT	AACCCTAATG
msa237456.2{328_CJB110}	TGCTTATATG	GATGAcGCTC	AAAAAGATTT	CAAACAAACT	AACCCTAATG
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	GTGAAAGCAT	TAGgGTTCAA	GCaGGcGATA	TGGTTGGAGC	AAGTCCAGCc
msa237456.2{328_2603}	GTGAAAGCAT	TAGgGTTCAA	GCaGGcGATA	TGGTTGGAGC	AAGTCCAGCc
msa237456.2{328_18RS21}	GTGAAAGCAT	TAGaGTTCAA	GcTGGtGATA	TGGTTGGAGC	AAGTCCAGCt
msa237456.2{328_H36B}	GTGAAAGCAT	TAGaGTTCAA	GcTGGtGATA	TGGTTGGAGC	AAGTCCAGCt
msa237456.2{328_COH1}	GTGAAAGCAT	TAGaGTTCAA	GcTGGtGATA	TGGTTGGAGC	AAGTCCAGCt
msa237456.2{328_M732}	GTGAAAGCAT	TAGaGTTCAA	GcTGGtGATA	TGGTTGGAGC	AAGTCCAGCt
msa237456.2{328_M781}	GTGAAAGCAT	TAGaGTTCAA	GcTGGtGATA	TGGTTGGAGC	AAGTCCAGCt
msa237456.2{328_JM9130013}	GTGAAAGCAT	TAGaGTTCAA	GcTGGtGATA	TGGTTGGAGC	AAGTCCAGCt
msa237456.2{328_A909}	GTGAAAGCAT	TAGaGTTCAA	GcTGGtGATA	TGGTTGGAGC	AAGTCCAGCt
msa237456.2{328_090}	GTGAAAGCAT	TAGaGTTCAA	GcTGGtGATA	TGGTTGGAGC	AAGTCCAGCt
msa237456.2{328_CJB110}	GTGAAAGCAT	TAGaGTTCAA	GcTGGtGATA	TGGTTGGAGC	AAGTCCAGCt
Consensus	*****	***-*****	**-***-*****	*****	*****-
msa237456.2{328_1169NT}	AACTCtGGGC	TTCTTCAAGA	TGAACCAACt	GTcAAAAaT	TTAATGCAAT
msa237456.2{328_2603}	AACTCtGGGC	TTCTTCAAGA	TGAACCAACt	GTcAAAAaT	TTAATGCAAT
msa237456.2{328_18RS21}	AACTCaGGGC	TTCTTCAAGA	TGAACCAACc	GTtAAAAcaT	TTAATGCAAT
msa237456.2{328_H36B}	AACTCaGGGC	TTCTTCAAGA	TGAACCAACc	GTtAAAAcaT	TTAATGCAAT
msa237456.2{328_COH1}	AACTCaGGGC	TTCTTCAAGA	TGAACCAACc	GTtAAAAcaT	TTAATGCAAT
msa237456.2{328_M732}	AACTCaGGGC	TTCTTCAAGA	TGAACCAACc	GTtAAAAcaT	TTAATGCAAT
msa237456.2{328_M781}	AACTCaGGGC	TTCTTCAAGA	TGAACCAACc	GTtAAAAcaT	TTAATGCAAT
msa237456.2{328_JM9130013}	AACTCaGGGC	TTCTTCAAGA	TGAACCAACc	GTtAAAAcaT	TTAATGCAAT
msa237456.2{328_A909}	AACTCaGGGC	TTCTTCAAGA	TGAACCAACc	GTtAAAAcaT	TTAATGCAAT
msa237456.2{328_090}	AACTCaGGGC	TTCTTCAAGA	TGAACCAACc	GTtAAAAcaT	TTAATGCAAT
msa237456.2{328_CJB110}	AACTCaGGGC	TTCTTCAAGA	TGAACCAACc	GTtAAAAcaT	TTAATGCAAT
Consensus	*****	*****	*****	**-*****	*****
msa237456.2{328_1169NT}	GAATGTTGAG	TATGGCACAT	TgGGTAACCA	TGAATTTGAT	GAAGGgTTGG
msa237456.2{328_2603}	GAATGTTGAG	TATGGCACAT	TgGGTAACCA	TGAATTTGAT	GAAGGgTTGG
msa237456.2{328_18RS21}	GAATGTTGAG	TATGGCACAT	TaGGTAACCA	TGAATTTGAT	GAAGGtTTGG
msa237456.2{328_H36B}	GAATGTTGAG	TATGGCACAT	TaGGTAACCA	TGAATTTGAT	GAAGGtTTGG
msa237456.2{328_COH1}	GAATGTTGAG	TATGGCACAT	TaGGTAACCA	TGAATTTGAT	GAAGGtTTGG
msa237456.2{328_M732}	GAATGTTGAG	TATGGCACAT	TaGGTAACCA	TGAATTTGAT	GAAGGtTTGG
msa237456.2{328_M781}	GAATGTTGAG	TATGGCACAT	TaGGTAACCA	TGAATTTGAT	GAAGGtTTGG
msa237456.2{328_JM9130013}	GAATGTTGAG	TATGGCACAT	TaGGTAACCA	TGAATTTGAT	GAAGGtTTGG
msa237456.2{328_A909}	GAATGTTGAG	TATGGCACAT	TaGGTAACCA	TGAATTTGAT	GAAGGtTTGG
msa237456.2{328_090}	GAATGTTGAG	TATGGCACAT	TaGGTAACCA	TGAATTTGAT	GAAGGtTTGG
msa237456.2{328_CJB110}	GAATGTTGAG	TATGGCACAT	TaGGTAACCA	TGAATTTGAT	GAAGGtTTGG
Consensus	*****	*****	*-*****	*****	*****
msa237456.2{328_1169NT}	CAGAATAtAA	TCGTATCGTT	ACTGGtAAaG	CCCCTGCTCC	AGATTCTAAT
msa237456.2{328_2603}	CAGAATAtAA	TCGTATCGTT	ACTGGtAAaG	CCCCTGCTCC	AGATTCTAAT
msa237456.2{328_18RS21}	CAGAATAcAA	TCGTATCGTT	ACTGGaAAgG	CCCCTGCTCC	AGATTCTAAT
msa237456.2{328_H36B}	CAGAATAcAA	TCGTATCGTT	ACTGGaAAgG	CCCCTGCTCC	AGATTCTAAT
msa237456.2{328_COH1}	CAGAATAcAA	TCGTATCGTT	ACTGGaAAgG	CCCCTGCTCC	AGATTCTAAT
msa237456.2{328_M732}	CAGAATAcAA	TCGTATCGTT	ACTGGaAAgG	CCCCTGCTCC	AGATTCTAAT
msa237456.2{328_M781}	CAGAATAcAA	TCGTATCGTT	ACTGGaAAgG	CCCCTGCTCC	AGATTCTAAT
msa237456.2{328_JM9130013}	CAGAATAcAA	TCGTATCGTT	ACTGGaAAgG	CCCCTGCTCC	AGATTCTAAT
msa237456.2{328_A909}	CAGAATAcAA	TCGTATCGTT	ACTGGaAAgG	CCCCTGCTCC	AGATTCTAAT
msa237456.2{328_090}	CAGAATAcAA	TCGTATCGTT	ACTGGaAAgG	CCCCTGCTCC	AGATTCTAAT
msa237456.2{328_CJB110}	CAGAATAcAA	TCGTATCGTT	ACTGGaAAgG	CCCCTGCTCC	AGATTCTAAT
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	ATtAATAATA	TTACGAAATC	ATACCCACAt	GAAGCTGCAA	AACAAGAAAT
msa237456.2{328_2603}	ATtAATAATA	TTACGAAATC	ATACCCACAt	GAAGCTGCAA	AACAAGAAAT
msa237456.2{328_18RS21}	ATaAATAATA	TTACGAAATC	ATACCCACAc	GAAGCTGCAA	AACAAGAAAT
msa237456.2{328_H36B}	ATaAATAATA	TTACGAAATC	ATACCCACAc	GAAGCTGCAA	AACAAGAAAT

Table 71: Comparative Sequences relating to SAG1333

msa237456.2{328_COH1}	ATaATAATA	TTACGAAATC	ATACCCACAc	GAAGCTGCAA	AACAAGAAAT
msa237456.2{328_M732}	ATaATAATA	TTACGAAATC	ATACCCACAc	GAAGCTGCAA	AACAAGAAAT
msa237456.2{328_M781}	ATaATAATA	TTACGAAATC	ATACCCACAc	GAAGCTGCAA	AACAAGAAAT
msa237456.2{328_JM9130013}	ATaATAATA	TTACGAAATC	ATACCCACAc	GAAGCTGCAA	AACAAGAAAT
msa237456.2{328_A909}	ATaATAATA	TTACGAAATC	ATACCCACAc	GAAGCTGCAA	AACAAGAAAT
msa237456.2{328_090}	ATaATAATA	TTACGAAATC	ATACCCACAc	GAAGCTGCAA	AACAAGAAAT
msa237456.2{328_CJB110}	ATaATAATA	TTACGAAATC	ATACCCACAc	GAAGCTGCAA	AACAAGAAAT
Consensus	***-*****	*****-*****	*****-*****	*****-*****	*****-*****
501					
msa237456.2{328_1169NT}	TGTAGTGGCA	AATGTTATTG	ATAAAGTTAA	CAAACAAATt	CCTTACAATT
msa237456.2{328_2603}	TGTAGTGGCA	AATGTTATTG	ATAAAGTTAA	CAAACAAATt	CCTTACAATT
msa237456.2{328_18RS21}	TGTAGTGGCA	AATGTTATTG	ATAAAGTTAA	CAAACAAATc	CCTTACAATT
msa237456.2{328_H36B}	TGTAGTGGCA	AATGTTATTG	ATAAAGTTAA	CAAACAAATc	CCTTACAATT
msa237456.2{328_COH1}	TGTAGTGGCA	AATGTTATTG	ATAAAGTTAA	CAAACAAATc	CCTTACAATT
msa237456.2{328_M732}	TGTAGTGGCA	AATGTTATTG	ATAAAGTTAA	CAAACAAATc	CCTTACAATT
msa237456.2{328_M781}	TGTAGTGGCA	AATGTTATTG	ATAAAGTTAA	CAAACAAATc	CCTTACAATT
msa237456.2{328_JM9130013}	TGTAGTGGCA	AATGTTATTG	ATAAAGTTAA	CAAACAAATc	CCTTACAATT
msa237456.2{328_A909}	TGTAGTGGCA	AATGTTATTG	ATAAAGTTAA	CAAACAAATc	CCTTACAATT
msa237456.2{328_090}	TGTAGTGGCA	AATGTTATTG	ATAAAGTTAA	CAAACAAATc	CCTTACAATT
msa237456.2{328_CJB110}	TGTAGTGGCA	AATGTTATTG	ATAAAGTTAA	CAAACAAATc	CCTTACAATT
Consensus	*****	***-*****	*****	*****-*****	*****
551					
msa237456.2{328_1169NT}	GGAAgCCTTA	CgCTATTAAA	AATATTCCCTG	TAAATAACAA	AAGTGTGAAC
msa237456.2{328_2603}	GGAAgCCTTA	CgCTATTAAA	AATATTCCCTG	TAAATAACAA	AAGTGTGAAC
msa237456.2{328_18RS21}	GGAAaCCTTA	CaCTATTAAA	AATATTCCCTG	TAAATAACAA	AAGTGTGAAC
msa237456.2{328_H36B}	GGAAaCCTTA	CaCTATTAAA	AATATTCCCTG	TAAATAACAA	AAGTGTGAAC
msa237456.2{328_COH1}	GGAAaCCTTA	CaCTATTAAA	AATATTCCCTG	TAAATAACAA	AAGTGTGAAC
msa237456.2{328_M732}	GGAAaCCTTA	CaCTATTAAA	AATATTCCCTG	TAAATAACAA	AAGTGTGAAC
msa237456.2{328_M781}	GGAAaCCTTA	CaCTATTAAA	AATATTCCCTG	TAAATAACAA	AAGTGTGAAC
msa237456.2{328_JM9130013}	GGAAaCCTTA	CaCTATTAAA	AATATTCCCTG	TAAATAACAA	AAGTGTGAAC
msa237456.2{328_A909}	GGAAaCCTTA	CaCTATTAAA	AATATTCCCTG	TAAATAACAA	AAGTGTGAAC
msa237456.2{328_090}	GGAAaCCTTA	CgCTATTAAA	AATATTCCCTG	TAAATAACAA	AAGTGTGAAC
msa237456.2{328_CJB110}	GGAAaCCTTA	CgCTATTAAA	AATATTCCCTG	TAAATAACAA	AAGTGTGAAC
Consensus	****-*****	*-*****	*****	*****	*****
601					
msa237456.2{328_1169NT}	GTTGGCTTTA	TCGGgATtGT	cACCAAAGAC	ATCCCAAACC	TTGTCTTACG
msa237456.2{328_2603}	GTTGGCTTTA	TCGGgATtGT	cACCAAAGAC	ATCCCAAACC	TTGTCTTACG
msa237456.2{328_18RS21}	GTTGGCTTTA	TCGGaATcGT	tACCAAAGAC	ATCCCAAACC	TTGTCTTACG
msa237456.2{328_H36B}	GTTGGCTTTA	TCGGaATcGT	tACCAAAGAC	ATCCCAAACC	TTGTCTTACG
msa237456.2{328_COH1}	GTTGGCTTTA	TCGGaATcGT	tACCAAAGAC	ATCCCAAACC	TTGTCTTACG
msa237456.2{328_M732}	GTTGGCTTTA	TCGGaATcGT	tACCAAAGAC	ATCCCAAACC	TTGTCTTACG
msa237456.2{328_M781}	GTTGGCTTTA	TCGGaATcGT	tACCAAAGAC	ATCCCAAACC	TTGTCTTACG
msa237456.2{328_JM9130013}	GTTGGCTTTA	TCGGaATcGT	tACCAAAGAC	ATCCCAAACC	TTGTCTTACG
msa237456.2{328_A909}	GTTGGCTTTA	TCGGaATcGT	tACCAAAGAC	ATCCCAAACC	TTGTCTTACG
msa237456.2{328_090}	GTTGGCTTTA	TCGGaATcGT	tACCAAAGAC	ATCCCAAACC	TTGTCTTACG
msa237456.2{328_CJB110}	GTTGGCTTTA	TCGGaATcGT	tACCAAAGAC	ATCCCAAACC	TTGTCTTACG
Consensus	*****	*****-***	-*****	*****	*****
651					
msa237456.2{328_1169NT}	TAAAAATTAT	GAACAATATG	AATTTTtTAGA	TGAAGCTGAA	ACAATCGTTA
msa237456.2{328_2603}	TAAAAATTAT	GAACAATATG	AATTTTtTAGA	TGAAGCTGAA	ACAATCGTTA
msa237456.2{328_18RS21}	TAAAAATTAT	GAACAATATG	AATTTTtTAGA	TGAAGCTGAA	ACAATCGTTA
msa237456.2{328_H36B}	TAAAAATTAT	GAACAATATG	AATTTTtTAGA	TGAAGCTGAA	ACAATCGTTA
msa237456.2{328_COH1}	TAAAAATTAT	GAACAATATG	AATTTTtTAGA	TGAAGCTGAA	ACAATCGTTA
msa237456.2{328_M732}	TAAAAATTAT	GAACAATATG	AATTTTtTAGA	TGAAGCTGAA	ACAATCGTTA
msa237456.2{328_M781}	TAAAAATTAT	GAACAATATG	AATTTTtTAGA	TGAAGCTGAA	ACAATCGTTA
msa237456.2{328_JM9130013}	TAAAAATTAT	GAACAATATG	AATTTTtTAGA	TGAAGCTGAA	ACAATCGTTA
msa237456.2{328_A909}	TAAAAATTAT	GAACAATATG	AATTTTtTAGA	TGAAGCTGAA	ACAATCGTTA
msa237456.2{328_090}	TAAAAATTAT	GAACAATATG	AATTTTtTAGA	TGAAGCTGAA	ACAATCGTTA
msa237456.2{328_CJB110}	TAAAAATTAT	GAACAATATG	AATTTTtTAGA	TGAAGCTGAA	ACAATCGTTA
Consensus	*****	*****	*****	*****	*****
701					
msa237456.2{328_1169NT}	AATACGCCAA	AGAATTACAA	GCTAAAAATG	TCAAaGCTAT	TGTAGTtCTc
msa237456.2{328_2603}	AATACGCCAA	AGAATTACAA	GCTAAAAATG	TCAAaGCTAT	TGTAGTtCTc
msa237456.2{328_18RS21}	AATACGCCAA	AGAATTACAA	GCTAAAAATG	TCAAaGCTAT	TGTAGTcCTt
msa237456.2{328_H36B}	AATACGCCAA	AGAATTACAA	GCTAAAAATG	TCAAaGCTAT	TGTAGTcCTt
msa237456.2{328_COH1}	AATACGCCAA	AGAATTACAA	GCTAAAAATG	TCAAaGCTAT	TGTAGTcCTt
msa237456.2{328_M732}	AATACGCCAA	AGAATTACAA	GCTAAAAATG	TCAAaGCTAT	TGTAGTcCTt
msa237456.2{328_M781}	AATACGCCAA	AGAATTACAA	GCTAAAAATG	TCAAaGCTAT	TGTAGTcCTt
msa237456.2{328_JM9130013}	AATACGCCAA	AGAATTACAA	GCTAAAAATG	TCAAaGCTAT	TGTAGTcCTt
msa237456.2{328_A909}	AATACGCCAA	AGAATTACAA	GCTAAAAATG	TCAAaGCTAT	TGTAGTcCTt
msa237456.2{328_090}	AATACGCCAA	AGAATTACAA	GCTAAAAATG	TCAAaGCTAT	TGTAGTcCTt
msa237456.2{328_CJB110}	AATACGCCAA	AGAATTACAA	GCTAAAAATG	TCAAaGCTAT	TGTAGTcCTt
Consensus	*****	*****	*****	*****-*****	*****-***
751					
msa237456.2{328_1169NT}	GCaCATGTAC	CTGCAACAAG	tAAaaATGAT	ATTGCTGAAG	GTGAAGCAGC
msa237456.2{328_2603}	GCaCATGTAC	CTGCAACAAG	tAAaaATGAT	ATTGCTGAAG	GTGAAGCAGC
msa237456.2{328_18RS21}	GCTCATGTAC	CTGCAACAAG	cAAggATGAT	ATTGCTGAAG	GTGAAGCAGC

Table 71: Comparative Sequences relating to SAG1333

msa237456.2{328_H36B}	GctCATGTAC	CTGCAACAAG	cAaggATGAT	ATTGCTGAAG	GTGAAGCAGC
msa237456.2{328_COH1}	GctCATGTAC	CTGCAACAAG	cAaggATGAT	ATTGCTGAAG	GTGAAGCAGC
msa237456.2{328_M732}	GctCATGTAC	CTGCAACAAG	cAaggATGAT	ATTGCTGAAG	GTGAAGCAGC
msa237456.2{328_M781}	GctCATGTAC	CTGCAACAAG	cAaggATGAT	ATTGCTGAAG	GTGAAGCAGC
msa237456.2{328_JM9130013}	GctCATGTAC	CTGCAACAAG	cAaggATGAT	ATTGCTGAAG	GTGAAGCAGC
msa237456.2{328_A909}	GctCATGTAC	CTGCAACAAG	cAaggATGAT	ATTGCTGAAG	GTGAAGCAGC
msa237456.2{328_090}	GctCATGTAC	CTGCAACAAG	cAaggATGAT	ATTGCTGAAG	GTGAAGCAGC
msa237456.2{328_CJB110}	GctCATGTAC	CTGCAACAAG	cAaggATGAT	ATTGCTGAAG	GTGAAGCAGC
Consensus	***-*****	*****	-***-*****	*****	*****
801					
msa237456.2{328_1169NT}	AGAAATGATG	AAAAAAGTCA	ATCAACTCTT	CCCTGAAAAT	AGCGTAGATA
msa237456.2{328_2603}	AGAAATGATG	AAAAAAGTCA	ATCAACTCTT	CCCTGAAAAT	AGCGTAGATA
msa237456.2{328_18RS21}	AGAAATGATG	AAAAAAGTCA	ATCAACTCTT	CCCTGAAAAT	AGCGTAGATA
msa237456.2{328_H36B}	AGAAATGATG	AAAAAAGTCA	ATCAACTCTT	CCCTGAAAAT	AGCGTAGATA
msa237456.2{328_COH1}	AGAAATGATG	AAAAAAGTCA	ATCAACTCTT	CCCTGAAAAT	AGCGTAGATA
msa237456.2{328_M732}	AGAAATGATG	AAAAAAGTCA	ATCAACTCTT	CCCTGAAAAT	AGCGTAGATA
msa237456.2{328_M781}	AGAAATGATG	AAAAAAGTCA	ATCAACTCTT	CCCTGAAAAT	AGCGTAGATA
msa237456.2{328_JM9130013}	AGAAATGATG	AAAAAAGTCA	ATCAACTCTT	CCCTGAAAAT	AGCGTAGATA
msa237456.2{328_A909}	AGAAATGATG	AAAAAAGTCA	ATCAACTCTT	CCCTGAAAAT	AGCGTAGATA
msa237456.2{328_090}	AGAAATGATG	AAAAAAGTCA	ATCAACTCTT	CCCTGAAAAT	AGCGTAGATA
msa237456.2{328_CJB110}	AGAAATGATG	AAAAAAGTCA	ATCAACTCTT	CCCTGAAAAT	AGCGTAGATA
Consensus	*****	*****	*****	*****	*****
851					
msa237456.2{328_1169NT}	TTGTCTTTGC	TGGACACAAT	CATCAATATA	CAAATGGTCT	TGTTGGTAAA
msa237456.2{328_2603}	TTGTCTTTGC	TGGACACAAT	CATCAATATA	CAAATGGTCT	TGTTGGTAAA
msa237456.2{328_18RS21}	TTGTCTTTGC	TGGACACAAT	CATCAATATA	CAAATGGTCT	TGTTGGTAAA
msa237456.2{328_H36B}	TTGTCTTTGC	TGGACACAAT	CATCAATATA	CAAATGGTCT	TGTTGGTAAA
msa237456.2{328_COH1}	TTGTCTTTGC	TGGACACAAT	CATCAATATA	CAAATGGTCT	TGTTGGTAAA
msa237456.2{328_M732}	TTGTCTTTGC	TGGACACAAT	CATCAATATA	CAAATGGTCT	TGTTGGTAAA
msa237456.2{328_M781}	TTGTCTTTGC	TGGACACAAT	CATCAATATA	CAAATGGTCT	TGTTGGTAAA
msa237456.2{328_JM9130013}	TTGTCTTTGC	TGGACACAAT	CATCAATATA	CAAATGGTCT	TGTTGGTAAA
msa237456.2{328_A909}	TTGTCTTTGC	TGGACACAAT	CATCAATATA	CAAATGGTCT	TGTTGGTAAA
msa237456.2{328_090}	TTGTCTTTGC	TGGACACAAT	CATCAATATA	CAAATGGTCT	TGTTGGTAAA
msa237456.2{328_CJB110}	TTGTCTTTGC	TGGACACAAT	CATCAATATA	CAAATGGTCT	TGTTGGTAAA
Consensus	*****	*****	*****	*****	*****
901					
msa237456.2{328_1169NT}	ACTCGtATTG	TACAAGCGCT	CTCTCAAGGA	AAAGCCTATG	CTGAtGTACG
msa237456.2{328_2603}	ACTCGtATTG	TACAAGCGCT	CTCTCAAGGA	AAAGCCTATG	CTGAtGTACG
msa237456.2{328_18RS21}	ACTCGtATTG	TACAAGCGCT	CTCTCAAGGA	AAAGCCTATG	CTGAtGTACG
msa237456.2{328_H36B}	ACTCGtATTG	TACAAGCGCT	CTCTCAAGGA	AAAGCCTATG	CTGAtGTACG
msa237456.2{328_COH1}	ACTCGtATTG	TACAAGCGCT	CTCTCAAGGA	AAAGCCTATG	CTGAtGTACG
msa237456.2{328_M732}	ACTCGtATTG	TACAAGCGCT	CTCTCAAGGA	AAAGCCTATG	CTGAtGTACG
msa237456.2{328_M781}	ACTCGtATTG	TACAAGCGCT	CTCTCAAGGA	AAAGCCTATG	CTGAtGTACG
msa237456.2{328_JM9130013}	ACTCGtATTG	TACAAGCGCT	CTCTCAAGGA	AAAGCCTATG	CTGAtGTACG
msa237456.2{328_A909}	ACTCGtATTG	TACAAGCGCT	CTCTCAAGGA	AAAGCCTATG	CTGAtGTACG
msa237456.2{328_090}	ACTCGcATTG	TACAAGCGCT	CTCTCAAGGA	AAAGCCTATG	CTGAcGTACG
msa237456.2{328_CJB110}	ACTCGcATTG	TACAAGCGCT	CTCTCAAGGA	AAAGCCTATG	CTGAcGTACG
Consensus	*****-****	*****	*****	*****	*****-*****
951					
msa237456.2{328_1169NT}	TGGTGTCTTA	GATACTGATA	CACAAGATTT	CATTGAaACC	CCTTCAGCTA
msa237456.2{328_2603}	TGGTGTCTTA	GATACTGATA	CACAAGATTT	CATTGAaACC	CCTTCAGCTA
msa237456.2{328_18RS21}	TGGTGTCTTA	GATACTGATA	CACAAGATTT	CATTGAaACC	CCTTCAGCTA
msa237456.2{328_H36B}	TGGTGTCTTA	GATACTGATA	CACAAGATTT	CATTGAaACC	CCTTCAGCTA
msa237456.2{328_COH1}	TGGTGTCTTA	GATACTGATA	CACAAGATTT	CATTGAaACC	CCTTCAGCTA
msa237456.2{328_M732}	TGGTGTCTTA	GATACTGATA	CACAAGATTT	CATTGAaACC	CCTTCAGCTA
msa237456.2{328_M781}	TGGTGTCTTA	GATACTGATA	CACAAGATTT	CATTGAaACC	CCTTCAGCTA
msa237456.2{328_JM9130013}	TGGTGTCTTA	GATACTGATA	CACAAGATTT	CATTGAaACC	CCTTCAGCTA
msa237456.2{328_A909}	TGGTGTCTTA	GATACTGATA	CACAAGATTT	CATTGAaACC	CCTTCAGCTA
msa237456.2{328_090}	TGGTGTCTTA	GATACTGATA	CACAAGATTT	CATTGAaACC	CCTTCAGCTA
msa237456.2{328_CJB110}	TGGTGTCTTA	GATACTGATA	CACAAGATTT	CATTGAaACC	CCTTCAGCTA
Consensus	*****-**	*****	*****	*****-***	*****
1001					
msa237456.2{328_1169NT}	AAGTAaTTGC	AGTTGCTCCT	GGTAAAAAAA	CAGGTAGTGC	CGATATTCAA
msa237456.2{328_2603}	AAGTAaTTGC	AGTTGCTCCT	GGTAAAAAAA	CAGGTAGTGC	CGATATTCAA
msa237456.2{328_18RS21}	AAGTAaTTGC	AGTTGCTCCT	GGTAAAAAAA	CAGGTAGTGC	CGATATTCAA
msa237456.2{328_H36B}	AAGTAaTTGC	AGTTGCTCCT	GGTAAAAAAA	CAGGTAGTGC	CGATATTCAA
msa237456.2{328_COH1}	AAGTAaTTGC	AGTTGCTCCT	GGTAAAAAAA	CAGGTAGTGC	CGATATTCAA
msa237456.2{328_M732}	AAGTAaTTGC	AGTTGCTCCT	GGTAAAAAAA	CAGGTAGTGC	CGATATTCAA
msa237456.2{328_M781}	AAGTAaTTGC	AGTTGCTCCT	GGTAAAAAAA	CAGGTAGTGC	CGATATTCAA
msa237456.2{328_JM9130013}	AAGTAaTTGC	AGTTGCTCCT	GGTAAAAAAA	CAGGTAGTGC	CGATATTCAA
msa237456.2{328_A909}	AAGTAaTTGC	AGTTGCTCCT	GGTAAAAAAA	CAGGTAGTGC	CGATATTCAA
msa237456.2{328_090}	AAGTAaTTGC	AGTTGCTCCT	GGTAAAAAAA	CAGGTAGTGC	CGATATTCAA
msa237456.2{328_CJB110}	AAGTAaTTGC	AGTTGCTCCT	GGTAAAAAAA	CAGGTAGTGC	CGATATTCAA
Consensus	*****-****	*****	*****	*****	*****
1051					
msa237456.2{328_1169NT}	GCCATTGTTG	ACCAAGCTAA	TACTATCGTT	AAACAAGTAA	CAGAAGCTAA
msa237456.2{328_2603}	GCCATTGTTG	ACCAAGCTAA	TACTATCGTT	AAACAAGTAA	CAGAAGCTAA

Table 71: Comparative Sequences relating to SAG1333

msa237456.2{328_18RS21}	GCCATTGTTG	ACCAAGCTAA	TACTATCGTT	AAACAAGTAA	CAGAAGCTAA
msa237456.2{328_H36B}	GCCATTGTTG	ACCAAGCTAA	TACTATCGTT	AAACAAGTAA	CAGAAGCTAA
msa237456.2{328_COH1}	GCCATTGTTG	ACCAAGCTAA	TACTATCGTT	AAACAAGTAA	CAGAAGCTAA
msa237456.2{328_M732}	GCCATTGTTG	ACCAAGCTAA	TACTATCGTT	AAACAAGTAA	CAGAAGCTAA
msa237456.2{328_M781}	GCCATTGTTG	ACCAAGCTAA	TACTATCGTT	AAACAAGTAA	CAGAAGCTAA
msa237456.2{328_JM9130013}	GCCATTGTTG	ACCAAGCTAA	TACTATCGTT	AAACAAGTAA	CAGAAGCTAA
msa237456.2{328_A909}	GCCATTGTTG	ACCAAGCTAA	TACTATCGTT	AAACAAGTAA	CAGAAGCTAA
msa237456.2{328_090}	GCCATTGTTG	ACCAAGCTAA	TACTATCGTT	AAACAAGTAA	CAGAAGCTAA
msa237456.2{328_CJB110}	GCCATTGTTG	ACCAAGCTAA	TACTATCGTT	AAACAAGTAA	CAGAAGCTAA
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	AATTGGTACT	GCCGAGGTAA	GTGtCATGAT	TACGCGTTCT	GTTGATCAAG
msa237456.2{328_2603}	AATTGGTACT	GCCGAGGTAA	GTGtCATGAT	TACGCGTTCT	GTTGATCAAG
msa237456.2{328_18RS21}	AATTGGTACT	GCCGAGGTAA	GTGgCATGAT	TACGCGTTCT	GTTGATCAAG
msa237456.2{328_H36B}	AATTGGTACT	GCCGAGGTAA	GTGgCATGAT	TACGCGTTCT	GTTGATCAAG
msa237456.2{328_COH1}	AATTGGTACT	GCCGAGGTAA	GTGgCATGAT	TACGCGTTCT	GTTGATCAAG
msa237456.2{328_M732}	AATTGGTACT	GCCGAGGTAA	GTGgCATGAT	TACGCGTTCT	GTTGATCAAG
msa237456.2{328_M781}	AATTGGTACT	GCCGAGGTAA	GTGgCATGAT	TACGCGTTCT	GTTGATCAAG
msa237456.2{328_JM9130013}	AATTGGTACT	GCCGAGGTAA	GTGgCATGAT	TACGCGTTCT	GTTGATCAAG
msa237456.2{328_A909}	AATTGGTACT	GCCGAGGTAA	GTGgCATGAT	TACGCGTTCT	GTTGATCAAG
msa237456.2{328_090}	AATTGGTACT	GCCGAGGTAA	GTGgCATGAT	TACGCGTTCT	GTTGATCAAG
msa237456.2{328_CJB110}	AATTGGTACT	GCCGAGGTAA	GTGgCATGAT	TACGCGTTCT	GTTGATCAAG
Consensus	*****	*****	***-*****	*****	*****
msa237456.2{328_1169NT}	ATAATGTTAG	TCCgGTAGGC	AGCCTCATCA	CAGAGGCTCA	ACTAGCAATT
msa237456.2{328_2603}	ATAATGTTAG	TCCgGTAGGC	AGCCTCATCA	CAGAGGCTCA	ACTAGCAATT
msa237456.2{328_18RS21}	ATAATGTTAG	TCCgGTAGGC	AGCCTCATCA	CAGAGGCTCA	ACTAGCAATT
msa237456.2{328_H36B}	ATAATGTTAG	TCCgGTAGGC	AGCCTCATCA	CAGAGGCTCA	ACTAGCAATT
msa237456.2{328_COH1}	ATAATGTTAG	TCCgGTAGGC	AGCCTCATCA	CAGAGGCTCA	ACTAGCAATT
msa237456.2{328_M732}	ATAATGTTAG	TCCgGTAGGC	AGCCTCATCA	CAGAGGCTCA	ACTAGCAATT
msa237456.2{328_M781}	ATAATGTTAG	TCCgGTAGGC	AGCCTCATCA	CAGAGGCTCA	ACTAGCAATT
msa237456.2{328_JM9130013}	ATAATGTTAG	TCCgGTAGGC	AGCCTCATCA	CAGAGGCTCA	ACTAGCAATT
msa237456.2{328_A909}	ATAATGTTAG	TCCgGTAGGC	AGCCTCATCA	CAGAGGCTCA	ACTAGCAATT
msa237456.2{328_090}	ATAATGTTAG	TCCgGTAGGC	AGCCTCATCA	CAGAGGCTCA	ACTAGCAATT
msa237456.2{328_CJB110}	ATAATGTTAG	TCCgGTAGGC	AGCCTCATCA	CAGAGGCTCA	ACTAGCAATT
Consensus	*****	***-*****	*****	*****	*****
msa237456.2{328_1169NT}	GCTCGAAAAA	GCTGGCCAGA	TATCGATTTT	GCCATGACAA	ATAATGGTGG
msa237456.2{328_2603}	GCTCGAAAAA	GCTGGCCAGA	TATCGATTTT	GCCATGACAA	ATAATGGTGG
msa237456.2{328_18RS21}	GCTCGAAAAA	GCTGGCCAGA	TATCGATTTT	GCCATGACAA	ATAATGGTGG
msa237456.2{328_H36B}	GCTCGAAAAA	GCTGGCCAGA	TATCGATTTT	GCCATGACAA	ATAATGGTGG
msa237456.2{328_COH1}	GCTCGAAAAA	GCTGGCCAGA	TATCGATTTT	GCCATGACAA	ATAATGGTGG
msa237456.2{328_M732}	GCTCGAAAAA	GCTGGCCAGA	TATCGATTTT	GCCATGACAA	ATAATGGTGG
msa237456.2{328_M781}	GCTCGAAAAA	GCTGGCCAGA	TATCGATTTT	GCCATGACAA	ATAATGGTGG
msa237456.2{328_JM9130013}	GCTCGAAAAA	GCTGGCCAGA	TATCGATTTT	GCCATGACAA	ATAATGGTGG
msa237456.2{328_A909}	GCTCGAAAAA	GCTGGCCAGA	TATCGATTTT	GCCATGACAA	ATAATGGTGG
msa237456.2{328_090}	GCTCGAAAAA	GCTGGCCAGA	TATCGATTTT	GCCATGACAA	ATAATGGTGG
msa237456.2{328_CJB110}	GCTCGAAAAA	GCTGGCCAGA	TATCGATTTT	GCCATGACAA	ATAATGGTGG
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	CATTTCGTGCT	GACTTACTCA	TCAAACCAGA	TGGAACAATC	ACCTGGGGAG
msa237456.2{328_2603}	CATTTCGTGCT	GACTTACTCA	TCAAACCAGA	TGGAACAATC	ACCTGGGGAG
msa237456.2{328_18RS21}	CATTTCGTGCT	GACTTACTCA	TCAAACCAGA	TGGAACAATC	ACCTGGGGAG
msa237456.2{328_H36B}	CATTTCGTGCT	GACTTACTCA	TCAAACCAGA	TGGAACAATC	ACCTGGGGAG
msa237456.2{328_COH1}	CATTTCGTGCT	GACTTACTCA	TCAAACCAGA	TGGAACAATC	ACCTGGGGAG
msa237456.2{328_M732}	CATTTCGTGCT	GACTTACTCA	TCAAACCAGA	TGGAACAATC	ACCTGGGGAG
msa237456.2{328_M781}	CATTTCGTGCT	GACTTACTCA	TCAAACCAGA	TGGAACAATC	ACCTGGGGAG
msa237456.2{328_JM9130013}	CATTTCGTGCT	GACTTACTCA	TCAAACCAGA	TGGAACAATC	ACCTGGGGAG
msa237456.2{328_A909}	CATTTCGTGCT	GACTTACTCA	TCAAACCAGA	TGGAACAATC	ACCTGGGGAG
msa237456.2{328_090}	CATTTCGTGCT	GACTTACTCA	TCAAACCAGA	TGGAACAATC	ACCTGGGGAG
msa237456.2{328_CJB110}	CATTTCGTGCT	GACTTACTCA	TCAAACCAGA	TGGAACAATC	ACCTGGGGAG
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	CTGCACAAGC	AGTTCAACCT	TTTGGTAATA	TCTTACAAGT	CGTCGAAATT
msa237456.2{328_2603}	CTGCACAAGC	AGTTCAACCT	TTTGGTAATA	TCTTACAAGT	CGTCGAAATT
msa237456.2{328_18RS21}	CTGCACAAGC	AGTTCAACCT	TTTGGTAATA	TCTTACAAGT	CGTCGAAATT
msa237456.2{328_H36B}	CTGCACAAGC	AGTTCAACCT	TTTGGTAATA	TCTTACAAGT	CGTCGAAATT
msa237456.2{328_COH1}	CTGCACAAGC	AGTTCAACCT	TTTGGTAATA	TCTTACAAGT	CGTCGAAATT
msa237456.2{328_M732}	CTGCACAAGC	AGTTCAACCT	TTTGGTAATA	TCTTACAAGT	CGTCGAAATT
msa237456.2{328_M781}	CTGCACAAGC	AGTTCAACCT	TTTGGTAATA	TCTTACAAGT	CGTCGAAATT
msa237456.2{328_JM9130013}	CTGCACAAGC	AGTTCAACCT	TTTGGTAATA	TCTTACAAGT	CGTCGAAATT
msa237456.2{328_A909}	CTGCACAAGC	AGTTCAACCT	TTTGGTAATA	TCTTACAAGT	CGTCGAAATT
msa237456.2{328_090}	CTGCACAAGC	AGTTCAACCT	TTTGGTAATA	TCTTACAAGT	CGTCGAAATT
msa237456.2{328_CJB110}	CTGCACAAGC	AGTTCAACCT	TTTGGTAATA	TCTTACAAGT	CGTCGAAATT
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	ACTGGTAGAG	ATCTTTTATAA	AGCACTCAAC	GAACAATACG	ACCAAAAACA

Table 71: Comparative Sequences relating to SAG1333

msa237456.2{328_2603}	ACTGGTAGAG	ATCTTTATAA	AGCACTCAAC	GAACAATACG	ACCAAAAACA
msa237456.2{328_18RS21}	ACTGGTAGAG	ATCTTTATAA	AGCACTCAAC	GAACAATACG	ACCAAAAACA
msa237456.2{328_H36B}	ACTGGTAGAG	ATCTTTATAA	AGCACTCAAC	GAACAATACG	ACCAAAAACA
msa237456.2{328_COH1}	ACTGGTAGAG	ATCTTTATAA	AGCACTCAAC	GAACAATACG	ACCAAAAACA
msa237456.2{328_M732}	ACTGGTAGAG	ATCTTTATAA	AGCACTCAAC	GAACAATACG	ACCAAAAACA
msa237456.2{328_M781}	ACTGGTAGAG	ATCTTTATAA	AGCACTCAAC	GAACAATACG	ACCAAAAACA
msa237456.2{328_JM9130013}	ACTGGTAGAG	ATCTTTATAA	AGCACTCAAC	GAACAATACG	ACCAAAAACA
msa237456.2{328_A909}	ACTGGTAGAG	ATCTTTATAA	AGCACTCAAC	GAACAATACG	ACCAAAAACA
msa237456.2{328_090}	ACTGGTAGAG	ATCTTTATAA	AGCACTCAAC	GAACAATACG	ACCAAAAACA
msa237456.2{328_CJB110}	ACTGGTAGAG	ATCTTTATAA	AGCACTCAAC	GAACAATACG	ACCAAAAACA
Consensus	*****	*****	*****	*****	*****
1401					
msa237456.2{328_1169NT}	AAATTTCTTC	CTTCAAATAG	CTGGTCTGCG	ATACACTTAC	ACAGATAATA
msa237456.2{328_2603}	AAATTTCTTC	CTTCAAATAG	CTGGTCTGCG	ATACACTTAC	ACAGATAATA
msa237456.2{328_18RS21}	AAATTTCTTC	CTTCAAATAG	CTGGTCTGCG	ATACACTTAC	ACAGATAATA
msa237456.2{328_H36B}	AAATTTCTTC	CTTCAAATAG	CTGGTCTGCG	ATACACTTAC	ACAGATAATA
msa237456.2{328_COH1}	AAATTTCTTC	CTTCAAATAG	CTGGTCTGCG	ATACACTTAC	ACAGATAATA
msa237456.2{328_M732}	AAATTTCTTC	CTTCAAATAG	CTGGTCTGCG	ATACACTTAC	ACAGATAATA
msa237456.2{328_M781}	AAATTTCTTC	CTTCAAATAG	CTGGTCTGCG	ATACACTTAC	ACAGATAATA
msa237456.2{328_JM9130013}	AAATTTCTTC	CTTCAAATAG	CTGGTCTGCG	ATACACTTAC	ACAGATAATA
msa237456.2{328_A909}	AAATTTCTTC	CTTCAAATAG	CTGGTCTGCG	ATACACTTAC	ACAGATAATA
msa237456.2{328_090}	AAATTTCTTC	CTTCAAATAG	CTGGTCTGCG	ATACACTTAC	ACAGATAATA
msa237456.2{328_CJB110}	AAATTTCTTC	CTTCAAATAG	CTGGTCTGCG	ATACACTTAC	ACAGATAATA
Consensus	*****	*****	*****	*****	*****
1451					
msa237456.2{328_1169NT}	AAGAGGGCGG	gGAAGAAACA	CCATTTAAAG	TTGTAAAAGC	TTATAAATCA
msa237456.2{328_2603}	AAGAGGGCGG	gGAAGAAACA	CCATTTAAAG	TTGTAAAAGC	TTATAAATCA
msa237456.2{328_18RS21}	AAGAGGGCGG	gGAAGAAACA	CCATTTAAAG	TTGTAAAAGC	TTATAAATCA
msa237456.2{328_H36B}	AAGAGGGCGG	gGAAGAAACA	CCATTTAAAG	TTGTAAAAGC	TTATAAATCA
msa237456.2{328_COH1}	AAGAGGGCGG	gGAAGAAACA	CCATTTAAAG	TTGTAAAAGC	TTATAAATCA
msa237456.2{328_M732}	AAGAGGGCGG	gGAAGAAACA	CCATTTAAAG	TTGTAAAAGC	TTATAAATCA
msa237456.2{328_M781}	AAGAGGGCGG	gGAAGAAACA	CCATTTAAAG	TTGTAAAAGC	TTATAAATCA
msa237456.2{328_JM9130013}	AAGAGGGCGG	gGAAGAAACA	CCATTTAAAG	TTGTAAAAGC	TTATAAATCA
msa237456.2{328_A909}	AAGAGGGCGG	gGAAGAAACA	CCATTTAAAG	TTGTAAAAGC	TTATAAATCA
msa237456.2{328_090}	AAGAGGGCGG	gGAAGAAACA	CCATTTAAAG	TTGTAAAAGC	TTATAAATCA
msa237456.2{328_CJB110}	AAGAGGGCGG	gGAAGAAACA	CCATTTAAAG	TTGTAAAAGC	TTATAAATCA
Consensus	*****	*****	*****	*****	*****
1501					
msa237456.2{328_1169NT}	AATGGTGAGG	AAATCAATCC	TGATGCAAAA	TACAAATTAG	TTATCAATGA
msa237456.2{328_2603}	AATGGTGAGG	AAATCAATCC	TGATGCAAAA	TACAAATTAG	TTATCAATGA
msa237456.2{328_18RS21}	AATGGTGAGG	AAATCAATCC	TGATGCAAAA	TACAAATTAG	TTATCAATGA
msa237456.2{328_H36B}	AATGGTGAGG	AAATCAATCC	TGATGCAAAA	TACAAATTAG	TTATCAATGA
msa237456.2{328_COH1}	AATGGTGAGG	AAATCAATCC	TGATGCAAAA	TACAAATTAG	TTATCAATGA
msa237456.2{328_M732}	AATGGTGAGG	AAATCAATCC	TGATGCAAAA	TACAAATTAG	TTATCAATGA
msa237456.2{328_M781}	AATGGTGAGG	AAATCAATCC	TGATGCAAAA	TACAAATTAG	TTATCAATGA
msa237456.2{328_JM9130013}	AATGGTGAGG	AAATCAATCC	TGATGCAAAA	TACAAATTAG	TTATCAATGA
msa237456.2{328_A909}	AATGGTGAGG	AAATCAATCC	TGATGCAAAA	TACAAATTAG	TTATCAATGA
msa237456.2{328_090}	AATGGTGAGG	AAATCAATCC	TGATGCAAAA	TACAAATTAG	TTATCAATGA
msa237456.2{328_CJB110}	AATGGTGAGG	AAATCAATCC	TGATGCAAAA	TACAAATTAG	TTATCAATGA
Consensus	*****	*****	*****	*****	*****
1551					
msa237456.2{328_1169NT}	CTTTTTATTTC	GGTGGTGGTG	ATGGCTTTGC	AAGCTTCAGA	AATGCCAAAC
msa237456.2{328_2603}	CTTTTTATTTC	GGTGGTGGTG	ATGGCTTTGC	AAGCTTCAGA	AATGCCAAAC
msa237456.2{328_18RS21}	CTTTTTATTTC	GGTGGTGGTG	ATGGCTTTGC	AAGCTTCAGA	AATGCCAAAC
msa237456.2{328_H36B}	CTTTTTATTTC	GGTGGTGGTG	ATGGCTTTGC	AAGCTTCAGA	AATGCCAAAC
msa237456.2{328_COH1}	CTTTTTATTTC	GGTGGTGGTG	ATGGCTTTGC	AAGCTTCAGA	AATGCCAAAC
msa237456.2{328_M732}	CTTTTTATTTC	GGTGGTGGTG	ATGGCTTTGC	AAGCTTCAGA	AATGCCAAAC
msa237456.2{328_M781}	CTTTTTATTTC	GGTGGTGGTG	ATGGCTTTGC	AAGCTTCAGA	AATGCCAAAC
msa237456.2{328_JM9130013}	CTTTTTATTTC	GGTGGTGGTG	ATGGCTTTGC	AAGCTTCAGA	AATGCCAAAC
msa237456.2{328_A909}	CTTTTTATTTC	GGTGGTGGTG	ATGGCTTTGC	AAGCTTCAGA	AATGCCAAAC
msa237456.2{328_090}	CTTTTTATTTC	GGTGGTGGTG	ATGGCTTTGC	AAGCTTCAGA	AATGCCAAAC
msa237456.2{328_CJB110}	CTTTTTATTTC	GGTGGTGGTG	ATGGCTTTGC	AAGCTTCAGA	AATGCCAAAC
Consensus	*****	*****	*****	*****	*****
1601					
msa237456.2{328_1169NT}	TTCTAGGAGC	CATTAAcCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_2603}	TTCTAGGAGC	CATTAAcCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_18RS21}	TTCTAGGAGC	CATTAAcCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_H36B}	TTCTAGGAGC	CATTAAcCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_COH1}	TTCTAGGAGC	CATTAAcCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_M732}	TTCTAGGAGC	CATTAAcCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_M781}	TTCTAGGAGC	CATTAAcCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_JM9130013}	TTCTAGGAGC	CATTAAcCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_A909}	TTCTAGGAGC	CATTAAcCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_090}	TTCTAGGAGC	CATTAAcCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_CJB110}	TTCTAGGAGC	CATTAAcCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
Consensus	*****	*****	*****	*****	*****
1651					
1700					

Table 71: Comparative Sequences relating to SAG1333

msa237456.2{328_1169NT}	GATTTAGAAA	AAGCTGGTAA	AAAAGTGAGC	gTTCCAAATA	ATAAACCTAA
msa237456.2{328_2603}	GATTTAGAAA	AAGCTGGTAA	AAAAGTGAGC	gTTCCAAATA	ATAAACCTAA
msa237456.2{328_18RS21}	GATTTAGAAA	AAGCTGGTAA	AAAAGTGAGC	gTTCCAAATA	ATAAACCTAA
msa237456.2{328_H36B}	GATTTAGAAA	AAGCTGGTAA	AAAAGTGAGC	gTTCCAAATA	ATAAACCTAA
msa237456.2{328_COH1}	GATTTAGAAA	AAGCTGGTAA	AAAAGTGAGC	aTTCCAAATA	ATAAACCTAA
msa237456.2{328_M732}	GATTTAGAAA	AAGCTGGTAA	AAAAGTGAGC	aTTCCAAATA	ATAAACCTAA
msa237456.2{328_M781}	GATTTAGAAA	AAGCTGGTAA	AAAAGTGAGC	aTTCCAAATA	ATAAACCTAA
msa237456.2{328_JM9130013}	GATTTAGAAA	AAGCTGGTAA	AAAAGTGAGC	gTTCCAAATA	ATAAACCTAA
msa237456.2{328_A909}	GATTTAGAAA	AAGCTGGTAA	AAAAGTGAGC	gTTCCAAATA	ATAAACCTAA
msa237456.2{328_090}	GATTTAGAAA	AAGCTGGTAA	AAAAGTGAGC	gTTCCAAATA	ATAAACCTAA
msa237456.2{328_CJB110}	GATTTAGAAA	AAGCTGGTAA	AAAAGTGAGC	gTTCCAAATA	ATAAACCTAA
Consensus	*****	*****	*****	-*****	*****
1701					
msa237456.2{328_1169NT}	AATCTATGTC	ACTATGAAGA	TGGTTAATGA	AACTATTACA	CAAAATGATG
msa237456.2{328_2603}	AATCTATGTC	ACTATGAAGA	TGGTTAATGA	AACTATTACA	CAAAATGATG
msa237456.2{328_18RS21}	AATCTATGTC	ACTATGAAGA	TGGTTAATGA	AACTATTACA	CAAAATGATG
msa237456.2{328_H36B}	AATCTATGTC	ACTATGAAGA	TGGTTAATGA	AACTATTACA	CAAAATGATG
msa237456.2{328_COH1}	AATCTATGTC	ACTATGAAGA	TGGTTAATGA	AACTATTACA	CAAAATGATG
msa237456.2{328_M732}	AATCTATGTC	ACTATGAAGA	TGGTTAATGA	AACTATTACA	CAAAATGATG
msa237456.2{328_M781}	AATCTATGTC	ACTATGAAGA	TGGTTAATGA	AACTATTACA	CAAAATGATG
msa237456.2{328_JM9130013}	AATCTATGTC	ACTATGAAGA	TGGTTAATGA	AACTATTACA	CAAAATGATG
msa237456.2{328_A909}	AATCTATGTC	ACTATGAAGA	TGGTTAATGA	AACTATTACA	CAAAATGATG
msa237456.2{328_090}	AATCTATGTC	ACTATGAAGA	TGGTTAATGA	AACTATTACA	CAAAATGATG
msa237456.2{328_CJB110}	AATCTATGTC	ACTATGAAGA	TGGTTAATGA	AACTATTACA	CAAAATGATG
Consensus	*****	*****	*****	*****	*****
1751					
msa237456.2{328_1169NT}	GTACAcATAG	CATTATTaAG	AAACTTTATT	TAGATCGACA	AGGAAATATT
msa237456.2{328_2603}	GTACAcATAG	CATTATTaAG	AAACTTTATT	TAGATCGACA	AGGAAATATT
msa237456.2{328_18RS21}	GTACAcATAG	CATTATTaAG	AAACTTTATT	TAGATCGACA	AGGAAATATT
msa237456.2{328_H36B}	GTACAcATAG	CATTATTaAG	AAACTTTATT	TAGATCGACA	AGGAAATATT
msa237456.2{328_COH1}	GTACAcATAG	CATTATTaAG	AAACTTTATT	TAGATCGACA	AGGAAATATT
msa237456.2{328_M732}	GTACAcATAG	CATTATTaAG	AAACTTTATT	TAGATCGACA	AGGAAATATT
msa237456.2{328_M781}	GTACAcATAG	CATTATTaAG	AAACTTTATT	TAGATCGACA	AGGAAATATT
msa237456.2{328_JM9130013}	GTACAcATAG	CATTATTgAG	AAACTTTATT	TAGATCGACA	AGGAAATATT
msa237456.2{328_A909}	GTACAcATAG	CATTATTaAG	AAACTTTATT	TAGATCGACA	AGGAAATATT
msa237456.2{328_090}	GTACAcATAG	CATTATTaAG	AAACTTTATT	TAGATCGACA	AGGAAATATT
msa237456.2{328_CJB110}	GTACAcATAG	CATTATTaAG	AAACTTTATT	TAGATCGACA	AGGAAATATT
Consensus	*****	*****	*****	*****	*****
1800					
1801					
msa237456.2{328_1169NT}	GTAGCACAAG	AGATTGTATC	AGACACTTTA	AACCAAACAA	AATCAAAATC
msa237456.2{328_2603}	GTAGCACAAG	AGATTGTATC	AGACACTTTA	AACCAAACAA	AATCAAAATC
msa237456.2{328_18RS21}	GTAGCACAAG	AGATTGTATC	AGACACTTTA	AACCAAACAA	AATCAAAATC
msa237456.2{328_H36B}	GTAGCACAAG	AGATTGTATC	AGACACTTTA	AACCAAACAA	AATCAAAATC
msa237456.2{328_COH1}	GTAGCACAAG	AGATTGTATC	AGACACTTTA	AACCAAACAA	AATCAAAATC
msa237456.2{328_M732}	GTAGCACAAG	AGATTGTATC	AGACACTTTA	AACCAAACAA	AATCAAAATC
msa237456.2{328_M781}	GTAGCACAAG	AGATTGTATC	AGACACTTTA	AACCAAACAA	AATCAAAATC
msa237456.2{328_JM9130013}	GTAGCACAAG	AGATTGTATC	AGACACTTTA	AACCAAACAA	AATCAAAATC
msa237456.2{328_A909}	GTAGCACAAG	AGATTGTATC	AGACACTTTA	AACCAAACAA	AATCAAAATC
msa237456.2{328_090}	GTAGCACAAG	AGATTGTATC	AGACACTTTA	AACCAAACAA	AATCAAAATC
msa237456.2{328_CJB110}	GTAGCACAAG	AGATTGTATC	AGACACTTTA	AACCAAACAA	AATCAAAATC
Consensus	*****	*****	*****	*****	*****
1851					
msa237456.2{328_1169NT}	TACAAAAATC	AACCCTGTAA	CTACAATTCA	CAAAAAACAA	TTACACCAAT
msa237456.2{328_2603}	TACAAAAATC	AACCCTGTAA	CTACAATTCA	CAAAAAACAA	TTACACCAAT
msa237456.2{328_18RS21}	TACAAAAATC	AACCCTGTAA	CTACAATTCA	CAAAAAACAA	TTACACCAAT
msa237456.2{328_H36B}	TACAAAAATC	AACCCTGTAA	CTACAATTCA	CAAAAAACAA	TTACACCAAT
msa237456.2{328_COH1}	TACAAAAATC	AACCCTGTAA	CTACAATTCA	CAAAAAACAA	TTACACCAAT
msa237456.2{328_M732}	TACAAAAATC	AACCCTGTAA	CTACAATTCA	CAAAAAACAA	TTACACCAAT
msa237456.2{328_M781}	TACAAAAATC	AACCCTGTAA	CTACAATTCA	CAAAAAACAA	TTACACCAAT
msa237456.2{328_JM9130013}	TACAAAAATC	AACCCTGTAA	CTACAATTCA	CAAAAAACAA	TTACACCAAT
msa237456.2{328_A909}	TACAAAAATC	AACCCTGTAA	CTACAATTCA	CAAAAAACAA	TTACACCAAT
msa237456.2{328_090}	TACAAAAATC	AACCCTGTAA	CTACAATTCA	CAAAAAACAA	TTACACCAAT
msa237456.2{328_CJB110}	TACAAAAATC	AACCCTGTAA	CTACAATTCA	CAAAAAACAA	TTACACCAAT
Consensus	*****	*****	*****	*****	*****
1901					
msa237456.2{328_1169NT}	TTACAGCTAT	TAACCCTATG	AGAAATTATG	GCAAACCATC	AAACTCCACT
msa237456.2{328_2603}	TTACAGCTAT	TAACCCTATG	AGAAATTATG	GCAAACCATC	AAACTCCACT
msa237456.2{328_18RS21}	TTACAGCTAT	TAACCCTATG	AGAAATTATG	GCAAACCATC	AAACTCCACT
msa237456.2{328_H36B}	TTACAGCTAT	TAACCCTATG	AGAAATTATG	GCAAACCATC	AAACTCCACT
msa237456.2{328_COH1}	TTACAGCTAT	TAACCCTATG	AGAAATTATG	GCAAACCATC	AAACTCCACT
msa237456.2{328_M732}	TTACAGCTAT	TAACCCTATG	AGAAATTATG	GCAAACCATC	AAACTCCACT
msa237456.2{328_M781}	TTACAGCTAT	TAACCCTATG	AGAAATTATG	GCAAACCATC	AAACTCCACT
msa237456.2{328_JM9130013}	TTACAGCTAT	TAACCCTATG	AGAAATTATG	GCAAACCATC	AAACTCCACT
msa237456.2{328_A909}	TTACAGCTAT	TAACCCTATG	AGAAATTATG	GCAAACCATC	AAACTCCACT
msa237456.2{328_090}	TTACAGCTAT	TAACCCTATG	AGAAATTATG	GCAAACCATC	AAACTCCACT
msa237456.2{328_CJB110}	TTACAGCTAT	TAACCCTATG	AGAAATTATG	GCAAACCATC	AAACTCCACT
Consensus	*****	*****	*****	*****	*****
1950					

Table 71: Comparative Sequences relating to SAG1333

	1951	2000
msa237456.2{328_1169NT}	ACTGTAAAAT CAaa-----	-----
msa237456.2{328_2603}	ACTGTAAAAT CAaaACAAtt accaaaaaca aactctgaat atggacaatc	-----
msa237456.2{328_18RS21}	ACTGTAAAAT CAaaA-----	-----
msa237456.2{328_H36B}	ACTGTAAAAT CAaa-----	-----
msa237456.2{328_COH1}	ACTGTAAAAT CAaa-----	-----
msa237456.2{328_M732}	ACTGTAAAAT CAaaACAA--	-----
msa237456.2{328_M781}	ACTGTAAAAT CAaa-----	-----
msa237456.2{328_JM9130013}	ACTGTAAAAT CAaaA-----	-----
msa237456.2{328_A909}	ACTGTAAAAT CAaaACAA--	-----
msa237456.2{328_090}	ACTGTAAAAT CAaaACAA--	-----
msa237456.2{328_CJB110}	ACTGTAAAAT CA-----	-----
Consensus	***** **_***** ***** ***** *****	*****
	2001	2050
msa237456.2{328_1169NT}	-----	-----
msa237456.2{328_2603}	attccttatg tctgtctttg gtgttggtact tataggaatt gcttttaata	-----
msa237456.2{328_18RS21}	-----	-----
msa237456.2{328_H36B}	-----	-----
msa237456.2{328_COH1}	-----	-----
msa237456.2{328_M732}	-----	-----
msa237456.2{328_M781}	-----	-----
msa237456.2{328_JM9130013}	-----	-----
msa237456.2{328_A909}	-----	-----
msa237456.2{328_090}	-----	-----
msa237456.2{328_CJB110}	-----	-----
Consensus	***** ***** ***** ***** *****	*****
	2051	2070
msa237456.2{328_1169NT}	-----	-----
msa237456.2{328_2603}	caaagaaaaa acatatgaaa	-----
msa237456.2{328_18RS21}	-----	-----
msa237456.2{328_H36B}	-----	-----
msa237456.2{328_COH1}	-----	-----
msa237456.2{328_M732}	-----	-----
msa237456.2{328_M781}	-----	-----
msa237456.2{328_JM9130013}	-----	-----
msa237456.2{328_A909}	-----	-----
msa237456.2{328_090}	-----	-----
msa237456.2{328_CJB110}	-----	-----
Consensus	***** *****	-----

SEQ ID NO. 7112

STRAIN 2603 frame: 1

MKKKI ILKSSVLGLVAGTSIMFSSVFADQVGQVIGVND F HGALDNTGTANMPDGK VANA
 GTAAQLDAYMDDAQKDFKQTNPNGESIRVQAGDMVGAS PANSGLLQDEPTVKNFNAMNVE
 YGTLGNHEFDEGLAEYNRI VTGKAPAPDSNINNITKSY PHEAAKQEI VVANVIDKVNKQI
 PYNWKPYAIKNI PVNNSVNVGFIGI VTKDIPNLVLRKNYEQYEF LDEAETIVKYAKELQ
 AKNVKAI VVLAHV PATSKNDIAEGEAAEMMKVNQLFPENSVDIVFAGHNHQYTNGLVGK
 TRIVQALSQ GKAYADVRGVLD TDTQDFIETPSAKVIAVAPGKKTGSADIQAI V DQANTI V
 KQVTEAKIGTAEVSMITRSVDQDNVSPVGS LITEAQLAIARKSWPDIDFAMTNNGGIRA
 DLLIKPDGTITWGAAQAVQPF GNILQVVEITGRDLYKALNEQYDQKQNF FLQIAGLRYTY
 TDNKEGGEETPFKVVKAYKSN GEEINPD AKYKLVINDFLFGG DGFASFRNAKLLGAINP
 DTEVF MAYITDLEKAGKKVSPNNKPKIYVTM K MVNETITQNDGTHSIIKKLYLDRQGN I
 VAQEI VSDTLNQTKSKSTKINPVTTIHKKQLHQFTAINPMRNYGKPSNSTTVKSKQLPKT
 NSEYGQSF LMSVFGVGLIGIALNTKKKHKM

SEQ ID NO. 7113

STRAIN 090 frame: 3

VGVQVIGVND F HGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIRV
 QAGDMVGAS PANSGLLQDEPTVKTFNAMNVEYGT LGNHEFDEGLAEYNRI VTGKAPAPDS
 NINNITKSY PHEAAKQEI VVANVIDKVNKQI PYNWKPYAIKNI PVNNSVNVGFIGI VTK
 DIPNLVLRKNYEQYEF LDEAETIVKYAKELQAKNVKAI VVLAHV PATSKDDIAEGEAAEM
 MKKNVQLFPENSVDIVFAGHNHQYTNGLVGKTRIVQALSQ GKAYADVRGVLD TDTQDFIE
 TPSAKVAVAPGKKTGSADIQAI V DQANTI VKQVTEAKIGTAEVSGMITRSVDQDNVSPV
 GSLITEAQLAIARKSWPDIDFAMTNNGGIRADLLIKPDGTITWGAAQAVQPF GNILQVVE
 ITGRDLYKALNEQYDQKQNF FLQIAGLRYTYTDNKEGGEETPFKVVKAYKSN GEEINPDA
 KYKLVINDFLFGG DGFASFRNAKLLGAINPDTEVF MAYITDLEKAGKKVSPNNKPKIY
 VTMK MVNETITQNDGTHSIIKKLYLDRQGN I VAQEI VSDTLNQTKSKSTKINPVTTIHKK
 QLHQFTAINPMRNYGKPSNSTTVKSKQ

SEQ ID NO. 7114

STRAIN A909 frame: 3

VNDFHGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIRVQAGDMVG
 ASPANSGLLQDEPTVKTFNAMNVEYGT LGNHEFDEGLAEYNRI VTGKAPAPDSNINNITK
 SYPHEAAKQEI VVANVIDKVNKQI PYNWKPYTIKNI PVNNSVNVGFIGI VTKDIPNLV
 RKNYEQYEF LDEAETIVKYAKELQAKNVKAI VVLAHV PATSKDDIAEGEAAEMMKVNQL
 FPENSVDIVFAGHNHQYTNGLVGKTRIVQALSQ GKAYADVRGVLD TDTQDFIETPSAKVI
 AVAPGKKTGSADIQAI V DQANTI VKQVTEAKIGTAEVSGMITRSVDQDNVSPVGS LITEA
 QLAIARKSWPDIDFAMTNNGGIRADLLIKPDGTITWGAAQAVQPF GNILQVVEITGRDLY
 KALNEQYDQKQNF FLQIAGLRYTYTDNKEGGEETPFKVVKAYKSN GEEINPD AKYKLVIN
 DFLFGG DGFASFRNAKLLGAINPDTEVF MAYITDLEKAGKKVSPNNKPKIYVTM K MVN
 ETITQNDGTHSIIKKLYLDRQGN I VAQEI VSDTLNQTKSKSTKINPVTTIHKKQLHQFTA

Table 71: Comparative Sequences relating to SAG1333

INPMRNYGKPSNSTTVKSKQ

SEQ ID NO. 7115

STRAIN H36B frame: 2

QVGVQVIGVND F HGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIR
 VQAGDMVGAS PANSGLLQDEPTVKT FNAMNVEYGT LGNHEFDEGLAEYNRI VTGKAPAPD
 SNINNITKSY PHEAAKQEI VVANVIDKVNKQI PYNWKPYTI KNI PVNNKSVNVGFIGIVT
 KDI PNLVLRKNYEQYEF LDEAETIVKYAKELQAKNVKAI VVLAHV PATSKDDIAEGEAAE
 MMKKVNQLFP ENSVDIVFAGHNHQYTNGLVGKTRIVQALSQ GKAYADVRGVLD TDTQDFI
 ETPSAKVIAVAPGKKTGSADIQAI VDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSP
 VGSLITEAQLAIARKSWPDIDFAMTNNGGIRADLLIKPDGTITWGAAQAVQPF GNILQVV
 EITGRDLYKALNEQYDQKQNF FLQIAGLRYTYTDNKEGGEETPFKVVKAYKSNGEEINPD
 AKYKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVF MAYITDLEKAGKKVSVPNKPKI
 YVTMKNVNETITQNDGTYSI IKKLYLDRQGNIVAQEIVSDTLNQTKSKSTKINPVTTIHK
 KQLHQFTAINPMRNYGKPSNSTTVKS

SEQ ID NO. 7116

STRAIN 18RS21 frame: 1

DQVGVQVIGVND F HGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIR
 RVQAGDMVGAS PANSGLLQDEPTVKT FNAMNVEYGT LGNHEFDEGLAEYNRI VTGKAPAPD
 DSNINNITKSY PHEAAKQEI VVANVIDKVNKQI PYNWKPYTI KNI PVNNKSVNVGFIGIVT
 TKDI PNLVLRKNYEQYEF LDEAETIVKYAKELQAKNVKAI VVLAHV PATSKDDIAEGEAAE
 EMMKKVNQLFP ENSVDIVFAGHNHQYTNGLVGKTRIVQALSQ GKAYADVRGVLD TDTQDFI
 IETPSAKVIAVAPGKKTGSADIQAI VDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSP
 PVGSLITEAQLAIARKSWPDIDFAMTNNGGIRADLLIKPDGTITWGAAQAVQPF GNILQVV
 VEITGRDLYKALNEQYDQKQNF FLQIAGLRYTYTDNKEGGEETPFKVVKAYKSNGEEINPD
 DAKYKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVF MAYITDLEKAGKKVSVPNKPKI
 IYVTMKNVNETITQNDGTYSI IKKLYLDRQGNIVAQEIVSDTLNQTKSKSTKINPVTTIHK
 KKQLHQFTAINPMRNYGKPSNSTTVKS

SEQ ID NO. 7117

STRAIN M732 frame: 3

QVGVQVIGVND F HGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIR
 VQAGDMVGAS PANSGLLQDEPTVKT FNAMNVEYGT LGNHEFDEGLAEYNRI VTGKAPAPD
 SNINNITKSY PHEAAKQEI VVANVIDKVNKQI PYNWKPYTI KNI PVNNKSVNVGFIGIVT
 KDI PNLVLRKNYEQYEF LDEAETIVKYAKELQAKNVKAI VVLAHV PATSKDDIAEGEAAE
 MMKKVNQLFP ENSVDIVFAGHNHQYTNGLVGKTRIVQALSQ GKAYADVRGVLD TDTQDFI
 ETPSAKVIAVAPGKKTGSADIQAI VDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSP
 VGSLITEAQLAIARKSWPDIDFAMTNNGGIRADLLIKPDGTITWGAAQAVQPF GNILQVV
 EITGRDLYKALNEQYDQKQNF FLQIAGLRYTYTDNKEGGEETPFKVVKAYKSNGEEINPD
 AKYKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVF MAYITDLEKAGKKVSI PNKPKI
 YVTMKNVNETITQNDGTYSI IKKLYLDRQGNIVAQEIVSDTLNQTKSKSTKINPVTTIHK
 KQLHQFTAINPMRNYGKPSNSTTVKSKQ

SEQ ID NO. 7118

STRAIN COH1 frame: 3

QVGVQVIGVND F HGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIR
 VQAGDMVGAS PANSGLLQDEPTVKT FNAMNVEYGT LGNHEFDEGLAEYNRI VTGKAPAPD
 SNINNITKSY PHEAAKQEI VVANVIDKVNKQI PYNWKPYTI KNI PVNNKSVNVGFIGIVT
 KDI PNLVLRKNYEQYEF LDEAETIVKYAKELQAKNVKAI VVLAHV PATSKDDIAEGEAAE
 MMKKVNQLFP ENSVDIVFAGHNHQYTNGLVGKTRIVQALSQ GKAYADVRGVLD TDTQDFI
 ETPSAKVIAVAPGKKTGSADIQAI VDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSP
 VGSLITEAQLAIARKSWPDIDFAMTNNGGIRADLLIKPDGTITWGAAQAVQPF GNILQVV
 EITGRDLYKALNEQYDQKQNF FLQIAGLRYTYTDNKEGGEETPFKVVKAYKSNGEEINPD
 AKYKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVF MAYITDLEKAGKKVSI PNKPKI
 YVTMKNVNETITQNDGTYSI IKKLYLDRQGNIVAQEIVSDTLNQTKSKSTKINPVTTIHK
 KQLHQFTAINPMRNYGKPSNSTTVKS

SEQ ID NO. 7119

STRAIN M781 frame: 1

QVGVQVIGVND F HGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIR
 VQAGDMVGAS PANSGLLQDEPTVKT FNAMNVEYGT LGNHEFDEGLAEYNRI VTGKAPAPD
 SNINNITKSY PHEAAKQEI VVANVIDKVNKQI PYNWKPYTI KNI PVNNKSVNVGFIGIVT
 KDI PNLVLRKNYEQYEF LDEAETIVKYAKELQAKNVKAI VVLAHV PATSKDDIAEGEAAE
 MMKKVNQLFP ENSVDIVFAGHNHQYTNGLVGKTRIVQALSQ GKAYADVRGVLD TDTQDFI
 ETPSAKVIAVAPGKKTGSADIQAI VDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSP
 VGSLITEAQLAIARKSWPDIDFAMTNNGGIRADLLIKPDGTITWGAAQAVQPF GNILQVV
 EITGRDLYKALNEQYDQKQNF FLQIAGLRYTYTDNKEGGEETPFKVVKAYKSNGEEINPD
 AKYKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVF MAYITDLEKAGKKVSI PNKPKI
 YVTMKNVNETITQNDGTYSI IKKLYLDRQGNIVAQEIVSDTLNQTKSKSTKINPVTTIHK
 KQLHQFTAINPMRNYGKPSNSTTVKS

SEQ ID NO. 7120

STRAIN CJB110 frame: 1

DQVGVQVIGVND F HGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIR
 RVQAGDMVGAS PANSGLLQDEPTVKT FNAMNVEYGT LGNHEFDEGLAEYNRI VTGKAPAPD
 DSNINNITKSY PHEAAKQEI VVANVIDKVNKQI PYNWKPYTI KNI PVNNKSVNVGFIGIVT
 TKDI PNLVLRKNYEQYEF LDEAETIVKYAKELQAKNVKAI VVLAHV PATSKDDIAEGEAAE
 EMMKKVNQLFP ENSVDIVFAGHNHQYTNGLVGKTRIVQALSQ GKAYADVRGVLD TDTQDFI
 IETPSAKVIAVAPGKKTGSADIQAI VDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSP
 PVGSLITEAQLAIARKSWPDIDFAMTNNGGIRADLLIKPDGTITWGAAQAVQPF GNILQVV
 VEITGRDLYKALNEQYDQKQNF FLQIAGLRYTYTDNKEGGEETPFKVVKAYKSNGEEINPD

Table 71: Comparative Sequences relating to SAG1333

DAKYKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVFMAIYITDLEKAGKKVSVPNKPK
IYVTMKNVNETITQNDGTHSIKKLYLDRQGNIVAQEIVSDTLNQTKSKSTKINPVTTIH
KKQLHQFTAINPMRNYGKPSNSTTVKS

SEQ ID NO. 7121

STRAIN 1169NT frame: 1

QVGQVIGVNDVDFHGALDNTGTANMPDGKVANAGTAAQLDAYMDDAQKDFKQTNPNGESIR
VQAGDMVGASPANSGLLQDEPTVKNFNAMNVEYGTGLGNHEFDEGLAEYNRIVTGKAPAPD
SNINNITKSYPHAAKQEIIVANVIDKVNKQIPYNWKPYAIKNIPVNNKSVNVGFIGIVT
KDIPNLVLRKNYEQYEFLEAETIVKYAKELQAKNVKAIIVLAHVPAATSKNDIAEGEAAE
MMKKVNQLFPENSVDIVFAGHNHQTNGLVGKTRIVQALSQGKAYADVRGVLDTDQDFI
ETPSAKVIAVAPGKKTGSADIQAIVDQANTIVKQVTEAKIGTAEVSMITRSVDQDNVSP
VGSLLITEAQLAIARKSWPDIDFAMTNNGGIRADLLIKPDGTITWGAAQAVQPFNGILQVV
EITGRDLYKALNEQYDQKQNFLLQIAGLRYTYTDNKEGGEETPFKVVKAYKSNGEIINPD
AKYKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVFMAIYITDLEKAGKKVSVPNKPKI
YVTMKNVNETITQNDGTHSIKKLYLDRQGNIVAQEIVSDTLNQTKSKSTKINPVTTIHK
KKQLHQFTAINPMRNYGKPSNSTTVKS

SEQ ID NO. 7122

STRAIN JM9130013 frame: 2

GVQVIGVNDVDFHGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIRVQ
AGDMVGASPANSGLLQDEPTVKTNFAMNVEYGTGLGNHEFDEGLAEYNRIVTGKAPAPDSN
INNITKSYPHAAKQEIIVANVIDKVNKQIPYNWKPYTIKNIPVNNKSVNVGFIGIVTKD
IPNLVLRKNYEQYEFLEAETIVKYAKELQAKNVKAIIVLAHVPAATSKDDIAEGEAAEMM
KKVNQLFPENSVDIVFAGHNHQTNGLVGKTRIVQALSQGKAYADVRGVLDTDQDFIET
PSAKVIAVAPGKKTGSADIQAIVDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSPVG
SLITEAQLAIARKSWPDIDFAMTNNGGIRADLLIKPDGTITWGAAQAVQPFNGILQVVEI
TGRDLYKALNEQYDQKQNFLLQIAGLRYTYTDNKEGGEETPFKVVKAYKSNGEIINPD
YKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVFMAIYITDLEKAGKKVSVPNKPKIYV
TMKNVNETITQNDGTYSIIEKLYLDRQGNIVAQEIVSDTLNQTKSKSTKINPVTTIHKKQ
LHQFTAINPMRNYGKPSNSTTVKSK

PRETTY of: /biotmp/msa237615.2{*} May 14, 2003 03:22 ..

	1		50
msa237615.2{328_1169NT}	~~~~~	~~~~~qv	gvqvigVNDF HGALDNTGTA
msa237615.2{328_2603}	mkkkkiilkss	vlglvagtsi mfssvfaDqv	gvqvigVNDF HGALDNTGTA
msa237615.2{328_A909}	~~~~~	~~~~~VNDF	HGALDNTGTA
msa237615.2{328_M732}	~~~~~	~~~~~qv	gvqvigVNDF HGALDNTGTA
msa237615.2{328_COH1}	~~~~~	~~~~~qv	gvqvigVNDF HGALDNTGTA
msa237615.2{328_M781}	~~~~~	~~~~~qv	gvqvigVNDF HGALDNTGTA
msa237615.2{328_H36B}	~~~~~	~~~~~qv	gvqvigVNDF HGALDNTGTA
msa237615.2{328_JM9130013}	~~~~~	~~~~~	gvqvigVNDF HGALDNTGTA
msa237615.2{328_18RS21}	~~~~~	~~~~~Dqv	gvqvigVNDF HGALDNTGTA
msa237615.2{328_090}	~~~~~	~~~~~v	gvqvigVNDF HGALDNTGTA
msa237615.2{328_CJB110}	~~~~~	~~~~~Dqv	gvqvigVNDF HGALDNTGTA
Consensus	*****	*****	*****

	51		100
msa237615.2{328_1169NT}	NMPDGKVANA GTAAQLDAYM DDAQKDFKQT	NPNGESIRVQ	AGDMVGASPA
msa237615.2{328_2603}	NMPDGKVANA GTAAQLDAYM DDAQKDFKQT	NPNGESIRVQ	AGDMVGASPA
msa237615.2{328_A909}	NMPDGKVtNA GTAAQLDAYM DDAQKDFKQT	NPNGESIRVQ	AGDMVGASPA
msa237615.2{328_M732}	NMPDGKVtNA GTAAQLDAYM DDAQKDFKQT	NPNGESIRVQ	AGDMVGASPA
msa237615.2{328_COH1}	NMPDGKVtNA GTAAQLDAYM DDAQKDFKQT	NPNGESIRVQ	AGDMVGASPA
msa237615.2{328_M781}	NMPDGKVtNA GTAAQLDAYM DDAQKDFKQT	NPNGESIRVQ	AGDMVGASPA
msa237615.2{328_H36B}	NMPDGKVtNA GTAAQLDAYM DDAQKDFKQT	NPNGESIRVQ	AGDMVGASPA
msa237615.2{328_JM9130013}	NMPDGKVtNA GTAAQLDAYM DDAQKDFKQT	NPNGESIRVQ	AGDMVGASPA
msa237615.2{328_18RS21}	NMPDGKVxNA GTAAQLDAYM DDAQKDFKQT	NPNGESIRVQ	AGDMVGASPA
msa237615.2{328_090}	NMPDGKVtNA GTAAQLDAYM DDAQKDFKQT	NPNGESIRVQ	AGDMVGASPA
msa237615.2{328_CJB110}	NMPDGKVtNA GTAAQLDAYM DDAQKDFKQT	NPNGESIRVQ	AGDMVGASPA
Consensus	*****	*****	*****

	101		150
msa237615.2{328_1169NT}	NSGLLQDEPT VKnFNAMNVE YGTGLGNHEFD	EGLAEYNRIV	TGKAPAPDSN
msa237615.2{328_2603}	NSGLLQDEPT VKnFNAMNVE YGTGLGNHEFD	EGLAEYNRIV	TGKAPAPDSN
msa237615.2{328_A909}	NSGLLQDEPT VKtFNAMNVE YGTGLGNHEFD	EGLAEYNRIV	TGKAPAPDSN
msa237615.2{328_M732}	NSGLLQDEPT VKtFNAMNVE YGTGLGNHEFD	EGLAEYNRIV	TGKAPAPDSN
msa237615.2{328_COH1}	NSGLLQDEPT VKtFNAMNVE YGTGLGNHEFD	EGLAEYNRIV	TGKAPAPDSN
msa237615.2{328_M781}	NSGLLQDEPT VKtFNAMNVE YGTGLGNHEFD	EGLAEYNRIV	TGKAPAPDSN
msa237615.2{328_H36B}	NSGLLQDEPT VKtFNAMNVE YGTGLGNHEFD	EGLAEYNRIV	TGKAPAPDSN
msa237615.2{328_JM9130013}	NSGLLQDEPT VKtFNAMNVE YGTGLGNHEFD	EGLAEYNRIV	TGKAPAPDSN
msa237615.2{328_18RS21}	NSGLLQDEPT VKtFNAMNVE YGTGLGNHEFD	EGLAEYNRIV	TGKAPAPDSN
msa237615.2{328_090}	NSGLLQDEPT VKtFNAMNVE YGTGLGNHEFD	EGLAEYNRIV	TGKAPAPDSN
msa237615.2{328_CJB110}	NSGLLQDEPT VKtFNAMNVE YGTGLGNHEFD	EGLAEYNRIV	TGKAPAPDSN
Consensus	*****	*****	*****

	151		200
msa237615.2{328_1169NT}	INNITKSYPH EAAKQEIIVA NVIDKVNKQI	PYNWKPYaIK	NIPVNNKSVN
msa237615.2{328_2603}	INNITKSYPH EAAKQEIIVA NVIDKVNKQI	PYNWKPYaIK	NIPVNNKSVN
msa237615.2{328_A909}	INNITKSYPH EAAKQEIIVA NVIDKVNKQI	PYNWKPYtIK	NIPVNNKSVN
msa237615.2{328_M732}	INNITKSYPH EAAKQEIIVA NVIDKVNKQI	PYNWKPYtIK	NIPVNNKSVN
msa237615.2{328_COH1}	INNITKSYPH EAAKQEIIVA NVIDKVNKQI	PYNWKPYtIK	NIPVNNKSVN
msa237615.2{328_M781}	INNITKSYPH EAAKQEIIVA NVIDKVNKQI	PYNWKPYtIK	NIPVNNKSVN

Table 71: Comparative Sequences relating to SAG1333

msa237615.2{328_H36B}	INNITKSYPH	EAAKQEIVVA	NVIDKVNKQI	PYNWKPYtIK	NIPVNNKSVN
msa237615.2{328_JM9130013}	INNITKSYPH	EAAKQEIVVA	NVIDKVNKQI	PYNWKPYtIK	NIPVNNKSVN
msa237615.2{328_18RS21}	INNITKSYPH	EAAKQEIVVA	NVIDKVNKQI	PYNWKPYtIK	NIPVNNKSVN
msa237615.2{328_090}	INNITKSYPH	EAAKQEIVVA	NVIDKVNKQI	PYNWKPYaIK	NIPVNNKSVN
msa237615.2{328_CJB110}	INNITKSYPH	EAAKQEIVVA	NVIDKVNKQI	PYNWKPYaIK	NIPVNNKSVN
Consensus	*****	*****	*****	*****-*	*****
201					
msa237615.2{328_1169NT}	VGFIGIVTKD	IPNLVLRKNY	EQYEFLDEAE	TIVKYAKELQ	AKNVKAIVVL
msa237615.2{328_2603}	VGFIGIVTKD	IPNLVLRKNY	EQYEFLDEAE	TIVKYAKELQ	AKNVKAIVVL
msa237615.2{328_A909}	VGFIGIVTKD	IPNLVLRKNY	EQYEFLDEAE	TIVKYAKELQ	AKNVKAIVVL
msa237615.2{328_M732}	VGFIGIVTKD	IPNLVLRKNY	EQYEFLDEAE	TIVKYAKELQ	AKNVKAIVVL
msa237615.2{328_COH1}	VGFIGIVTKD	IPNLVLRKNY	EQYEFLDEAE	TIVKYAKELQ	AKNVKAIVVL
msa237615.2{328_M781}	VGFIGIVTKD	IPNLVLRKNY	EQYEFLDEAE	TIVKYAKELQ	AKNVKAIVVL
msa237615.2{328_H36B}	VGFIGIVTKD	IPNLVLRKNY	EQYEFLDEAE	TIVKYAKELQ	AKNVKAIVVL
msa237615.2{328_JM9130013}	VGFIGIVTKD	IPNLVLRKNY	EQYEFLDEAE	TIVKYAKELQ	AKNVKAIVVL
msa237615.2{328_18RS21}	VGFIGIVTKD	IPNLVLRKNY	EQYEFLDEAE	TIVKYAKELQ	AKNVKAIVVL
msa237615.2{328_090}	VGFIGIVTKD	IPNLVLRKNY	EQYEFLDEAE	TIVKYAKELQ	AKNVKAIVVL
msa237615.2{328_CJB110}	VGFIGIVTKD	IPNLVLRKNY	EQYEFLDEAE	TIVKYAKELQ	AKNVKAIVVL
Consensus	*****	*****	*****	*****	*****
251					
msa237615.2{328_1169NT}	AHVPATSKnD	IAEGEAAEMM	KKNVQLFPEN	SVDIVFAGHN	HQYTNGLVGK
msa237615.2{328_2603}	AHVPATSKnD	IAEGEAAEMM	KKNVQLFPEN	SVDIVFAGHN	HQYTNGLVGK
msa237615.2{328_A909}	AHVPATSKdD	IAEGEAAEMM	KKNVQLFPEN	SVDIVFAGHN	HQYTNGLVGK
msa237615.2{328_M732}	AHVPATSKdD	IAEGEAAEMM	KKNVQLFPEN	SVDIVFAGHN	HQYTNGLVGK
msa237615.2{328_COH1}	AHVPATSKdD	IAEGEAAEMM	KKNVQLFPEN	SVDIVFAGHN	HQYTNGLVGK
msa237615.2{328_M781}	AHVPATSKdD	IAEGEAAEMM	KKNVQLFPEN	SVDIVFAGHN	HQYTNGLVGK
msa237615.2{328_H36B}	AHVPATSKdD	IAEGEAAEMM	KKNVQLFPEN	SVDIVFAGHN	HQYTNGLVGK
msa237615.2{328_JM9130013}	AHVPATSKdD	IAEGEAAEMM	KKNVQLFPEN	SVDIVFAGHN	HQYTNGLVGK
msa237615.2{328_18RS21}	AHVPATSKdD	IAEGEAAEMM	KKNVQLFPEN	SVDIVFAGHN	HQYTNGLVGK
msa237615.2{328_090}	AHVPATSKdD	IAEGEAAEMM	KKNVQLFPEN	SVDIVFAGHN	HQYTNGLVGK
msa237615.2{328_CJB110}	AHVPATSKdD	IAEGEAAEMM	KKNVQLFPEN	SVDIVFAGHN	HQYTNGLVGK
Consensus	*****-*	*****	*****	*****	*****
301					
msa237615.2{328_1169NT}	TRIVQALSQG	KAYADVRGVL	DTDTQDFIET	PSAKViAVAP	GKKTGSADIQ
msa237615.2{328_2603}	TRIVQALSQG	KAYADVRGVL	DTDTQDFIET	PSAKViAVAP	GKKTGSADIQ
msa237615.2{328_A909}	TRIVQALSQG	KAYADVRGVL	DTDTQDFIET	PSAKViAVAP	GKKTGSADIQ
msa237615.2{328_M732}	TRIVQALSQG	KAYADVRGVL	DTDTQDFIET	PSAKViAVAP	GKKTGSADIQ
msa237615.2{328_COH1}	TRIVQALSQG	KAYADVRGVL	DTDTQDFIET	PSAKViAVAP	GKKTGSADIQ
msa237615.2{328_M781}	TRIVQALSQG	KAYADVRGVL	DTDTQDFIET	PSAKViAVAP	GKKTGSADIQ
msa237615.2{328_H36B}	TRIVQALSQG	KAYADVRGVL	DTDTQDFIET	PSAKViAVAP	GKKTGSADIQ
msa237615.2{328_JM9130013}	TRIVQALSQG	KAYADVRGVL	DTDTQDFIET	PSAKViAVAP	GKKTGSADIQ
msa237615.2{328_18RS21}	TRIVQALSQG	KAYADVRGVL	DTDTQDFIET	PSAKViAVAP	GKKTGSADIQ
msa237615.2{328_090}	TRIVQALSQG	KAYADVRGVL	DTDTQDFIET	PSAKVvAVAP	GKKTGSADIQ
msa237615.2{328_CJB110}	TRIVQALSQG	KAYADVRGVL	DTDTQDFIET	PSAKVvAVAP	GKKTGSADIQ
Consensus	*****	*****	*****	*****-*****	*****
351					
msa237615.2{328_1169NT}	AIVDQANTIV	KQVTEAKIGT	AEVSvMITRS	VDQDNVSPVG	SLITEAQLAI
msa237615.2{328_2603}	AIVDQANTIV	KQVTEAKIGT	AEVSvMITRS	VDQDNVSPVG	SLITEAQLAI
msa237615.2{328_A909}	AIVDQANTIV	KQVTEAKIGT	AEVSgMITRS	VDQDNVSPVG	SLITEAQLAI
msa237615.2{328_M732}	AIVDQANTIV	KQVTEAKIGT	AEVSgMITRS	VDQDNVSPVG	SLITEAQLAI
msa237615.2{328_COH1}	AIVDQANTIV	KQVTEAKIGT	AEVSgMITRS	VDQDNVSPVG	SLITEAQLAI
msa237615.2{328_M781}	AIVDQANTIV	KQVTEAKIGT	AEVSgMITRS	VDQDNVSPVG	SLITEAQLAI
msa237615.2{328_H36B}	AIVDQANTIV	KQVTEAKIGT	AEVSgMITRS	VDQDNVSPVG	SLITEAQLAI
msa237615.2{328_JM9130013}	AIVDQANTIV	KQVTEAKIGT	AEVSgMITRS	VDQDNVSPVG	SLITEAQLAI
msa237615.2{328_18RS21}	AIVDQANTIV	KQVTEAKIGT	AEVSgMITRS	VDQDNVSPVG	SLITEAQLAI
msa237615.2{328_090}	AIVDQANTIV	KQVTEAKIGT	AEVSgMITRS	VDQDNVSPVG	SLITEAQLAI
msa237615.2{328_CJB110}	AIVDQANTIV	KQVTEAKIGT	AEVSgMITRS	VDQDNVSPVG	SLITEAQLAI
Consensus	*****	*****	*****-*****	*****	*****
401					
msa237615.2{328_1169NT}	ARKSWPDIDF	AMTNNGGIRA	DLLIKPDGTI	TWGAAQAVQP	FGNILQVVEI
msa237615.2{328_2603}	ARKSWPDIDF	AMTNNGGIRA	DLLIKPDGTI	TWGAAQAVQP	FGNILQVVEI
msa237615.2{328_A909}	ARKSWPDIDF	AMTNNGGIRA	DLLIKPDGTI	TWGAAQAVQP	FGNILQVVEI
msa237615.2{328_M732}	ARKSWPDIDF	AMTNNGGIRA	DLLIKPDGTI	TWGAAQAVQP	FGNILQVVEI
msa237615.2{328_COH1}	ARKSWPDIDF	AMTNNGGIRA	DLLIKPDGTI	TWGAAQAVQP	FGNILQVVEI
msa237615.2{328_M781}	ARKSWPDIDF	AMTNNGGIRA	DLLIKPDGTI	TWGAAQAVQP	FGNILQVVEI
msa237615.2{328_H36B}	ARKSWPDIDF	AMTNNGGIRA	DLLIKPDGTI	TWGAAQAVQP	FGNILQVVEI
msa237615.2{328_JM9130013}	ARKSWPDIDF	AMTNNGGIRA	DLLIKPDGTI	TWGAAQAVQP	FGNILQVVEI
msa237615.2{328_18RS21}	ARKSWPDIDF	AMTNNGGIRA	DLLIKPDGTI	TWGAAQAVQP	FGNILQVVEI
msa237615.2{328_090}	ARKSWPDIDF	AMTNNGGIRA	DLLIKPDGTI	TWGAAQAVQP	FGNILQVVEI
msa237615.2{328_CJB110}	ARKSWPDIDF	AMTNNGGIRA	DLLIKPDGTI	TWGAAQAVQP	FGNILQVVEI
Consensus	*****	*****	*****	*****	*****
451					
msa237615.2{328_1169NT}	TGRDLYKALN	EQYDQKQNF	LQIAGLRYTY	TDNKEGGEET	PFKVVKAYKS
msa237615.2{328_2603}	TGRDLYKALN	EQYDQKQNF	LQIAGLRYTY	TDNKEGGEET	PFKVVKAYKS
msa237615.2{328_A909}	TGRDLYKALN	EQYDQKQNF	LQIAGLRYTY	TDNKEGGEET	PFKVVKAYKS
msa237615.2{328_M732}	TGRDLYKALN	EQYDQKQNF	LQIAGLRYTY	TDNKEGGEET	PFKVVKAYKS
msa237615.2{328_COH1}	TGRDLYKALN	EQYDQKQNF	LQIAGLRYTY	TDNKEGGEET	PFKVVKAYKS

Table 71: Comparative Sequences relating to SAG1333

msa237615.2{328_M781}	TGRDLYKALN	EQYDQKQNF	LQIAGLRYTY	TDNKEGGEET	PFKVVKAYKS
msa237615.2{328_H36B}	TGRDLYKALN	EQYDQKQNF	LQIAGLRYTY	TDNKEGGEET	PFKVVKAYKS
msa237615.2{328_JM9130013}	TGRDLYKALN	EQYDQKQNF	LQIAGLRYTY	TDNKEGGEET	PFKVVKAYKS
msa237615.2{328_18RS21}	TGRDLYKALN	EQYDQKQNF	LQIAGLRYTY	TDNKEGGEET	PFKVVKAYKS
msa237615.2{328_090}	TGRDLYKALN	EQYDQKQNF	LQIAGLRYTY	TDNKEGGEET	PFKVVKAYKS
msa237615.2{328_CJB110}	TGRDLYKALN	EQYDQKQNF	LQIAGLRYTY	TDNKEGGEET	PFKVVKAYKS
Consensus	*****	*****	*****	*****	*****
501					
msa237615.2{328_1169NT}	NGEEINPDAK	YKLVINDFLF	GGGDGFASFR	NAKLLGAINP	DTEVFMAYIT
msa237615.2{328_2603}	NGEEINPDAK	YKLVINDFLF	GGGDGFASFR	NAKLLGAINP	DTEVFMAYIT
msa237615.2{328_A909}	NGEEINPDAK	YKLVINDFLF	GGGDGFASFR	NAKLLGAINP	DTEVFMAYIT
msa237615.2{328_M732}	NGEEINPDAK	YKLVINDFLF	GGGDGFASFR	NAKLLGAINP	DTEVFMAYIT
msa237615.2{328_COH1}	NGEEINPDAK	YKLVINDFLF	GGGDGFASFR	NAKLLGAINP	DTEVFMAYIT
msa237615.2{328_M781}	NGEEINPDAK	YKLVINDFLF	GGGDGFASFR	NAKLLGAINP	DTEVFMAYIT
msa237615.2{328_H36B}	NGEEINPDAK	YKLVINDFLF	GGGDGFASFR	NAKLLGAINP	DTEVFMAYIT
msa237615.2{328_JM9130013}	NGEEINPDAK	YKLVINDFLF	GGGDGFASFR	NAKLLGAINP	DTEVFMAYIT
msa237615.2{328_18RS21}	NGEEINPDAK	YKLVINDFLF	GGGDGFASFR	NAKLLGAINP	DTEVFMAYIT
msa237615.2{328_090}	NGEEINPDAK	YKLVINDFLF	GGGDGFASFR	NAKLLGAINP	DTEVFMAYIT
msa237615.2{328_CJB110}	NGEEINPDAK	YKLVINDFLF	GGGDGFASFR	NAKLLGAINP	DTEVFMAYIT
Consensus	*****	*****	*****	*****	*****
551					
msa237615.2{328_1169NT}	DLEKAGKKVS	vPNNKPKIYV	TMKMNVTIT	QNDGThSIik	KLYLDRQGNi
msa237615.2{328_2603}	DLEKAGKKVS	vPNNKPKIYV	TMKMNVTIT	QNDGThSIik	KLYLDRQGNi
msa237615.2{328_A909}	DLEKAGKKVS	vPNNKPKIYV	TMKMNVTIT	QNDGTySIik	KLYLDRQGNi
msa237615.2{328_M732}	DLEKAGKKVS	iPNNKPKIYV	TMKMNVTIT	QNDGTySIik	KLYLDRQGNi
msa237615.2{328_COH1}	DLEKAGKKVS	iPNNKPKIYV	TMKMNVTIT	QNDGTySIik	KLYLDRQGNi
msa237615.2{328_M781}	DLEKAGKKVS	iPNNKPKIYV	TMKMNVTIT	QNDGTySIik	KLYLDRQGNi
msa237615.2{328_H36B}	DLEKAGKKVS	vPNNKPKIYV	TMKMNVTIT	QNDGTySIik	KLYLDRQGNi
msa237615.2{328_JM9130013}	DLEKAGKKVS	vPNNKPKIYV	TMKMNVTIT	QNDGTySIie	KLYLDRQGNi
msa237615.2{328_18RS21}	DLEKAGKKVS	vPNNKPKIYV	TMKMNVTIT	QNDGTySIik	KLYLDRQGNi
msa237615.2{328_090}	DLEKAGKKVS	vPNNKPKIYV	TMKMNVTIT	QNDGThSIik	KLYLDRQGNi
msa237615.2{328_CJB110}	DLEKAGKKVS	vPNNKPKIYV	TMKMNVTIT	QNDGThSIik	KLYLDRQGNi
Consensus	*****	*****	*****	*****	*****
601					
msa237615.2{328_1169NT}	VAQEIVSDTL	NQTKSKSTKI	NPVTTIHKKQ	LHQFTAINPM	RNYGKPSNST
msa237615.2{328_2603}	VAQEIVSDTL	NQTKSKSTKI	NPVTTIHKKQ	LHQFTAINPM	RNYGKPSNST
msa237615.2{328_A909}	VAQEIVSDTL	NQTKSKSTKI	NPVTTIHKKQ	LHQFTAINPM	RNYGKPSNST
msa237615.2{328_M732}	VAQEIVSDTL	NQTKSKSTKI	NPVTTIHKKQ	LHQFTAINPM	RNYGKPSNST
msa237615.2{328_COH1}	VAQEIVSDTL	NQTKSKSTKI	NPVTTIHKKQ	LHQFTAINPM	RNYGKPSNST
msa237615.2{328_M781}	VAQEIVSDTL	NQTKSKSTKI	NPVTTIHKKQ	LHQFTAINPM	RNYGKPSNST
msa237615.2{328_H36B}	VAQEIVSDTL	NQTKSKSTKI	NPVTTIHKKQ	LHQFTAINPM	RNYGKPSNST
msa237615.2{328_JM9130013}	VAQEIVSDTL	NQTKSKSTKI	NPVTTIHKKQ	LHQFTAINPM	RNYGKPSNST
msa237615.2{328_18RS21}	VAQEIVSDTL	NQTKSKSTKI	NPVTTIHKKQ	LHQFTAINPM	RNYGKPSNST
msa237615.2{328_090}	VAQEIVSDTL	NQTKSKSTKI	NPVTTIHKKQ	LHQFTAINPM	RNYGKPSNST
msa237615.2{328_CJB110}	VAQEIVSDTL	NQTKSKSTKI	NPVTTIHKKQ	LHQFTAINPM	RNYGKPSNST
Consensus	*****	*****	*****	*****	*****
651					
msa237615.2{328_1169NT}	TVKS-----	-----	-----	-----	-----
msa237615.2{328_2603}	TVKSKQlpkt	nseygqsflm	svfgvgligi	alntkkkchmk	-----
msa237615.2{328_A909}	TVKSKQ----	-----	-----	-----	-----
msa237615.2{328_M732}	TVKSKQ----	-----	-----	-----	-----
msa237615.2{328_COH1}	TVKS-----	-----	-----	-----	-----
msa237615.2{328_M781}	TVKS-----	-----	-----	-----	-----
msa237615.2{328_H36B}	TVKS-----	-----	-----	-----	-----
msa237615.2{328_JM9130013}	TVKSK-----	-----	-----	-----	-----
msa237615.2{328_18RS21}	TVKSK-----	-----	-----	-----	-----
msa237615.2{328_090}	TVKSKQ----	-----	-----	-----	-----
msa237615.2{328_CJB110}	TVKS-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
690					

Table 72: Comparative Sequences relating to SAG0941

SEQ ID NO. 7201

STRAIN 2603

ATGAATAAACGCGTAAAAATCGTTGCAACACTTGGTCCTGCGGTTGAATTCCGTGGTG
 GTAAGAAGTTTGGTGAGTCTGGATACTGGGGTGAAAGCCTTGACGTAGAAGCTTCAGCAG
 AAAAAATTGCTCAATTGATTAAAGAAGGTGCTAACGTTTTCCGTTTCAACTTCTCACATG
 GAGATCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTGTAAGCAGAAGAGATTGCAG
 GACAAAAAGTTGGCTTCCCTCCTTGATACTAAAGGACCTGAAATTTCGTACAGAAGCTTTTG
 AAGATGGTGACAGATTTCCATTTCATATACAACAGGTACAAAATTACGTGTTGCTACTAAGC
 AAGGTATCAAATCAACTCCAGAAGTGATTGCATTGAATGTTGCTGGTGGACTTGACATCT
 TTGATGACGTTGAAGTTGGTAAGCAAATCCTTGTTGATGATGGTAACTAGGTCTTACTG
 TGTGTCAAAAGATAAAGACACTCGTGAATTTGAAGTAGTTGTTGAGAATGATGGCCTTA
 TTGGTAAACAAAAAGGTGTAACATCCCTTATACTAAAATTCTTTCCCAGCACTTGCAG
 AACGCGATAATGCTGATATCCGTTTTGGACTTGAGCAAGGACTTAACTTTATTGCTATCT
 CATTTGTACGTACTGCTAAAGATGTTAATGAAGTTCGTGCTATTTGTGAAGAACTGGsm
 ATGGACACGTTAAGTTGTTTGCTAAAATTGAAAATCAACAAGGTATCGATAATATTGATG
 AGATTATCGAAGCAGCAGATGGTATTATGATTGCTCGTGGTGATATGGGTATCGAAGTTC
 CATTTGAAATGGTTCCAGTTTACCAAAAAATGATCATTACTAAAGTTAATGCAGCTGGTA
 AAGCAGTTATTACAGCAACAAATATGCTTgAAACAATGACTGATAAACCACGTGCGACTC
 GTTCAGAAGTATCTGATGTCTTCAATGCTGTTATTGATGGTACTGATGCTACAATGCTTT
 CAGGTGAGTCAGCTAATGGTAAATACCCAGTTGAGTCAGTTCGTACAATGGCTACTATTG
 ATAAAAATGCTCAAACATTACTCAATGAGTATGGTCGCTTAGACTCATCTGCATTCCAC
 GTAATAACAAAACCTGATGTTATTGCATCTGCGGTTAAAGATGCAACACACTCAATGGATA
 TCAAACTTGTGTTGAACAATTACTGAAACAGGTAAATACAGCTCGTGCCATTTCTAAATTCC
 GTCCAGATGCAGACATTTTGGCTGTTACATTTGATGAAAAAGTACAACGTTCAATTGATGA
 TTAAGTGGGGTGTATCCCTGTCTTGCAGACAAACCAGCATCTACAGATGATATGTTTG
 AGGTGTCAGAACGTGTAGCACTTGAAGCAGGATTTGTTGAATCAGGCGATAATATCGTTA
 TCGTTGCAGGTGTTCTGTAGGTACAGGTGGAACATAACAATGCGTGTTCGTACTGTTA
 AA

SEQ ID NO. 7202

STRAIN 090

AATAAACGCGTAAAAATCGTTGCAACACT

TGGTCCTGCGGTAGAATTCCGTGGTGGTAAGAAGTTTGGTGAGTCTGGAT
 ACTGGGGTGAAAGCCTTGACGTAGAAGCTTCAGCAGAAAAAATTGCTCAA
 TTGATTAAAGAAGGTGCTAACGTTTTCCGTTTCAACTTCTCACATGGAGA
 TCGTGTGAGCAAGGAGCTCGTATGGCTACTGTTGTAAGCAGAAGAGA
 TTGCAGGACAAAAAGTTGGCTTCCCTCCTTGATACTAAAGGACCTGAAATT
 CGTACAGAAGCTTTTGAAGATGGTTGAGTTTCCATTTCATATACAACAGG
 TACAGAATTACGTGTTGCTACTAAGCAAGGTATCAAATCAACTCCAGAAG
 TGATTGCATTGAATGTTGCTGGTGGACTTGACATCTTTGATGACGTTGAA
 GTTGGTAAGCAAATCCTTGTGTTGATGATGGTAACTAGGTCTTACTGTGTT
 TGCAAAAGATAAAGACACTCgTGAATTTGAAGTAGTTGTTGAGAATGATG
 GCCTTATTGGTAAACAaaaaGGTGTAAACATCCCTTATACTAaAATTCTT
 TTCCCAgCACITGCGAAGCGGATAATGCTGATATCCGTTTTGGACTTGA
 GCAAGGACTTAACTTTATTGCTATCTCATTGTTACGTACTGCTAAAGATG
 TTAATGAAGTTTCGTGCTATTGTTGAAGAACTGGCAATGGACATGTTAAG
 TTGTTTGCTAAAATTGAAAATCAACAAGGTATCGATAATATTGATGAGAT
 TATCGAAGCAGCAGATGGTATTATGATTGCTCGTGGTGATATGGGTATCG
 AAGTTCCATTGGAATGGTTCCAGTTTACCAAAAAATGATCATTACTAAA
 GTTAATGCAGCTGGTAAAGCAGTTATTACAGCAACAAATATGCTTGAAAC
 AATGACTGATAAACCACGTGCGACTCGTTCAGAAGTATCTGATGTCTTCA
 ATGCTGTTATTGATGGTACTGATGCTACAATGCTTTCAGGTGAGTCAGCT
 AATGGTAAATACCCAGTTGAGTCAGTTCGTACAATGGCTACTATTGATAA
 AAATGCTCAAACATTACTCAATGAGTATGGTCGCTTAGACTCATCTGCAT
 TCCCACGTAATAACAAAACCTGATGTTATTGCATCTGCGGTTAAAGATGCA
 ACACACTCAATGGATATCAAACCTGTTGTGACAATTACTGAAACAGGTAA
 TACAGCTCGTGCCATTTCTAAATCCGTCCAGATGCAGACATTTTGGCTG
 TTACATTTGATGAAAAAGTACAACGTTCAATTGATGATTAACTGGGGTGT
 ATCCCTGTCTTGCAGACAAACCAGCATCTACAGATGATATGTTTGAGGT
 TGCAGAACGTGTAGCACTTGAAGCAGGACTTGTGTAATCAGGCGATAATA
 TCGTTATCGTTGCAGGTGTTCTGTAGGTACAGGTGGAACATAACAATG
 CGTGTTCGTACTGTAAA

SEQ ID NO. 7203

STRAIN A909

AATAAACGCGTAAAAATCGTTGCAACACTTGGTC

CTGCGGTTGAATTCCGTGGTGGTAAGAAGTTTGGTGAGTCTGGATACTGG
 GGTGAAAGCCTTGACGTAGAAGCTTCAGCAGAAAAAATTGCTCAATTGAT
 TAAAGAAGGTGCTAACGTTTTCCGTTTCAACTTCTCACATGGAGATCATG
 CTGAGCAAGGAGCTCGTATGGCTACTGTTGTAAGCAGAAGAGATTGCA
 GGACAAAAAGTTGGCTTCCCTCCTTGATACTAAAGGACCTGAAATTTCGTAC
 AGAAGCTTTTGAAGATGGTGACAGATTTCCATTTCATATACAACAGGTACAA
 AATTACGTGTTGCTACTAAGCAAGGTATCAAATCAACTCCAGAAGTGATT
 GCATTGAATGTTGCTGGTGGACTTGACATCTTTGATGACGTTGAAGTTGG
 TAAGCAAATCCTTGTGATGATGGTAACTAGGTCTTACTGTGTTTGCAA
 AAGATAAAGACACTCGTGAATTTGAAGTAGTTGTTGAGAATGATGGCCTT
 ATTGGTAAACAAAAAGGTGTAACATCCCTTATACTAAAATTCTTTCCC
 AGCACTTGCAAGAACGCGATAATGCTGATATCCGTTTTGGACTTGAGCAAG
 GACTTAACTTTATTGCTATCTCATTGTTACGTACTGCTAAAGATGTTAAT
 GAAGTTTCGTGCTATTGTTGAAGAACTGGCAATGGACACGTTAAGTTGTT
 TGCTAAAATTGAAAATCAACAAGGTATCGATAATATTGATGAGATTATCG
 AAGCAGCAGATGGTATTATGATTGCTCGTGGTGATATGGGTATCGAAGTT
 CCATTTGAAATGGTTCCAGTTTACCAAAAAATGATCATTACTAAAGTTAA

Table 72: Comparative Sequences relating to SAG0941

TGCAGCTGGTAAAGCAGTTATTACAGCAACAAATATGCTTGAAACAATGA
 CTGATAAACCCACGTGCGACTCGTTCAGAAGTATCTGATGTCTTCAATGCT
 GTTATTGATGGTACTGATGCTACAATGCTTTCAGGTGAGTCAGCTAATGG
 TAAATACCCAGTTGAGTCAGTTTCGTACAATGGCTACTATTGATAAAAAATG
 CTCAAACATTACTCAATGAGTATGGTCGCTTAGACTCATCTGCATTCCCA
 CGTAATAACAAAACTGATGTTATTGTCATCTGCGGTTAAAGATGCAACACA
 CTCAATGGATATCAAACCTTGTGTAACAATTACTGAAACAGGTAATACAG
 CTCGTGCCATTTCTAAATTCCTGCCAGATGCAGACATTTTGGCTGTTACA
 TTTGATGAAAAAGTACAACGTTTATTGATGATTAACCTGGGGTGTATCCC
 TGTCCCTGCAGACAAACCAGCATCTACAGATGATATGTTTGAGGTTGCAG
 AACGTGTAGCACTTGAAGCAGGATTTGTTGAATCAGGCGATAATATCGTT
 ATCGTTGCAGGTGTTCCCTGTAGGTACAGGTGGAAC TAACACAATGCGTGT
 TCGTACTGTTAAA

SEQ ID NO. 7204

STRAIN H36B

AATAAACGCGTAAAAATCGTTGCAAC

ACTTGGTCCTGCGGTTGAATTCCGTGGTGGTAAGAAGTTTGGTGAGTCTG
 GATACTGGGGTGAAAGCCTTGACGTAGAAGCTTCAGCAGAAAAAATTGCT
 CAATTGATTAAAGAAGGTGCTAACGTTTTCCGTTTCACTTCTCACATGG
 AGATCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTTCGTAAAGCAGAAG
 AGATTGCAGGACAAAAAGTTGGCTTCCTCCTTGATACTAAAGGACCTGAA
 ATTTCGTACAGAACTTTTGAAGATGGTGCAGATTTCCATTATATACAAC
 AGGTACAAAAATTACGTGTTGCTACTAAGCAAGGTATCAAATCAACTCCAG
 AAGTGATTGCATTGAATGTTGCTGGTGGACTTGACATCTTTGATGACGTT
 GAAGTTGGTAAGCAAATCCTTGTGATGATGGTAAACTAGGTCTTACTGT
 GTTTGC AAAAGATAAAGACACTCGTGAATTTGAAGTAGTTGTTGAGAATG
 ATGGCCTTATTGGTAAACAAAAAGGTGTAAACATCCCTTATACTAAAATT
 CCTTTCAGCACTTGCAAGACGCGATAATGCTGATATCCGTTTTGGACT
 TGAGCAAGGACTTAACCTTATTGCTATCTCATTTGTACGTACTGCTAAAG
 ATGTTAATGAAGTTTCGTGCTATTTGTGAAGAACTGGCAATGGACACGTT
 AAGTTGTTTGTCTAAAATTGAAAATCAACAAGGTATCGATAATATTGATGA
 GATTATCGAAGCAGCAGATGGTATTATGATTGCTCGTGGTGATATGGGTA
 TCGAAGTTCCATTTGAAATGGTTCAGTTTACCAAAAAATGATCATTACT
 AAAGTTAATGCAGCTGGTAAAGCAGTTATTACAGCAACAAATATGCTTGA
 AACAAATGAaTGATAAACCACGTGCGACTCGTTTCAAGATATCTGATGTCT
 TCAATGCTGTTATTGATGGTACTGATGCTACAATGCTTTCAGGTGAGTCA
 GCTAATGGTAAATACCCAGTTGAGTCAGTTTCGTACAATGGCTACTATTGA
 TAAAAATGCTCAAACATTACTCAATGAGTATGGTCGCTTAGACTCATCTG
 CATTCCCACGTAATAACAAAACCTGATGTTATTGCATCTGCGGTTAAAGAT
 GCAACACACTCAATGGATATCAAACCTTGTGTAACAATTACTGAAACAGG
 TAATACAGCTCGTGCCATTTCTAAATTCCGTCCAGATGCAGACATTTTGG
 CTGTTACATTTGATGAAAAAGTACAACGTTTATTGATGATTAACTGGGGT
 GTTATCCCTGTCTTGCAGACAAACCAGCATCTACAGATGATATGTTTGA
 GGTTGCAGAACGTGTAGCACTTGAAGCAGGATTTGTTGAATCAGGCGATA
 ATATCGTTATCGTTGCAGGTGTTCCCTGTAGGTACAGGTGGAAC TAACACA
 ATGCGTGTTTCGTACTGTTAAA

SEQ ID NO. 7205

STRAIN 18RS21

AATAAACGCGTAAAAATCGTTGCAAC

ACTTGGTCCTGCGGTTGAATTCCGTGGTGGTAAGAAGTTTGGTGAGTCTG
 GATACTGGGGTGAAAGCCTTGACGTAGAAGCTTCAGCAGAAAAAATTGCT
 CAATTGATTAAAGAAGGTGCTAACGTTTTCCGTTTCACTTCTCACATGG
 AGATCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTTCGTAAAGCAGAAG
 AGATTGCAGGACAAAAAGTTGGCTTCCTCCTTGATACTAAAGGACCTGAA
 ATTTCGTACAGAACTTTTTGAAGATGGTGCAGATTTCCATTATATACAAC
 AGGTACAAAAATTACGTGTTGCTACTAAGCAAGGTATCAAATCAACTCCAG
 AAGTGATTGCATTGAATGTTGCTGGTGGACTTGACATCTTTGATGACGTT
 GAAGTTGGTAAGCAAATCCTTGTGATGATGGTAAACTAGGTCTTACTGT
 GTTTGCAAAAGATAAAGACACTCGTGAATTTGAAGTAGTTGTTGAGAATG
 ATGGCCTTATTGGTAAACAAAAAGGTGTAAACATCCCTTATACTAAAATT
 CCTTTCAGCACTTGCAAGACGCGATAATGCTGATATCCGTTTTGGACT
 TGAGCAAGGACTTAACCTTATTGCTATCTCATTTGTACGTACTGCTAAAG
 ATGTTAATGAAGTTTCGTGCTATTTGTGAAGAACTGGCAATGGACACGTT
 AAGTTGTTTGTCTAAAATTGAAAATCAACAAGGTATCGATAATATTGATGA
 GATTATCGAAGCAGCAGATGGTATTATGATTGCTCGTGGTGATATGGGTA
 TCGAAGTTCCATTTGAAATGGTTCAGTTTACCAAAAAATGATCATTACT
 AAAGTTAATGCAGCTGGTAAAGCAGTTATTACAGCAACAAATATGCTTGA
 AACAAATGAaTGATAAACCACGTGCGACTCGTTTCAAGATATCTGATGTCT
 TCAATGCTGTTATTGATGGTACTGATGCTACAATGCTTTCAGGTGAGTCA
 GCTAATGGTAAATACCCAGTTGAGTCAGTTTCGTACAATGGCTACTATTGA
 TAAAAATGCTCAAACATTACTCAATGAGTATGGTCGCTTAGACTCATCTG
 CATTCCCACGTAATAACAAAACCTGATGTTATTGCATCTGCGGTTAAAGAT
 GCAACACACTCAATGGATATCAAACCTTGTGTAACAATTACTGAAACAGG
 TAATACAGCTCGTGCCATTTCTAAATTCCGTCCAGATGCAGACATTTTGG
 CTGTTACATTTGATGAAAAAGTACAACGTTTATTGATGATTAACTGGGGT
 GTTATCCCTGTCTTGCAGACAAACCAGCATCTACAGATGATATGTTTGA
 GGTTGCAGAACGTGTAGCACTTGAAGCAGGATTTGTTGAATCAGGCGATA
 ATATCGTTATCGTTGCAGGTGTTCCCTGTAGGTACAGGTGGAAC TAACACA
 ATGCGTGTTTCGTACTGTTAAA

SEQ ID NO. 7206

Table 72: Comparative Sequences relating to SAG0941**STRAIN M732**

AATAAACGCGTAAAAATCGTTGCAAC
 ACTTGGTCCTGCGGTAGAATTCCGTGGTGGTAAGAAGTTTGGTGAGTCTG
 GATACTGGGGTGAAAGCCTTGACGTAGAAGCTTCAGCAGAAAAAATTGCT
 CAATTGATTAAAGAAGGTGCTAACGTTTTCCGTTTCAACTTCTCACATGG
 AGATCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTGTAAGCAGAAG
 AGATTGCAGGACAAAAAGTTGGCTTCCTCCTTGATACTAAAGGACCTGAA
 ATTTCGTACAGAACTTTTTGAAGATGGTGCAGATTTCCATTTCATATACAAC
 AGGTACAAAAATTACGTGTTGCTACTAAGCAAGGTATCAAATCAACTCCAG
 AAGTGATTGCATTGAATGTTGCTGGTGGACTTGACATCTTTGATGACGTT
 GAAGTTGGTAAGCAAATCCTTGTTGATGATGGTAAACTAGGTCTTACTGT
 GTTTGCAAAAAGATAAAGACACTCGTGAATTTGAAGTAGTTGTTGAGAATG
 ATGGCCTTATTGGTAAACAAAAAGGTGTAAACATCCCTTATACTAAAATT
 CCTTTCCAGCACTTGACAGAACGCGATAATGCTGATATCCGTTTTGGACT
 TGAGCAAGGACTTAACTTTATTGCTATCTCATTTGTACGTACTGCTAAAG
 ATGTTAATGAAGTTTCGTGCTATTTGTGAAGAACTGGCAATGGACACGTT
 AAGTTGTTTGTCTAAAATTGAAAATCAACAAGGTATCGATAATATTGATGA
 GATTATCGAAGCAGCAGATGGTATTATGATTGCTCGTGGTGATATGGGTA
 TCGAAGTTCCATTTGAAATGGTTCCAGTTTACCAAAAAATGATCATTACT
 AAAGTTAATGCAGCTGGTAAAGCAGTTATTACAGCAACAAATATGCTTGA
 AACAAATGACTGATAAACCACGTGCGACTCGTTTCAAGATATCTGATGTCT
 TCAATGCTGTTATTGATGGTACTGATGCTACAATGCTTTTCCAGGTGAGTCA
 GCTAATGGTAAATACCCAGTTGAGTCAGTTTCGTACAATGGCTACTATTGA
 TAAAAATGCTCAAACATTACTCAATGAGTATGGTTCGCTTAGACTCATCTG
 CATTTCCACGTAATAACAAAACCTGATGTTATTGTCATCTGCGGTTAAAGAT
 GCAACACACTCAATGGATATCAAACCTTGTTGTAAACAATTACTGAAACAGG
 TAATACAGCTCGTGCCATTTCTAAATTCGGTCCAGATGCAGACATTTTGG
 CTGTTACATTTGATGAAAAAGTACAACGTTTATTGATGATTAACTGGGGT
 GTTATCCCTGTCCTTGACAGACAAACCAGCATCTACAGATGATATGTTTGA
 GGTGTCAGAACGTGTAGCACTTGAAGCAGGACTTGTGTAATCAGGCGATA
 ATATCGTTATCGTTGCAGGTGTTCTGTAGGTACAGGTGGAACCTAACACA
 ATGCGTGTTTCGTACTGTTAAA

SEQ ID NO. 7207**STRAIN COH1**

AATAAACGCGTAAAAATCGTTGCAAC
 ACTTGGTCCTGCGGTAGAATTCCGTGGTGGTAAGAAGTTTGGTGAGTCTG
 GATACTGGGGTGAAAGCCTTGACGTAGAAGCTTCAGCAGAAAAAATTGCT
 CAATTGATTAAAGAAGGTGCTAACGTTTTCCGTTTCAACTTCTCACATGG
 AGATCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTGTAAGCAGAAG
 AGATTGCAGGACAAAAAGTTGGCTTCCTCCTTGATACTAAAGGACCTGAA
 ATTTCGTACAGAACTTTTTGAAGATGGTGCAGATTTCCATTTCATATACAAC
 AGGTACAAAAATTACGTGTTGCTACTAAGCAAGGTATCAAATCAACTCCAG
 AAGTGATTGCATTGAATGTTGCTGGTGGACTTGACATCTTTGATGACGTT
 GAAGTTGGTAAGCAAATCCTTGTTGATGATGGTAAACTAGGTCTTACTGT
 GTTTGCAAAAAGATAAAGACACTCGTGAATTTGAAGTAGTTGTTGAGAATG
 ATGGCCTTATTGGTAAACAAAAAGGTGTAAACATCCCTTATACTAAAATT
 CCTTTCCAGCACTTGACAGAACGCGATAATGCTGATATCCGTTTTGGACT
 TGAGCAAGGACTTAACTTTATTGCTATCTCATTTGTACGTACTGCTAAAG
 ATGTTAATGAAGTTTCGTGCTATTTGTGAAGAACTGGCAATGGACACGTT
 AAGTTGTTTGTCTAAAATTGAAAATCAACAAGGTATCGATAATATTGATGA
 GATTATCGAAGCAGCAGATGGTATTATGATTGCTCGTGGTGATATGGGTA
 TCGAAGTTCCATTTGAAATGGTTCCAGTTTACCAAAAAATGATCATTACT
 AAAGTTAATGCAGCTGGTAAAGCAGTTATTACAGCAACAAATATGCTTGA
 AACAAATGACTGATAAACCACGTGCGACTCGTTTCAAGATATCTGATGTCT
 TCAATGCTGTTATTGATGGTACTGATGCTACAATGCTTTCAGGTGAGTCA
 GCTAATGGTAAATACCCAGTTGAGTCAGTTTCGTACAATGGCTACTATTGA
 TAAAAATGCTCAAACATTACTCAATGAGTATGGTTCGCTTAGACTCATCTG
 CATTTCCACGTAATAACAAAACCTGATGTTATTGTCATCTGCGGTTAAAGAT
 GCAACACACTCAATGGATATCAAACCTTGTTGTAAACAATTACTGAAACAGG
 TAATACAGCTCGTGCCATTTCTAAATTCGGTCCAGATGCAGACATTTTGG
 CTGTTACATTTGATGAAAAAGTACAACGTTTATTGATGATTAACTGGGGT
 GTTATCCCTGTCCTTGACAGACAAACCAGCATCTACAGATGATATGTTTGA
 GGTGTCAGAACGTGTAGCACTTGAAGCAGGACTTGTGTAATCAGGCGATA
 ATATCGTTATCGTTGCAGGTGTTCTGTAGGTACAGGTGGAACCTAACACA
 ATGCGTGTTTCGTACTGTTAAA

SEQ ID NO. 7208**STRAIN M781**

AATAAACGCGTAAAAATCGTTGCAAC
 ACTTGGTCCTGCGGTAGAATTCCGTGGTGGTAAGAAGTTTGGTGAGTCTG
 GATACTGGGGTGAAAGCCTTGACGTAGAAGCTTCAGCAGAAAAAATTGCT
 CAATTGATTAAAGAAGGTGCTAACGTTTTCCGTTTCAACTTCTCACATGG
 AGATCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTGTAAGCAGAAG
 AGATTGCAGGACAAAAAGTTGGCTTCCTCCTTGATACTAAAGGACCTGAA
 ATTTCGTACAGAACTTTTTGAAGATGGTGCAGATTTCCATTTCATATACAAC
 AGGTACAAAAATTACGTGTTGCTACTAAGCAAGGTATCAAATCAACTCCAG
 AAGTGATTGCATTGAATGTTGCTGGTGGACTTGACATCTTTGATGACGTT
 GAAGTTGGTAAGCAAATCCTTGTTGATGATGGTAAACTAGGTCTTACTGT
 GTTTGCAAAAAGATAAAGACACTCGTGAATTTGAAGTAGTTGTTGAGAATG
 ATGGCCTTATTGGTAAACAAAAAGGTGTAAACATCCCTTATACTAAAATT
 CCTTTCCAGCACTTGACAGAACGCGATAATGCTGATATCCGTTTTGGACT
 TGAGCAAGGACTTAACTTTATTGCTATCTCATTTGTACGTACTGCTAAAG

Table 72: Comparative Sequences relating to SAG0941

ATGTTAATGAAGTTCGTGCTATTTGTGAAGAACTGGCAATGGACACGTT
 AAGTTGTTTGGCTAAAATTGAAAATCAACAAGGTATCGATAATATTGATGA
 GATTATCGAAGCAGCAGATGGTATTATGATTGCTCGTGGTGATATGGGTA
 TCGAAGTTCATTTGAAATGGTTCAGTTTACCAAAAAATGATCATTACT
 AAAGTTAATGCAGCTGGTAAAGCAGTTATTACAGCAACAAATATGCTTGA
 AACAATGACTGATAAACCACGTGCGACTCGTTCAGAAGTATCTGATGTCT
 TCAATGCTGTTATTGATGGTACTGATGCTACAATGCTTTAGGTGAGTCA
 GCTAATGGTAAATACCCAGTTGAGTCAGTTCGTACAATGGCTACTATTGA
 TAAAAATGCTCAAACATTACTCAATGAGTATGGTCGCTTAGACTCATCTG
 CATTCCCACGTAATAACAAAACCTGATGTTATTGCATCTGCGGTTAAAGAT
 GCAACACACTCAATGGATATCAAACCTGTTGTAACAATTACTGAAACAGG
 TAATACAGCTCGTGCCATTTCTAAGTTCGGTCCAGATGCAGACATTTTGG
 CTGTTACATTTGATGAAAAAGTACAACGTTTATTGATGATTAACTGGGGT
 GTTATCCCTGTCTTGCAGACAAACCAGCATCTACAGATGATATGTTTGA
 GGTGTCAGAACGTGTAGCACTTGAAGCAGGACTTGTGTAATCAGGCGATA
 ATATCGTTATCGTTGCAGGTGTTCTGTAGGTACAGGTGGAACTAACACA
 ATGCGTGTTCGTACTGTTAAA

SEQ ID NO. 7209

STRAIN CJB110

AATAAACGCGTAAAAATCGTTGCAAC

ACTTGGTCCTGCGGTTGAATTCGGTGGTGAAGAAGTTTGGTGAGTCTG
 GATACTGGGGTGAAAGCCTTGACGTAGAAGCTTCAGCAGAAAAAATGCT
 CAATTGATTAAAGAAGGTGCTAACGTTTTCCGTTTCAACTTCTCATATGG
 AGATCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTGTAAGCAGAAG
 AGATTGCAGGACAAAAAGTTGGCTTCTCCTTGATACTAAAGGACCTGAA
 ATTTCGTACAGAACTTTTTGAAGATGGTGCAGATTTCCATTATATACAAC
 AGGTACAAAATTACGTGTTGCTACTAAGCAAGGTATCAAATCAACTCCAG
 AAGTGATTGCATTGAATGTTGCTGGTGGACTTGACATCTTGATGACGTT
 GAAGTTGGTAAGCAAATCCTTGTTGATGATGGTAAACTAGGTCTTACTGT
 GTTTGCAAAAGATAAAGACACTCGTGAATTTGAAGTAGTTGTTGAGAATG
 ATGGCCTTATGGTAAACAAAAAGGTGTAAACATCCCTTATACTAAAATT
 CCTTTCCAGCACTTGCAAGACGCGATAATGCTGATATCCGTTTGGACT
 TGAACAAGGACTTAACTTTATTGCTATCTCATTTGTACGTACTGCTAAAG
 ATGTTAATGAAGTTCTGCTATTTGTGAAGAACTGGCAATGGACACGTT
 AAGTTGTTTGGCTAAAATTGAAAATCAACAAGGTATCGATAATATTGATGA
 GATTATCGAAGCAGCAGATGGTATTATGATTGCTCGTGGTGATATGGGTA
 TCGAAGTTCATTTGAAATGGTTCAGTTTACCAAAAAATGATCATTACT
 AAAGTTAATGCAGCTGGTAAAGCAGTTATTACAGCAACAAATATGCTTGA
 AACAATGACTGATAAACCACGTGCGACTCGTTCAGAAGTATCTGATGTCT
 TCAATGCTGTTATTGATGGTACTGATGCTACAATGCTTTAGGTGAGTCA
 GCTAATGGTAAATACCCAGTTGAGTCAGTTCGTACAATGGCTACTATTGA
 TAAAAATGCTCAAACATTACTCAATGAGTATGGTCGCTTAGACTCATCTG
 CATTCCCACGTAATAACAAAACCTGATGTTATTGCATCTGCGGTTAAAGAT
 GCAACACACTCAATGGATATCAAACCTGTTGTAACAATTACTGAAACAGG
 TAATACAGCTCGTGCCATTTCTAAATTCCGTCCAGATGCAGACATTTTGG
 CTGTTACATTTGATGAAAAAGTACAACGTTTATTGATGATTAACTGGGGT
 GTTATCCCTGTCTTGCAGACAAACCAGCATCTACAGATGATATGTTTGA
 GGTGTCAGAACGTGTAGCACTTGAAGCAGGATTTGTTGAATCAGGCGATA
 ATATCGTTATCGTTGCAGGTGTTCTGTAGGTACAGGTGGAACTAACACA
 ATGCGTGTTCGTACTGTTAAA

SEQ ID NO. 7210

STRAIN 1169NT

AATAAACGCGTAAAAATCGTTGCAAC

ACTTGGTCCTGCGGTAGAATTCCGTGGTGGTAAGAAGTTTGGTGAGTCTG
 GATACTGGGGTGAAAGCCTTGACGTAGAAGCTTCAGCAGAAAAAATGCT
 CAATTGATTAAAGAAGGTGCTAACGTTTTCCGTTTCAACTTCTCATATGG
 AGATCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTGTAAGCAGAAG
 AGATTGCAGGACAAAAAGTTGGCTTCTCCTTGATACTAAAGGACCTGAA
 ATTTCGTACAGAACTTTTTGAAGATGGTGCAGATTTCCATTATATACAAC
 AGGTACAAAATTACGTGTTGCTACTAAGCAAGGTATCAAATCAACTCCAG
 AAGTGATTGCATTGAATGTTGCTGGTGGACTTGACATCTTGATGACGTT
 GAAGTTGGTAAGCAAATCCTTGTTGATGATGGTAAACTAGGTCTTACTGT
 GTTTGCAAAAGATAAAGACACTCGTGAATTTGAAGTAGTTGTTGAGAATG
 ATGGCCTTATTGGTAAACAAAAAGGTGTAAACATCCCTTATACTAAAATT
 CCTTTCCAGCACTTGCAAGACGCGATAATGCTGATATCCGTTTGGACT
 TGAGCAAGGACTTAACTTTATTGCTATCTCATTTGTACGTACTGCTAAAG
 ATGTTAATGAAGTTCTGCTATTTGTGAAGAACTGGCAATGGACACGTT
 AAGTTGTTTGGCTAAAATTGAAAATCAACAAGGTATCGATAATATTGATGA
 GATTATCGAAGCAGCAGATGGTATTATGATTGCTCGTGGTGATATGGGTA
 TCGAAGTTCCATTTGAAATGGTTCAGTTTACCAAAAAATGATCATTACT
 AaAGTTAATGCAGCTGGTAAAGCAGTTATTACAGCAACAAATATGCTTGA
 AACAATGACTGATAAACCACGTGCGACTCGTTCAGAAGTATCTGATGTCT
 TCAATGCTGTTATTGATGGTACTGATGCTACAATGCTTTAGGTGAGTCA
 GCTAATGGTAAATACCCAGTTGAGTCAGTTCGTACAATGGCTACTATTGA
 TAAAAATGCTCAAACATTAATCAATGAGTATGGTCGCTTAGACTCATCTG
 CATTCCCACGTAATAACAAAACCTGATGTTATTGCATCTGCGGTTAAAGAT
 GCAACACACTCAATGGATATCAAACCTGTTGTAACAATTACTGAAACAGG
 TAATACAGCTCGTGCCATTTCTAAATTCCGTCCAGATGCAGACATTTTGG
 CTGTTACATTTGATGAAAAAGTACAACGTTTATTGATGATTAACTGGGGT
 GTTATCCCTGTCTTGCAGACAAACCAGCATCTACAGATGATATGTTTGA
 GGTGTCAGAACGTGTAGCACTTGAAGCAGGACTTGTGTAATCAGGCGATA
 ATATCGTTATCGTTGCAGGTGTTCTGTAGGTACAGGTGGAACTAACACA
 ATGCGTGTTCGTACTGTTAAA

Table 72: Comparative Sequences relating to SAG0941

ATATCGTTATCGTTGCAGGTGTTCTCTGTAGGTACAGGTGGAACCTAACACA
ATGCGTGTTCGTACTGTTAAA

SEQ ID NO. 7211

STRAIN JM9130013

AATAAACGCGTAAAAATCGTTGCAAC

ACTTGGTCCTGCGGTAGAATTCCGTGGTGGTAAGAAGTTTGGTGAGTCTG
GATACTGGGGTGAAAGCCTTGACGTAGAAGCTTCAGCAGAAAAAATTGCT
CAATTGATTAAAGAAGGTGCTAACGTTTTCCGTTTCAACTTCTCACATGG
AGATCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTTCGTAAAGCAGAAG
AGATTGCAGGACAAAAAGTTGGCTTCCTCCTTGATACTAAAGGACCTGAA
ATTTCGTACAGAACTTTTGAAGATGGTTCAGATTTCCATTTCATATACAAC
AGGTACAAAATTACGTGTGCTACTAAGCAAGGTATCAAATCAACTCCAG
AAGTGATTGCATTGAATGTTGCTGGTGGACTTGACATCTTGATGACGTT
GAAGTTGGTAAGCAAATCCTTGTGATGATGGTAAACTAGGTCCTACTGT
GTTTGCAAAGATAAAGACACTCGTGAATTTGAAGTAGTTGTTGAGAATG
ATGGCCTTATTGGTAAACAAAAAGGTGTAACATCCCTTATACTAAAAAT
CCTTTCCAGCACTTGAGAACGCGATAATGCTGATATCCGTTTGGACT
TGAGCAAGGACTTAACTTTATTGCTATCTCATTTGTACGTACTGCTAAAG
ATGTTAATGAAGTTCGTGCTATTTGTGAAGAACTGGCAATGGACATGTT
AAGTTGTTTGCTAAAATTGAAATCAaCAAGGTATCGATAATATTGATGA
GATTATCGAAGCAGCAGATGGTATTATGATTGCTCGTGGTGAATGGGTA
TCGAAGTTCCATTGAAATGGTTCAGTTTACCAAAAAATGATCATTACT
AAAGTTAATGCAGCTGGTAAAGCAGTTATtACAGCAACAAATATGCTTGA
AACAATGACTGATAAACACCGTCCGACTCGTTCAGAAGTATCTGATGTCT
TCAATGCTGTTATTGATGGTACTGATGCTACAATGCTTTCAGGTGAGTCA
GCTAATGGTAAATACCCAGTTGAGTCAGTTTCGTACAATGGCTACTATTGA
TAAAAATGCTCAAACATTACTCAATGAGTATGGTTCGCTTAGACTCATCTG
CATTCCCACGTAATAaCAAACTGATGTTATTGCTCTGCGGTTAAAGAT
GCAACACACTCAATGGATATCAAACCTTGTGTGACAATTACTGAAACAGG
TAATACAGCTCGTGCCATTTCTAAATTCCGTCCAGATGCAGACATTTTGG
CTGTTACATTTGATGAAAAAGTACAACGTTTCAATGATGATTAACCTGGGGT
GTTATCCCTGTCTTGCAGACAAACCAGCATCTACAGATGATATGTTTGA
GGTTGCAGAACGTTGTAgaCTTGAAGCAGGACTTGTGAATCAGGCGATA
ATATCGTTATCGTTGCAGGTGTTCTCTGTAGGTACAGGTGGAACCTAACACA
ATGCGTGTTCGTACTGTTAAA

PRETTY of: /biotmp/msa277466.2{*} February 24, 2003 01:44 ..

	1		50
msa277466.2{330_090}	---AATAAAC	GCGTAAAAAT	CGTTGCAACA CTTGGTCCTG CCGTaGAATT
msa277466.2{330_JM9130013}	---AATAAAC	GCGTAAAAAT	CGTTGCAACA CTTGGTCCTG CCGTaGAATT
msa277466.2{330_18RS21}	---AATAAAC	GCGTAAAAAT	CGTTGCAACA CTTGGTCCTG CCGTtGAATT
msa277466.2{330_2603}	atgAATAAAC	GCGTAAAAAT	CGTTGCAACA CTTGGTCCTG CCGTtGAATT
msa277466.2{330_A909}	---AATAAAC	GCGTAAAAAT	CGTTGCAACA CTTGGTCCTG CCGTtGAATT
msa277466.2{330_H36B}	---AATAAAC	GCGTAAAAAT	CGTTGCAACA CTTGGTCCTG CCGTtGAATT
msa277466.2{330_CJB110}	---AATAAAC	GCGTAAAAAT	CGTTGCAACA CTTGGTCCTG CCGTtGAATT
msa277466.2{330_COH1}	---AATAAAC	GCGTAAAAAT	CGTTGCAACA CTTGGTCCTG CCGTaGAATT
msa277466.2{330_M732}	---AATAAAC	GCGTAAAAAT	CGTTGCAACA CTTGGTCCTG CCGTaGAATT
msa277466.2{330_1169NT}	---AATAAAC	GCGTAAAAAT	CGTTGCAACA CTTGGTCCTG CCGTaGAATT
msa277466.2{330_M781}	---AATAAAC	GCGTAAAAAT	CGTTGCAACA CTTGGTCCTG CCGTaGAATT
Consensus	*****	*****	*****
	51		100
msa277466.2{330_090}	CCGTGGTGGT	AAGAAGTTTG	GTGAGTCTGG ATACTGGGGT GAAAGCCTTG
msa277466.2{330_JM9130013}	CCGTGGTGGT	AAGAAGTTTG	GTGAGTCTGG ATACTGGGGT GAAAGCCTTG
msa277466.2{330_18RS21}	CCGTGGTGGT	AAGAAGTTTG	GTGAGTCTGG ATACTGGGGT GAAAGCCTTG
msa277466.2{330_2603}	CCGTGGTGGT	AAGAAGTTTG	GTGAGTCTGG ATACTGGGGT GAAAGCCTTG
msa277466.2{330_A909}	CCGTGGTGGT	AAGAAGTTTG	GTGAGTCTGG ATACTGGGGT GAAAGCCTTG
msa277466.2{330_H36B}	CCGTGGTGGT	AAGAAGTTTG	GTGAGTCTGG ATACTGGGGT GAAAGCCTTG
msa277466.2{330_CJB110}	CCGTGGTGGT	AAGAAGTTTG	GTGAGTCTGG ATACTGGGGT GAAAGCCTTG
msa277466.2{330_COH1}	CCGTGGTGGT	AAGAAGTTTG	GTGAGTCTGG ATACTGGGGT GAAAGCCTTG
msa277466.2{330_M732}	CCGTGGTGGT	AAGAAGTTTG	GTGAGTCTGG ATACTGGGGT GAAAGCCTTG
msa277466.2{330_1169NT}	CCGTGGTGGT	AAGAAGTTTG	GTGAGTCTGG ATACTGGGGT GAAAGCCTTG
msa277466.2{330_M781}	CCGTGGTGGT	AAGAAGTTTG	GTGAGTCTGG ATACTGGGGT GAAAGCCTTG
Consensus	*****	*****	*****
	101		150
msa277466.2{330_090}	ACGTAGAAGC	TTCAGCAGAA	AAAATTGCTC AATTGATTAA AGAAGGTGCT
msa277466.2{330_JM9130013}	ACGTAGAAGC	TTCAGCAGAA	AAAATTGCTC AATTGATTAA AGAAGGTGCT
msa277466.2{330_18RS21}	ACGTAGAAGC	TTCAGCAGAA	AAAATTGCTC AATTGATTAA AGAAGGTGCT
msa277466.2{330_2603}	ACGTAGAAGC	TTCAGCAGAA	AAAATTGCTC AATTGATTAA AGAAGGTGCT
msa277466.2{330_A909}	ACGTAGAAGC	TTCAGCAGAA	AAAATTGCTC AATTGATTAA AGAAGGTGCT
msa277466.2{330_H36B}	ACGTAGAAGC	TTCAGCAGAA	AAAATTGCTC AATTGATTAA AGAAGGTGCT
msa277466.2{330_CJB110}	ACGTAGAAGC	TTCAGCAGAA	AAAATTGCTC AATTGATTAA AGAAGGTGCT
msa277466.2{330_COH1}	ACGTAGAAGC	TTCAGCAGAA	AAAATTGCTC AATTGATTAA AGAAGGTGCT
msa277466.2{330_M732}	ACGTAGAAGC	TTCAGCAGAA	AAAATTGCTC AATTGATTAA AGAAGGTGCT
msa277466.2{330_1169NT}	ACGTAGAAGC	TTCAGCAGAA	AAAATTGCTC AATTGATTAA AGAAGGTGCT
msa277466.2{330_M781}	ACGTAGAAGC	TTCAGCAGAA	AAAATTGCTC AATTGATTAA AGAAGGTGCT
Consensus	*****	*****	*****
	151		200
msa277466.2{330_090}	AACGTTTTCC	GTTTCAACTT	CTCACATGGA GATCATGCTG AGCAAGGAGC

Table 72: Comparative Sequences relating to SAG0941

msa277466.2{330_JM9130013}	AACGTTTTCC	GTTTCAACTT	CTCACATGGA	GATCATGCTG	AGCAAGGAGC
msa277466.2{330_18RS21}	AACGTTTTCC	GTTTCAACTT	CTCACATGGA	GATCATGCTG	AGCAAGGAGC
msa277466.2{330_2603}	AACGTTTTCC	GTTTCAACTT	CTCACATGGA	GATCATGCTG	AGCAAGGAGC
msa277466.2{330_A909}	AACGTTTTCC	GTTTCAACTT	CTCACATGGA	GATCATGCTG	AGCAAGGAGC
msa277466.2{330_H36B}	AACGTTTTCC	GTTTCAACTT	CTCACATGGA	GATCATGCTG	AGCAAGGAGC
msa277466.2{330_CJB110}	AACGTTTTCC	GTTTCAACTT	CTCACATGGA	GATCATGCTG	AGCAAGGAGC
msa277466.2{330_COH1}	AACGTTTTCC	GTTTCAACTT	CTCACATGGA	GATCATGCTG	AGCAAGGAGC
msa277466.2{330_M732}	AACGTTTTCC	GTTTCAACTT	CTCACATGGA	GATCATGCTG	AGCAAGGAGC
msa277466.2{330_1169NT}	AACGTTTTCC	GTTTCAACTT	CTCACATGGA	GATCATGCTG	AGCAAGGAGC
msa277466.2{330_M781}	AACGTTTTCC	GTTTCAACTT	CTCACATGGA	GATCATGCTG	AGCAAGGAGC
Consensus	*****	*****	*****	*****	*****
msa277466.2{330_090}	TCGTATGGCT	ACTGTTTCGTA	AAGCAGAAGA	GATTGCAGGA	CAAAAAGTTG
msa277466.2{330_JM9130013}	TCGTATGGCT	ACTGTTTCGTA	AAGCAGAAGA	GATTGCAGGA	CAAAAAGTTG
msa277466.2{330_18RS21}	TCGTATGGCT	ACTGTTTCGTA	AAGCAGAAGA	GATTGCAGGA	CAAAAAGTTG
msa277466.2{330_2603}	TCGTATGGCT	ACTGTTTCGTA	AAGCAGAAGA	GATTGCAGGA	CAAAAAGTTG
msa277466.2{330_A909}	TCGTATGGCT	ACTGTTTCGTA	AAGCAGAAGA	GATTGCAGGA	CAAAAAGTTG
msa277466.2{330_H36B}	TCGTATGGCT	ACTGTTTCGTA	AAGCAGAAGA	GATTGCAGGA	CAAAAAGTTG
msa277466.2{330_CJB110}	TCGTATGGCT	ACTGTTTCGTA	AAGCAGAAGA	GATTGCAGGA	CAAAAAGTTG
msa277466.2{330_COH1}	TCGTATGGCT	ACTGTTTCGTA	AAGCAGAAGA	GATTGCAGGA	CAAAAAGTTG
msa277466.2{330_M732}	TCGTATGGCT	ACTGTTTCGTA	AAGCAGAAGA	GATTGCAGGA	CAAAAAGTTG
msa277466.2{330_1169NT}	TCGTATGGCT	ACTGTTTCGTA	AAGCAGAAGA	GATTGCAGGA	CAAAAAGTTG
msa277466.2{330_M781}	TCGTATGGCT	ACTGTTTCGTA	AAGCAGAAGA	GATTGCAGGA	CAAAAAGTTG
Consensus	*****	*****	*****	*****	*****
msa277466.2{330_090}	GCTTCCTCCT	TGATACTAAA	GGACCTGAAA	TTCGTACAGA	ACTTTTTGAA
msa277466.2{330_JM9130013}	GCTTCCTCCT	TGATACTAAA	GGACCTGAAA	TTCGTACAGA	ACTTTTTGAA
msa277466.2{330_18RS21}	GCTTCCTCCT	TGATACTAAA	GGACCTGAAA	TTCGTACAGA	ACTTTTTGAA
msa277466.2{330_2603}	GCTTCCTCCT	TGATACTAAA	GGACCTGAAA	TTCGTACAGA	ACTTTTTGAA
msa277466.2{330_A909}	GCTTCCTCCT	TGATACTAAA	GGACCTGAAA	TTCGTACAGA	ACTTTTTGAA
msa277466.2{330_H36B}	GCTTCCTCCT	TGATACTAAA	GGACCTGAAA	TTCGTACAGA	ACTTTTTGAA
msa277466.2{330_CJB110}	GCTTCCTCCT	TGATACTAAA	GGACCTGAAA	TTCGTACAGA	ACTTTTTGAA
msa277466.2{330_COH1}	GCTTCCTCCT	TGATACTAAA	GGACCTGAAA	TTCGTACAGA	ACTTTTTGAA
msa277466.2{330_M732}	GCTTCCTCCT	TGATACTAAA	GGACCTGAAA	TTCGTACAGA	ACTTTTTGAA
msa277466.2{330_1169NT}	GCTTCCTCCT	TGATACTAAA	GGACCTGAAA	TTCGTACAGA	ACTTTTTGAA
msa277466.2{330_M781}	GCTTCCTCCT	TGATACTAAA	GGACCTGAAA	TTCGTACAGA	ACTTTTTGAA
Consensus	*****	*****	*****	*****	*****
msa277466.2{330_090}	GATGGTtCAG	ATTTCCATTC	ATATACAACA	GGTACaAAT	TACGTGTTGC
msa277466.2{330_JM9130013}	GATGGTtCAG	ATTTCCATTC	ATATACAACA	GGTACaAAT	TACGTGTTGC
msa277466.2{330_18RS21}	GATGGTgCAG	ATTTCCATTC	ATATACAACA	GGTACaAAT	TACGTGTTGC
msa277466.2{330_2603}	GATGGTgCAG	ATTTCCATTC	ATATACAACA	GGTACaAAT	TACGTGTTGC
msa277466.2{330_A909}	GATGGTgCAG	ATTTCCATTC	ATATACAACA	GGTACaAAT	TACGTGTTGC
msa277466.2{330_H36B}	GATGGTgCAG	ATTTCCATTC	ATATACAACA	GGTACaAAT	TACGTGTTGC
msa277466.2{330_CJB110}	GATGGTgCAG	ATTTCCATTC	ATATACAACA	GGTACaAAT	TACGTGTTGC
msa277466.2{330_COH1}	GATGGTgCAG	ATTTCCATTC	ATATACAACA	GGTACaAAT	TACGTGTTGC
msa277466.2{330_M732}	GATGGTgCAG	ATTTCCATTC	ATATACAACA	GGTACaAAT	TACGTGTTGC
msa277466.2{330_1169NT}	GATGGTgCAG	ATTTCCATTC	ATATACAACA	GGTACaAAT	TACGTGTTGC
msa277466.2{330_M781}	GATGGTgCAG	ATTTCCATTC	ATATACAACA	GGTACaAAT	TACGTGTTGC
Consensus	*****_***	*****	*****	*****_***	*****
msa277466.2{330_090}	TACTAAGCAA	GGTATCAAAT	CAACTCCAGA	AGTGATTGCA	TTGAATGTTG
msa277466.2{330_JM9130013}	TACTAAGCAA	GGTATCAAAT	CAACTCCAGA	AGTGATTGCA	TTGAATGTTG
msa277466.2{330_18RS21}	TACTAAGCAA	GGTATCAAAT	CAACTCCAGA	AGTGATTGCA	TTGAATGTTG
msa277466.2{330_2603}	TACTAAGCAA	GGTATCAAAT	CAACTCCAGA	AGTGATTGCA	TTGAATGTTG
msa277466.2{330_A909}	TACTAAGCAA	GGTATCAAAT	CAACTCCAGA	AGTGATTGCA	TTGAATGTTG
msa277466.2{330_H36B}	TACTAAGCAA	GGTATCAAAT	CAACTCCAGA	AGTGATTGCA	TTGAATGTTG
msa277466.2{330_CJB110}	TACTAAGCAA	GGTATCAAAT	CAACTCCAGA	AGTGATTGCA	TTGAATGTTG
msa277466.2{330_COH1}	TACTAAGCAA	GGTATCAAAT	CAACTCCAGA	AGTGATTGCA	TTGAATGTTG
msa277466.2{330_M732}	TACTAAGCAA	GGTATCAAAT	CAACTCCAGA	AGTGATTGCA	TTGAATGTTG
msa277466.2{330_1169NT}	TACTAAGCAA	GGTATCAAAT	CAACTCCAGA	AGTGATTGCA	TTGAATGTTG
msa277466.2{330_M781}	TACTAAGCAA	GGTATCAAAT	CAACTCCAGA	AGTGATTGCA	TTGAATGTTG
Consensus	*****	*****	*****	*****	*****
msa277466.2{330_090}	CTGGTGGACT	TGACATCTTT	GATGACGTTG	AAGTTGGTAA	GCAAATCCTT
msa277466.2{330_JM9130013}	CTGGTGGACT	TGACATCTTT	GATGACGTTG	AAGTTGGTAA	GCAAATCCTT
msa277466.2{330_18RS21}	CTGGTGGACT	TGACATCTTT	GATGACGTTG	AAGTTGGTAA	GCAAATCCTT
msa277466.2{330_2603}	CTGGTGGACT	TGACATCTTT	GATGACGTTG	AAGTTGGTAA	GCAAATCCTT
msa277466.2{330_A909}	CTGGTGGACT	TGACATCTTT	GATGACGTTG	AAGTTGGTAA	GCAAATCCTT
msa277466.2{330_H36B}	CTGGTGGACT	TGACATCTTT	GATGACGTTG	AAGTTGGTAA	GCAAATCCTT
msa277466.2{330_CJB110}	CTGGTGGACT	TGACATCTTT	GATGACGTTG	AAGTTGGTAA	GCAAATCCTT
msa277466.2{330_COH1}	CTGGTGGACT	TGACATCTTT	GATGACGTTG	AAGTTGGTAA	GCAAATCCTT
msa277466.2{330_M732}	CTGGTGGACT	TGACATCTTT	GATGACGTTG	AAGTTGGTAA	GCAAATCCTT
msa277466.2{330_1169NT}	CTGGTGGACT	TGACATCTTT	GATGACGTTG	AAGTTGGTAA	GCAAATCCTT
msa277466.2{330_M781}	CTGGTGGACT	TGACATCTTT	GATGACGTTG	AAGTTGGTAA	GCAAATCCTT
Consensus	*****	*****	*****	*****	*****
451					500

Table 72: Comparative Sequences relating to SAG0941

msa277466.2{330_090}	GTTGATGATG	GTAAACTAGG	TCTTACTGTG	TTTGCAAAAG	ATAAAGACAC
msa277466.2{330_JM9130013}	GTTGATGATG	GTAAACTAGG	TCTTACTGTG	TTTGCAAAAG	ATAAAGACAC
msa277466.2{330_18RS21}	GTTGATGATG	GTAAACTAGG	TCTTACTGTG	TTTGCAAAAG	ATAAAGACAC
msa277466.2{330_2603}	GTTGATGATG	GTAAACTAGG	TCTTACTGTG	TTTGCAAAAG	ATAAAGACAC
msa277466.2{330_A909}	GTTGATGATG	GTAAACTAGG	TCTTACTGTG	TTTGCAAAAG	ATAAAGACAC
msa277466.2{330_H36B}	GTTGATGATG	GTAAACTAGG	TCTTACTGTG	TTTGCAAAAG	ATAAAGACAC
msa277466.2{330_CJB110}	GTTGATGATG	GTAAACTAGG	TCTTACTGTG	TTTGCAAAAG	ATAAAGACAC
msa277466.2{330_COH1}	GTTGATGATG	GTAAACTAGG	TCTTACTGTG	TTTGCAAAAG	ATAAAGACAC
msa277466.2{330_M732}	GTTGATGATG	GTAAACTAGG	TCTTACTGTG	TTTGCAAAAG	ATAAAGACAC
msa277466.2{330_1169NT}	GTTGATGATG	GTAAACTAGG	TCTTACTGTG	TTTGCAAAAG	ATAAAGACAC
msa277466.2{330_M781}	GTTGATGATG	GTAAACTAGG	TCTTACTGTG	TTTGCAAAAG	ATAAAGACAC
Consensus	*****	*****	*****	*****	*****
msa277466.2{330_090}	TCGTGAATTT	GAAGTAGTTG	TTGAGAATGA	TGGCCTTATT	GGTAAACAAA
msa277466.2{330_JM9130013}	TCGTGAATTT	GAAGTAGTTG	TTGAGAATGA	TGGCCTTATT	GGTAAACAAA
msa277466.2{330_18RS21}	TCGTGAATTT	GAAGTAGTTG	TTGAGAATGA	TGGCCTTATT	GGTAAACAAA
msa277466.2{330_2603}	TCGTGAATTT	GAAGTAGTTG	TTGAGAATGA	TGGCCTTATT	GGTAAACAAA
msa277466.2{330_A909}	TCGTGAATTT	GAAGTAGTTG	TTGAGAATGA	TGGCCTTATT	GGTAAACAAA
msa277466.2{330_H36B}	TCGTGAATTT	GAAGTAGTTG	TTGAGAATGA	TGGCCTTATT	GGTAAACAAA
msa277466.2{330_CJB110}	TCGTGAATTT	GAAGTAGTTG	TTGAGAATGA	TGGCCTTATT	GGTAAACAAA
msa277466.2{330_COH1}	TCGTGAATTT	GAAGTAGTTG	TTGAGAATGA	TGGCCTTATT	GGTAAACAAA
msa277466.2{330_M732}	TCGTGAATTT	GAAGTAGTTG	TTGAGAATGA	TGGCCTTATT	GGTAAACAAA
msa277466.2{330_1169NT}	TCGTGAATTT	GAAGTAGTTG	TTGAGAATGA	TGGCCTTATT	GGTAAACAAA
msa277466.2{330_M781}	TCGTGAATTT	GAAGTAGTTG	TTGAGAATGA	TGGCCTTATT	GGTAAACAAA
Consensus	*****	*****	*****	*****	*****
msa277466.2{330_090}	AAGGTGTAAA	CATCCCTTAT	ACTAAAATTC	CTTCCCAGC	ACTTGCAGAA
msa277466.2{330_JM9130013}	AAGGTGTAAA	CATCCCTTAT	ACTAAAATTC	CTTCCCAGC	ACTTGCAGAA
msa277466.2{330_18RS21}	AAGGTGTAAA	CATCCCTTAT	ACTAAAATTC	CTTCCCAGC	ACTTGCAGAA
msa277466.2{330_2603}	AAGGTGTAAA	CATCCCTTAT	ACTAAAATTC	CTTCCCAGC	ACTTGCAGAA
msa277466.2{330_A909}	AAGGTGTAAA	CATCCCTTAT	ACTAAAATTC	CTTCCCAGC	ACTTGCAGAA
msa277466.2{330_H36B}	AAGGTGTAAA	CATCCCTTAT	ACTAAAATTC	CTTCCCAGC	ACTTGCAGAA
msa277466.2{330_CJB110}	AAGGTGTAAA	CATCCCTTAT	ACTAAAATTC	CTTCCCAGC	ACTTGCAGAA
msa277466.2{330_COH1}	AAGGTGTAAA	CATCCCTTAT	ACTAAAATTC	CTTCCCAGC	ACTTGCAGAA
msa277466.2{330_M732}	AAGGTGTAAA	CATCCCTTAT	ACTAAAATTC	CTTCCCAGC	ACTTGCAGAA
msa277466.2{330_1169NT}	AAGGTGTAAA	CATCCCTTAT	ACTAAAATTC	CTTCCCAGC	ACTTGCAGAA
msa277466.2{330_M781}	AAGGTGTAAA	CATCCCTTAT	ACTAAAATTC	CTTCCCAGC	ACTTGCAGAA
Consensus	*****	*****	*****	*****	*****
msa277466.2{330_090}	CGCGATAATG	CTGATATCCG	TTTGGACTT	GAGCAAGGAC	TTAACTTTAT
msa277466.2{330_JM9130013}	CGCGATAATG	CTGATATCCG	TTTGGACTT	GAGCAAGGAC	TTAACTTTAT
msa277466.2{330_18RS21}	CGCGATAATG	CTGATATCCG	TTTGGACTT	GAGCAAGGAC	TTAACTTTAT
msa277466.2{330_2603}	CGCGATAATG	CTGATATCCG	TTTGGACTT	GAGCAAGGAC	TTAACTTTAT
msa277466.2{330_A909}	CGCGATAATG	CTGATATCCG	TTTGGACTT	GAGCAAGGAC	TTAACTTTAT
msa277466.2{330_H36B}	CGCGATAATG	CTGATATCCG	TTTGGACTT	GAGCAAGGAC	TTAACTTTAT
msa277466.2{330_CJB110}	CGCGATAATG	CTGATATCCG	TTTGGACTT	GAGCAAGGAC	TTAACTTTAT
msa277466.2{330_COH1}	CGCGATAATG	CTGATATCCG	TTTGGACTT	GAGCAAGGAC	TTAACTTTAT
msa277466.2{330_M732}	CGCGATAATG	CTGATATCCG	TTTGGACTT	GAGCAAGGAC	TTAACTTTAT
msa277466.2{330_1169NT}	CGCGATAATG	CTGATATCCG	TTTGGACTT	GAGCAAGGAC	TTAACTTTAT
msa277466.2{330_M781}	CGCGATAATG	CTGATATCCG	TTTGGACTT	GAGCAAGGAC	TTAACTTTAT
Consensus	*****	*****	*****	*****	*****
msa277466.2{330_090}	TGCTATCTCA	TTTGTACGTA	CTGCTAAAGA	TGTTAATGAA	GTTTCGTGCTA
msa277466.2{330_JM9130013}	TGCTATCTCA	TTTGTACGTA	CTGCTAAAGA	TGTTAATGAA	GTTTCGTGCTA
msa277466.2{330_18RS21}	TGCTATCTCA	TTTGTACGTA	CTGCTAAAGA	TGTTAATGAA	GTTTCGTGCTA
msa277466.2{330_2603}	TGCTATCTCA	TTTGTACGTA	CTGCTAAAGA	TGTTAATGAA	GTTTCGTGCTA
msa277466.2{330_A909}	TGCTATCTCA	TTTGTACGTA	CTGCTAAAGA	TGTTAATGAA	GTTTCGTGCTA
msa277466.2{330_H36B}	TGCTATCTCA	TTTGTACGTA	CTGCTAAAGA	TGTTAATGAA	GTTTCGTGCTA
msa277466.2{330_CJB110}	TGCTATCTCA	TTTGTACGTA	CTGCTAAAGA	TGTTAATGAA	GTTTCGTGCTA
msa277466.2{330_COH1}	TGCTATCTCA	TTTGTACGTA	CTGCTAAAGA	TGTTAATGAA	GTTTCGTGCTA
msa277466.2{330_M732}	TGCTATCTCA	TTTGTACGTA	CTGCTAAAGA	TGTTAATGAA	GTTTCGTGCTA
msa277466.2{330_1169NT}	TGCTATCTCA	TTTGTACGTA	CTGCTAAAGA	TGTTAATGAA	GTTTCGTGCTA
msa277466.2{330_M781}	TGCTATCTCA	TTTGTACGTA	CTGCTAAAGA	TGTTAATGAA	GTTTCGTGCTA
Consensus	*****	*****	*****	*****	*****
msa277466.2{330_090}	TTTGTGAAGA	AACTGGcaAT	GGACAcGTTA	AGTTGTTTGC	TAAAATTGAA
msa277466.2{330_JM9130013}	TTTGTGAAGA	AACTGGcaAT	GGACAcGTTA	AGTTGTTTGC	TAAAATTGAA
msa277466.2{330_18RS21}	TTTGTGAAGA	AACTGGcaAT	GGACAcGTTA	AGTTGTTTGC	TAAAATTGAA
msa277466.2{330_2603}	TTTGTGAAGA	AACTGGsmAT	GGACAcGTTA	AGTTGTTTGC	TAAAATTGAA
msa277466.2{330_A909}	TTTGTGAAGA	AACTGGcaAT	GGACAcGTTA	AGTTGTTTGC	TAAAATTGAA
msa277466.2{330_H36B}	TTTGTGAAGA	AACTGGcaAT	GGACAcGTTA	AGTTGTTTGC	TAAAATTGAA
msa277466.2{330_CJB110}	TTTGTGAAGA	AACTGGcaAT	GGACAcGTTA	AGTTGTTTGC	TAAAATTGAA
msa277466.2{330_COH1}	TTTGTGAAGA	AACTGGcaAT	GGACAcGTTA	AGTTGTTTGC	TAAAATTGAA
msa277466.2{330_M732}	TTTGTGAAGA	AACTGGcaAT	GGACAcGTTA	AGTTGTTTGC	TAAAATTGAA
msa277466.2{330_1169NT}	TTTGTGAAGA	AACTGGcaAT	GGACAcGTTA	AGTTGTTTGC	TAAAATTGAA
msa277466.2{330_M781}	TTTGTGAAGA	AACTGGcaAT	GGACAcGTTA	AGTTGTTTGC	TAAAATTGAA
Consensus	*****	*****	*****	*****	*****

Table 72: Comparative Sequences relating to SAG0941

	751				800
msa277466.2{330_090}	AATCAACAAG	GTATCGATAA	TATTGATGAG	ATTATCGAAG	CAGCAGATGG
msa277466.2{330_JM9130013}	AATCAACAAG	GTATCGATAA	TATTGATGAG	ATTATCGAAG	CAGCAGATGG
msa277466.2{330_18RS21}	AATCAACAAG	GTATCGATAA	TATTGATGAG	ATTATCGAAG	CAGCAGATGG
msa277466.2{330_2603}	AATCAACAAG	GTATCGATAA	TATTGATGAG	ATTATCGAAG	CAGCAGATGG
msa277466.2{330_A909}	AATCAACAAG	GTATCGATAA	TATTGATGAG	ATTATCGAAG	CAGCAGATGG
msa277466.2{330_H36B}	AATCAACAAG	GTATCGATAA	TATTGATGAG	ATTATCGAAG	CAGCAGATGG
msa277466.2{330_CJB110}	AATCAACAAG	GTATCGATAA	TATTGATGAG	ATTATCGAAG	CAGCAGATGG
msa277466.2{330_COH1}	AATCAACAAG	GTATCGATAA	TATTGATGAG	ATTATCGAAG	CAGCAGATGG
msa277466.2{330_M732}	AATCAACAAG	GTATCGATAA	TATTGATGAG	ATTATCGAAG	CAGCAGATGG
msa277466.2{330_1169NT}	AATCAACAAG	GTATCGATAA	TATTGATGAG	ATTATCGAAG	CAGCAGATGG
msa277466.2{330_M781}	AATCAACAAG	GTATCGATAA	TATTGATGAG	ATTATCGAAG	CAGCAGATGG
Consensus	*****	*****	*****	*****	*****
	801				850
msa277466.2{330_090}	TATTATGATT	GCTCGTGGTG	ATATGGGTAT	CGAAGTTCCA	TTTGAAATGG
msa277466.2{330_JM9130013}	TATTATGATT	GCTCGTGGTG	ATATGGGTAT	CGAAGTTCCA	TTTGAAATGG
msa277466.2{330_18RS21}	TATTATGATT	GCTCGTGGTG	ATATGGGTAT	CGAAGTTCCA	TTTGAAATGG
msa277466.2{330_2603}	TATTATGATT	GCTCGTGGTG	ATATGGGTAT	CGAAGTTCCA	TTTGAAATGG
msa277466.2{330_A909}	TATTATGATT	GCTCGTGGTG	ATATGGGTAT	CGAAGTTCCA	TTTGAAATGG
msa277466.2{330_H36B}	TATTATGATT	GCTCGTGGTG	ATATGGGTAT	CGAAGTTCCA	TTTGAAATGG
msa277466.2{330_CJB110}	TATTATGATT	GCTCGTGGTG	ATATGGGTAT	CGAAGTTCCA	TTTGAAATGG
msa277466.2{330_COH1}	TATTATGATT	GCTCGTGGTG	ATATGGGTAT	CGAAGTTCCA	TTTGAAATGG
msa277466.2{330_M732}	TATTATGATT	GCTCGTGGTG	ATATGGGTAT	CGAAGTTCCA	TTTGAAATGG
msa277466.2{330_1169NT}	TATTATGATT	GCTCGTGGTG	ATATGGGTAT	CGAAGTTCCA	TTTGAAATGG
msa277466.2{330_M781}	TATTATGATT	GCTCGTGGTG	ATATGGGTAT	CGAAGTTCCA	TTTGAAATGG
Consensus	*****	*****	*****	*****	*****
	851				900
msa277466.2{330_090}	TTCCAGTTTA	CCAAAAAATG	ATCATTACTA	AAGTTAATGC	AGCTGGTAAA
msa277466.2{330_JM9130013}	TTCCAGTTTA	CCAAAAAATG	ATCATTACTA	AAGTTAATGC	AGCTGGTAAA
msa277466.2{330_18RS21}	TTCCAGTTTA	CCAAAAAATG	ATCATTACTA	AAGTTAATGC	AGCTGGTAAA
msa277466.2{330_2603}	TTCCAGTTTA	CCAAAAAATG	ATCATTACTA	AAGTTAATGC	AGCTGGTAAA
msa277466.2{330_A909}	TTCCAGTTTA	CCAAAAAATG	ATCATTACTA	AAGTTAATGC	AGCTGGTAAA
msa277466.2{330_H36B}	TTCCAGTTTA	CCAAAAAATG	ATCATTACTA	AAGTTAATGC	AGCTGGTAAA
msa277466.2{330_CJB110}	TTCCAGTTTA	CCAAAAAATG	ATCATTACTA	AAGTTAATGC	AGCTGGTAAA
msa277466.2{330_COH1}	TTCCAGTTTA	CCAAAAAATG	ATCATTACTA	AAGTTAATGC	AGCTGGTAAA
msa277466.2{330_M732}	TTCCAGTTTA	CCAAAAAATG	ATCATTACTA	AAGTTAATGC	AGCTGGTAAA
msa277466.2{330_1169NT}	TTCCAGTTTA	CCAAAAAATG	ATCATTACTA	AAGTTAATGC	AGCTGGTAAA
msa277466.2{330_M781}	TTCCAGTTTA	CCAAAAAATG	ATCATTACTA	AAGTTAATGC	AGCTGGTAAA
Consensus	*****	*****	*****	*****	*****
	901				950
msa277466.2{330_090}	GCAGTTATTA	CAGCAACAAA	TATGCTTGAA	ACAATGACTG	ATAAACCACG
msa277466.2{330_JM9130013}	GCAGTTATTA	CAGCAACAAA	TATGCTTGAA	ACAATGACTG	ATAAACCACG
msa277466.2{330_18RS21}	GCAGTTATTA	CAGCAACAAA	TATGCTTGAA	ACAATGACTG	ATAAACCACG
msa277466.2{330_2603}	GCAGTTATTA	CAGCAACAAA	TATGCTTGAA	ACAATGACTG	ATAAACCACG
msa277466.2{330_A909}	GCAGTTATTA	CAGCAACAAA	TATGCTTGAA	ACAATGACTG	ATAAACCACG
msa277466.2{330_H36B}	GCAGTTATTA	CAGCAACAAA	TATGCTTGAA	ACAATGACTG	ATAAACCACG
msa277466.2{330_CJB110}	GCAGTTATTA	CAGCAACAAA	TATGCTTGAA	ACAATGACTG	ATAAACCACG
msa277466.2{330_COH1}	GCAGTTATTA	CAGCAACAAA	TATGCTTGAA	ACAATGACTG	ATAAACCACG
msa277466.2{330_M732}	GCAGTTATTA	CAGCAACAAA	TATGCTTGAA	ACAATGACTG	ATAAACCACG
msa277466.2{330_1169NT}	GCAGTTATTA	CAGCAACAAA	TATGCTTGAA	ACAATGACTG	ATAAACCACG
msa277466.2{330_M781}	GCAGTTATTA	CAGCAACAAA	TATGCTTGAA	ACAATGACTG	ATAAACCACG
Consensus	*****	*****	*****	*****	*****
	951				1000
msa277466.2{330_090}	TGCGACTCGT	TCAGAAAGTAT	CTGATGTCTT	CAATGCTGTT	ATTGATGGTA
msa277466.2{330_JM9130013}	TGCGACTCGT	TCAGAAAGTAT	CTGATGTCTT	CAATGCTGTT	ATTGATGGTA
msa277466.2{330_18RS21}	TGCGACTCGT	TCAGAAAGTAT	CTGATGTCTT	CAATGCTGTT	ATTGATGGTA
msa277466.2{330_2603}	TGCGACTCGT	TCAGAAAGTAT	CTGATGTCTT	CAATGCTGTT	ATTGATGGTA
msa277466.2{330_A909}	TGCGACTCGT	TCAGAAAGTAT	CTGATGTCTT	CAATGCTGTT	ATTGATGGTA
msa277466.2{330_H36B}	TGCGACTCGT	TCAGAAAGTAT	CTGATGTCTT	CAATGCTGTT	ATTGATGGTA
msa277466.2{330_CJB110}	TGCGACTCGT	TCAGAAAGTAT	CTGATGTCTT	CAATGCTGTT	ATTGATGGTA
msa277466.2{330_COH1}	TGCGACTCGT	TCAGAAAGTAT	CTGATGTCTT	CAATGCTGTT	ATTGATGGTA
msa277466.2{330_M732}	TGCGACTCGT	TCAGAAAGTAT	CTGATGTCTT	CAATGCTGTT	ATTGATGGTA
msa277466.2{330_1169NT}	TGCGACTCGT	TCAGAAAGTAT	CTGATGTCTT	CAATGCTGTT	ATTGATGGTA
msa277466.2{330_M781}	TGCGACTCGT	TCAGAAAGTAT	CTGATGTCTT	CAATGCTGTT	ATTGATGGTA
Consensus	*****	*****	*****	*****	*****
	1001				1050
msa277466.2{330_090}	CTGATGCTAC	AATGCTTTCA	GGTGAGTCAG	CTAATGGTAA	ATACCCAGTT
msa277466.2{330_JM9130013}	CTGATGCTAC	AATGCTTTCA	GGTGAGTCAG	CTAATGGTAA	ATACCCAGTT
msa277466.2{330_18RS21}	CTGATGCTAC	AATGCTTTCA	GGTGAGTCAG	CTAATGGTAA	ATACCCAGTT
msa277466.2{330_2603}	CTGATGCTAC	AATGCTTTCA	GGTGAGTCAG	CTAATGGTAA	ATACCCAGTT
msa277466.2{330_A909}	CTGATGCTAC	AATGCTTTCA	GGTGAGTCAG	CTAATGGTAA	ATACCCAGTT
msa277466.2{330_H36B}	CTGATGCTAC	AATGCTTTCA	GGTGAGTCAG	CTAATGGTAA	ATACCCAGTT
msa277466.2{330_CJB110}	CTGATGCTAC	AATGCTTTCA	GGTGAGTCAG	CTAATGGTAA	ATACCCAGTT
msa277466.2{330_COH1}	CTGATGCTAC	AATGCTTTCA	GGTGAGTCAG	CTAATGGTAA	ATACCCAGTT
msa277466.2{330_M732}	CTGATGCTAC	AATGCTTTCA	GGTGAGTCAG	CTAATGGTAA	ATACCCAGTT
msa277466.2{330_1169NT}	CTGATGCTAC	AATGCTTTCA	GGTGAGTCAG	CTAATGGTAA	ATACCCAGTT
msa277466.2{330_M781}	CTGATGCTAC	AATGCTTTCA	GGTGAGTCAG	CTAATGGTAA	ATACCCAGTT
Consensus	*****	*****	*****	*****	*****

Table 72: Comparative Sequences relating to SAG0941

		1051			1100
msa277466.2{330_090}	GAGTCAGTTC	GTACAATGGC	TACTATTGAT	AAAAATGCTC	AAACATTACT
msa277466.2{330_JM9130013}	GAGTCAGTTC	GTACAATGGC	TACTATTGAT	AAAAATGCTC	AAACATTACT
msa277466.2{330_18RS21}	GAGTCAGTTC	GTACAATGGC	TACTATTGAT	AAAAATGCTC	AAACATTACT
msa277466.2{330_2603}	GAGTCAGTTC	GTACAATGGC	TACTATTGAT	AAAAATGCTC	AAACATTACT
msa277466.2{330_A909}	GAGTCAGTTC	GTACAATGGC	TACTATTGAT	AAAAATGCTC	AAACATTACT
msa277466.2{330_H36B}	GAGTCAGTTC	GTACAATGGC	TACTATTGAT	AAAAATGCTC	AAACATTACT
msa277466.2{330_CJB110}	GAGTCAGTTC	GTACAATGGC	TACTATTGAT	AAAAATGCTC	AAACATTACT
msa277466.2{330_COH1}	GAGTCAGTTC	GTACAATGGC	TACTATTGAT	AAAAATGCTC	AAACATTACT
msa277466.2{330_M732}	GAGTCAGTTC	GTACAATGGC	TACTATTGAT	AAAAATGCTC	AAACATTACT
msa277466.2{330_1169NT}	GAGTCAGTTC	GTACAATGGC	TACTATTGAT	AAAAATGCTC	AAACATTACT
msa277466.2{330_M781}	GAGTCAGTTC	GTACAATGGC	TACTATTGAT	AAAAATGCTC	AAACATTACT
Consensus	*****	*****	*****	*****	*****
		1101			1150
msa277466.2{330_090}	CAATGAGTAT	GGTCGcTTAG	ACTCATCTGC	ATTCCCACGT	AATAACAAAA
msa277466.2{330_JM9130013}	CAATGAGTAT	GGTCGcTTAG	ACTCATCTGC	ATTCCCACGT	AATAACAAAA
msa277466.2{330_18RS21}	CAATGAGTAT	GGTCGcTTAG	ACTCATCTGC	ATTCCCACGT	AATAACAAAA
msa277466.2{330_2603}	CAATGAGTAT	GGTCGcTTAG	ACTCATCTGC	ATTCCCACGT	AATAACAAAA
msa277466.2{330_A909}	CAATGAGTAT	GGTCGcTTAG	ACTCATCTGC	ATTCCCACGT	AATAACAAAA
msa277466.2{330_H36B}	CAATGAGTAT	GGTCGcTTAG	ACTCATCTGC	ATTCCCACGT	AATAACAAAA
msa277466.2{330_CJB110}	CAATGAGTAT	GGTCGcTTAG	ACTCATCTGC	ATTCCCACGT	AATAACAAAA
msa277466.2{330_COH1}	CAATGAGTAT	GGTCGcTTAG	ACTCATCTGC	ATTCCCACGT	AATAACAAAA
msa277466.2{330_M732}	CAATGAGTAT	GGTCGcTTAG	ACTCATCTGC	ATTCCCACGT	AATAACAAAA
msa277466.2{330_1169NT}	CAATGAGTAT	GGTCGcTTAG	ACTCATCTGC	ATTCCCACGT	AATAACAAAA
msa277466.2{330_M781}	CAATGAGTAT	GGTCGcTTAG	ACTCATCTGC	ATTCCCACGT	AATAACAAAA
Consensus	*****	*****	*****	*****	*****
		1151			1200
msa277466.2{330_090}	CTGATGTTAT	TGCATCTGCG	GTTAAAGATG	CAACACACTC	AATGGATATC
msa277466.2{330_JM9130013}	CTGATGTTAT	TGCATCTGCG	GTTAAAGATG	CAACACACTC	AATGGATATC
msa277466.2{330_18RS21}	CTGATGTTAT	TGCATCTGCG	GTTAAAGATG	CAACACACTC	AATGGATATC
msa277466.2{330_2603}	CTGATGTTAT	TGCATCTGCG	GTTAAAGATG	CAACACACTC	AATGGATATC
msa277466.2{330_A909}	CTGATGTTAT	TGCATCTGCG	GTTAAAGATG	CAACACACTC	AATGGATATC
msa277466.2{330_H36B}	CTGATGTTAT	TGCATCTGCG	GTTAAAGATG	CAACACACTC	AATGGATATC
msa277466.2{330_CJB110}	CTGATGTTAT	TGCATCTGCG	GTTAAAGATG	CAACACACTC	AATGGATATC
msa277466.2{330_COH1}	CTGATGTTAT	TGCATCTGCG	GTTAAAGATG	CAACACACTC	AATGGATATC
msa277466.2{330_M732}	CTGATGTTAT	TGCATCTGCG	GTTAAAGATG	CAACACACTC	AATGGATATC
msa277466.2{330_1169NT}	CTGATGTTAT	TGCATCTGCG	GTTAAAGATG	CAACACACTC	AATGGATATC
msa277466.2{330_M781}	CTGATGTTAT	TGCATCTGCG	GTTAAAGATG	CAACACACTC	AATGGATATC
Consensus	*****	*****	*****	*****	*****
		1201			1250
msa277466.2{330_090}	AAACTTGTTG	TgACAATTAC	TGAAACAGGT	AATACAGCTC	GTGCCATTTT
msa277466.2{330_JM9130013}	AAACTTGTTG	TgACAATTAC	TGAAACAGGT	AATACAGCTC	GTGCCATTTT
msa277466.2{330_18RS21}	AAACTTGTTG	TaACAATTAC	TGAAACAGGT	AATACAGCTC	GTGCCATTTT
msa277466.2{330_2603}	AAACTTGTTG	TaACAATTAC	TGAAACAGGT	AATACAGCTC	GTGCCATTTT
msa277466.2{330_A909}	AAACTTGTTG	TaACAATTAC	TGAAACAGGT	AATACAGCTC	GTGCCATTTT
msa277466.2{330_H36B}	AAACTTGTTG	TaACAATTAC	TGAAACAGGT	AATACAGCTC	GTGCCATTTT
msa277466.2{330_CJB110}	AAACTTGTTG	TaACAATTAC	TGAAACAGGT	AATACAGCTC	GTGCCATTTT
msa277466.2{330_COH1}	AAACTTGTTG	TaACAATTAC	TGAAACAGGT	AATACAGCTC	GTGCCATTTT
msa277466.2{330_M732}	AAACTTGTTG	TaACAATTAC	TGAAACAGGT	AATACAGCTC	GTGCCATTTT
msa277466.2{330_1169NT}	AAACTTGTTG	TaACAATTAC	TGAAACAGGT	AATACAGCTC	GTGCCATTTT
msa277466.2{330_M781}	AAACTTGTTG	TaACAATTAC	TGAAACAGGT	AATACAGCTC	GTGCCATTTT
Consensus	*****	*-*****	*****	*****	*****
		1251			1300
msa277466.2{330_090}	TAAaTTCCGT	CCAGATGCAG	ACATTTTGGC	TGTTACATTT	GATGAAAAAG
msa277466.2{330_JM9130013}	TAAaTTCCGT	CCAGATGCAG	ACATTTTGGC	TGTTACATTT	GATGAAAAAG
msa277466.2{330_18RS21}	TAAaTTCCGT	CCAGATGCAG	ACATTTTGGC	TGTTACATTT	GATGAAAAAG
msa277466.2{330_2603}	TAAaTTCCGT	CCAGATGCAG	ACATTTTGGC	TGTTACATTT	GATGAAAAAG
msa277466.2{330_A909}	TAAaTTCCGT	CCAGATGCAG	ACATTTTGGC	TGTTACATTT	GATGAAAAAG
msa277466.2{330_H36B}	TAAaTTCCGT	CCAGATGCAG	ACATTTTGGC	TGTTACATTT	GATGAAAAAG
msa277466.2{330_CJB110}	TAAaTTCCGT	CCAGATGCAG	ACATTTTGGC	TGTTACATTT	GATGAAAAAG
msa277466.2{330_COH1}	TAAaTTCCGT	CCAGATGCAG	ACATTTTGGC	TGTTACATTT	GATGAAAAAG
msa277466.2{330_M732}	TAAaTTCCGT	CCAGATGCAG	ACATTTTGGC	TGTTACATTT	GATGAAAAAG
msa277466.2{330_1169NT}	TAAaTTCCGT	CCAGATGCAG	ACATTTTGGC	TGTTACATTT	GATGAAAAAG
msa277466.2{330_M781}	TAAgTTCCGT	CCAGATGCAG	ACATTTTGGC	TGTTACATTT	GATGAAAAAG
Consensus	***-*****	*****	*****	*****	*****
		1301			1350
msa277466.2{330_090}	TACAACGTTT	ATTGATGATT	AACTGGGGTG	TTATCCCTGT	CCTTGCAGAC
msa277466.2{330_JM9130013}	TACAACGTTT	ATTGATGATT	AACTGGGGTG	TTATCCCTGT	CCTTGCAGAC
msa277466.2{330_18RS21}	TACAACGTTT	ATTGATGATT	AACTGGGGTG	TTATCCCTGT	CCTTGCAGAC
msa277466.2{330_2603}	TACAACGTTT	ATTGATGATT	AACTGGGGTG	TTATCCCTGT	CCTTGCAGAC
msa277466.2{330_A909}	TACAACGTTT	ATTGATGATT	AACTGGGGTG	TTATCCCTGT	CCTTGCAGAC
msa277466.2{330_H36B}	TACAACGTTT	ATTGATGATT	AACTGGGGTG	TTATCCCTGT	CCTTGCAGAC
msa277466.2{330_CJB110}	TACAACGTTT	ATTGATGATT	AACTGGGGTG	TTATCCCTGT	CCTTGCAGAC
msa277466.2{330_COH1}	TACAACGTTT	ATTGATGATT	AACTGGGGTG	TTATCCCTGT	CCTTGCAGAC
msa277466.2{330_M732}	TACAACGTTT	ATTGATGATT	AACTGGGGTG	TTATCCCTGT	CCTTGCAGAC
msa277466.2{330_1169NT}	TACAACGTTT	ATTGATGATT	AACTGGGGTG	TTATCCCTGT	CCTTGCAGAC
msa277466.2{330_M781}	TACAACGTTT	ATTGATGATT	AACTGGGGTG	TTATCCCTGT	CCTTGCAGAC

Table 72: Comparative Sequences relating to SAG0941

Consensus	*****	*****	*****	*****	*****
	1351				1400
msa277466.2{330_090}	AAACCAGCAT	CTACAGATGA	TATGTTTGAG	GTTGCAGAAC	GTGTAGCACT
msa277466.2{330_JM9130013}	AAACCAGCAT	CTACAGATGA	TATGTTTGAG	GTTGCAGAAC	GTGTAGCACT
msa277466.2{330_18RS21}	AAACCAGCAT	CTACAGATGA	TATGTTTGAG	GTTGCAGAAC	GTGTAGCACT
msa277466.2{330_2603}	AAACCAGCAT	CTACAGATGA	TATGTTTGAG	GTTGCAGAAC	GTGTAGCACT
msa277466.2{330_A909}	AAACCAGCAT	CTACAGATGA	TATGTTTGAG	GTTGCAGAAC	GTGTAGCACT
msa277466.2{330_H36B}	AAACCAGCAT	CTACAGATGA	TATGTTTGAG	GTTGCAGAAC	GTGTAGCACT
msa277466.2{330_CJB110}	AAACCAGCAT	CTACAGATGA	TATGTTTGAG	GTTGCAGAAC	GTGTAGCACT
msa277466.2{330_COH1}	AAACCAGCAT	CTACAGATGA	TATGTTTGAG	GTTGCAGAAC	GTGTAGCACT
msa277466.2{330_M732}	AAACCAGCAT	CTACAGATGA	TATGTTTGAG	GTTGCAGAAC	GTGTAGCACT
msa277466.2{330_1169NT}	AAACCAGCAT	CTACAGATGA	TATGTTTGAG	GTTGCAGAAC	GTGTAGCACT
msa277466.2{330_M781}	AAACCAGCAT	CTACAGATGA	TATGTTTGAG	GTTGCAGAAC	GTGTAGCACT
Consensus	*****	*****	*****	*****	*****
	1401				1450
msa277466.2{330_090}	TGAAGCAGGA	cTTGTTGAAT	CAGGCGATAA	TATCGTTATC	GTTGCAGGTG
msa277466.2{330_JM9130013}	TGAAGCAGGA	cTTGTTGAAT	CAGGCGATAA	TATCGTTATC	GTTGCAGGTG
msa277466.2{330_18RS21}	TGAAGCAGGA	tTTGTTGAAT	CAGGCGATAA	TATCGTTATC	GTTGCAGGTG
msa277466.2{330_2603}	TGAAGCAGGA	tTTGTTGAAT	CAGGCGATAA	TATCGTTATC	GTTGCAGGTG
msa277466.2{330_A909}	TGAAGCAGGA	tTTGTTGAAT	CAGGCGATAA	TATCGTTATC	GTTGCAGGTG
msa277466.2{330_H36B}	TGAAGCAGGA	tTTGTTGAAT	CAGGCGATAA	TATCGTTATC	GTTGCAGGTG
msa277466.2{330_CJB110}	TGAAGCAGGA	tTTGTTGAAT	CAGGCGATAA	TATCGTTATC	GTTGCAGGTG
msa277466.2{330_COH1}	TGAAGCAGGA	cTTGTTGAAT	CAGGCGATAA	TATCGTTATC	GTTGCAGGTG
msa277466.2{330_M732}	TGAAGCAGGA	cTTGTTGAAT	CAGGCGATAA	TATCGTTATC	GTTGCAGGTG
msa277466.2{330_1169NT}	TGAAGCAGGA	cTTGTTGAAT	CAGGCGATAA	TATCGTTATC	GTTGCAGGTG
msa277466.2{330_M781}	TGAAGCAGGA	cTTGTTGAAT	CAGGCGATAA	TATCGTTATC	GTTGCAGGTG
Consensus	*****	-*****	*****	*****	*****
	1451				1500
msa277466.2{330_090}	TTCCTGTAGG	TACAGGTGGA	ACTAACACAA	TGCGTGTTCG	TACTGTTAAA
msa277466.2{330_JM9130013}	TTCCTGTAGG	TACAGGTGGA	ACTAACACAA	TGCGTGTTCG	TACTGTTAAA
msa277466.2{330_18RS21}	TTCCTGTAGG	TACAGGTGGA	ACTAACACAA	TGCGTGTTCG	TACTGTTAAA
msa277466.2{330_2603}	TTCCTGTAGG	TACAGGTGGA	ACTAACACAA	TGCGTGTTCG	TACTGTTAAA
msa277466.2{330_A909}	TTCCTGTAGG	TACAGGTGGA	ACTAACACAA	TGCGTGTTCG	TACTGTTAAA
msa277466.2{330_H36B}	TTCCTGTAGG	TACAGGTGGA	ACTAACACAA	TGCGTGTTCG	TACTGTTAAA
msa277466.2{330_CJB110}	TTCCTGTAGG	TACAGGTGGA	ACTAACACAA	TGCGTGTTCG	TACTGTTAAA
msa277466.2{330_COH1}	TTCCTGTAGG	TACAGGTGGA	ACTAACACAA	TGCGTGTTCG	TACTGTTAAA
msa277466.2{330_M732}	TTCCTGTAGG	TACAGGTGGA	ACTAACACAA	TGCGTGTTCG	TACTGTTAAA
msa277466.2{330_1169NT}	TTCCTGTAGG	TACAGGTGGA	ACTAACACAA	TGCGTGTTCG	TACTGTTAAA
msa277466.2{330_M781}	TTCCTGTAGG	TACAGGTGGA	ACTAACACAA	TGCGTGTTCG	TACTGTTAAA
Consensus	*****	*****	*****	*****	*****

SEQ ID NO. 7212

STRAIN 2603 frame: 1

MNKRVKIVATLGPVAFRGGKKFGESGYWGESLDVEASAEKIAQLIKEGANVFRFNFSHG
 DHAEQGARMATVRKAEEIAGQKVGFLDLTKGPEIRTELFEDGADFSYTTGTLRVATKQ
 GIKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGTLVFAKDKDTREFEVVVENDGLI
 GKQKGVNIPYTKIPFPALAERDNADIRFGLAQGLNFIAISFVRTAKDVNEVRAICEETGX
 GHVKLFAKIEHQGIDNIDEIIEAADGIMIAARGDMGIEVPFEMVPVYQKMIITKVNAAGK
 AVITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATID
 KNAQTLLNEYGRDLSSAFPRNNKTDVIAAVKDATHSMDIKLVVTITETGNTARAI SKFR
 PDADILAVTFDEKVQRSLMINWGVIPVLADKPASTDDMFEVAERVALEAGFVESGDNIIV
 VAGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7213

STRAIN 090 frame: 1

NKRVKIVATLGPVAFRGGKKFGESGYWGESLDVEASAEKIAQLIKEGANVFRFNFSHGD
 HAEQGARMATVRKAEEIAGQKVGFLDLTKGPEIRTELFEDGSDFSYTTGTLRVATKQG
 IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGTLVFAKDKDTREFEVVVENDGLIG
 KQKGVNIPYTKIPFPALAERDNADIRFGLAQGLNFIAISFVRTAKDVNEVRAICEETGNG
 HVKLFAKIEHQGIDNIDEIIEAADGIMIAARGDMGIEVPFEMVPVYQKMIITKVNAAGKA
 VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
 NAQTLLNEYGRDLSSAFPRNNKTDVIAAVKDATHSMDIKLVVTITETGNTARAI SKFRP
 DADILAVTFDEKVQRSLMINWGVIPVLADKPASTDDMFEVAERVALEAGLVESGDNIIV
 AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7214

STRAIN A909 frame: 1

NKRVKIVATLGPVAFRGGKKFGESGYWGESLDVEASAEKIAQLIKEGANVFRFNFSHGD
 HAEQGARMATVRKAEEIAGQKVGFLDLTKGPEIRTELFEDGADFSYTTGTLRVATKQG
 IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGTLVFAKDKDTREFEVVVENDGLIG
 KQKGVNIPYTKIPFPALAERDNADIRFGLAQGLNFIAISFVRTAKDVNEVRAICEETGNG
 HVKLFAKIEHQGIDNIDEIIEAADGIMIAARGDMGIEVPFEMVPVYQKMIITKVNAAGKA
 VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
 NAQTLLNEYGRDLSSAFPRNNKTDVIAAVKDATHSMDIKLVVTITETGNTARAI SKFRP
 DADILAVTFDEKVQRSLMINWGVIPVLADKPASTDDMFEVAERVALEAGFVESGDNIIV
 AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7215

STRAIN H36B frame: 1

Table 72: Comparative Sequences relating to SAG0941

NKRVKIVATLGPVAFRGGKKFGESGYWGESLDVEASAEDIAQLIKEGANVFRFNFSHGD
 HAEQGARMATVRKAEEIAGQKVGFLDITKGPEIRTELFEDGADFSYTTGTCLRATKQG
 IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGTLVFAKDKDTREFEVVVENDGLIG
 KQKGVNIPYTKIPFPALAEARNADIRFGLEQGLNFIAISFVRTAKDVNEVRAICEETGNG
 HVKLFAKIENQQGIDNIDEIEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGKA
 VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
 NAQTLLNEYGRDSSAFPRNNKTDVIASAVKDATHSMDIKLVVTITETGNTARAI SKFRP
 DADILAVTFDEKVQRSLMINWGVIPVLADKPASTDDMFEVAERVALEAGFVESGDNIIV
 AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7216

STRAIN 18RS21 frame: 1

NKRVKIVATLGPVAFRGGKKFGESGYWGESLDVEASAEDIAQLIKEGANVFRFNFSHGD
 HAEQGARMATVRKAEEIAGQKVGFLDITKGPEIRTELFEDGADFSYTTGTCLRATKQG
 IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGTLVFAKDKDTREFEVVVENDGLIG
 KQKGVNIPYTKIPFPALAEARNADIRFGLEQGLNFIAISFVRTAKDVNEVRAICEETGNG
 HVKLFAKIENQQGIDNIDEIEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGKA
 VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
 NAQTLLNEYGRDSSAFPRNNKTDVIASAVKDATHSMDIKLVVTITETGNTARAI SKFRP
 DADILAVTFDEKVQRSLMINWGVIPVLADKPASTDDMFEVAERVALEAGFVESGDNIIV
 AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7217

STRAIN M732 frame: 1

NKRVKIVATLGPVAFRGGKKFGESGYWGESLDVEASAEDIAQLIKEGANVFRFNFSHGD
 HAEQGARMATVRKAEEIAGQKVGFLDITKGPEIRTELFEDGADFSYTTGTCLRATKQG
 IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGTLVFAKDKDTREFEVVVENDGLIG
 KQKGVNIPYTKIPFPALAEARNADIRFGLEQGLNFIAISFVRTAKDVNEVRAICEETGNG
 HVKLFAKIENQQGIDNIDEIEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGKA
 VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
 NAQTLLNEYGRDSSAFPRNNKTDVIASAVKDATHSMDIKLVVTITETGNTARAI SKFRP
 DADILAVTFDEKVQRSLMINWGVIPVLADKPASTDDMFEVAERVALEAGFVESGDNIIV
 AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7218

STRAIN COH1 frame: 1

NKRVKIVATLGPVAFRGGKKFGESGYWGESLDVEASAEDIAQLIKEGANVFRFNFSHGD
 HAEQGARMATVRKAEEIAGQKVGFLDITKGPEIRTELFEDGADFSYTTGTCLRATKQG
 IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGTLVFAKDKDTREFEVVVENDGLIG
 KQKGVNIPYTKIPFPALAEARNADIRFGLEQGLNFIAISFVRTAKDVNEVRAICEETGNG
 HVKLFAKIENQQGIDNIDEIEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGKA
 VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
 NAQTLLNEYGRDSSAFPRNNKTDVIASAVKDATHSMDIKLVVTITETGNTARAI SKFRP
 DADILAVTFDEKVQRSLMINWGVIPVLADKPASTDDMFEVAERVALEAGFVESGDNIIV
 AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7219

STRAIN M781 frame: 1

NKRVKIVATLGPVAFRGGKKFGESGYWGESLDVEASAEDIAQLIKEGANVFRFNFSHGD
 HAEQGARMATVRKAEEIAGQKVGFLDITKGPEIRTELFEDGADFSYTTGTCLRATKQG
 IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGTLVFAKDKDTREFEVVVENDGLIG
 KQKGVNIPYTKIPFPALAEARNADIRFGLEQGLNFIAISFVRTAKDVNEVRAICEETGNG
 HVKLFAKIENQQGIDNIDEIEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGKA
 VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
 NAQTLLNEYGRDSSAFPRNNKTDVIASAVKDATHSMDIKLVVTITETGNTARAI SKFRP
 DADILAVTFDEKVQRSLMINWGVIPVLADKPASTDDMFEVAERVALEAGFVESGDNIIV
 AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7220

STRAIN CJB110 frame: 1

NKRVKIVATLGPVAFRGGKKFGESGYWGESLDVEASAEDIAQLIKEGANVFRFNFSHGD
 HAEQGARMATVRKAEEIAGQKVGFLDITKGPEIRTELFEDGADFSYTTGTCLRATKQG
 IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGTLVFAKDKDTREFEVVVENDGLIG
 KQKGVNIPYTKIPFPALAEARNADIRFGLEQGLNFIAISFVRTAKDVNEVRAICEETGNG
 HVKLFAKIENQQGIDNIDEIEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGKA
 VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
 NAQTLLNEYGRDSSAFPRNNKTDVIASAVKDATHSMDIKLVVTITETGNTARAI SKFRP
 DADILAVTFDEKVQRSLMINWGVIPVLADKPASTDDMFEVAERVALEAGFVESGDNIIV
 AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7221

STRAIN 1169NT frame: 1

NKRVKIVATLGPVAFRGGKKFGESGYWGESLDVEASAEDIAQLIKEGANVFRFNFSHGD
 HAEQGARMATVRKAEEIAGQKVGFLDITKGPEIRTELFEDGADFSYTTGTCLRATKQG
 IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGTLVFAKDKDTREFEVVVENDGLIG
 KQKGVNIPYTKIPFPALAEARNADIRFGLEQGLNFIAISFVRTAKDVNEVRAICEETGNG
 HVKLFAKIENQQGIDNIDEIEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGKA
 VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
 NAQTLLNEYGRDSSAFPRNNKTDVIASAVKDATHSMDIKLVVTITETGNTARAI SKFRP
 DADILAVTFDEKVQRSLMINWGVIPVLADKPASTDDMFEVAERVALEAGFVESGDNIIV
 AGVPVGTGGTNTMRVRTVK

Table 72: Comparative Sequences relating to SAG0941

SEQ ID NO. 7222

STRAIN JM9130013 frame: 1

NKRVKIVATLGPVAVFRGGKKFGESGYWGESLDVEASAEKIAQLIKEGANVFRFNFSHGD
 HAEQGMATVRKAEIAGQKVGFLDLTKGPEIRTELFEDGSDFSYTTGTLRVATKQG
 IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGTLVFAKDKDTREFEVVENDGLIG
 KQKGVNIPYTKIPFPALAEKQGLNFIAISFVRTAKDVNEVRAICEETGNG
 HVKLFKAIENQOQIDNIDEIEAADGIMIARGDMGIEVPFEMVVPVYQKMIITKVNAAGKA
 VITATNMLETMDKPRATRSEVSDVFNVIDGTATMLSGESANGKYPVESVRTMATIDK
 NAQTLLENYGRDLSSAFPRNNKTDVIASAVKDATHSMDIKLVTTITETGNTARAISKFRP
 DADILAVTFDEKVQRSLMINWGVIPVLADKPASTDDMFEVAERVALEAGLVESGDNIVIV
 AGVPVGTGGTNTMRVRTVK

PRETTY of: /biotmp/msa277662.2{*} February 24, 2003 01:49 ..

	1				50
msa277662.2{330_18RS21}	~NKRVKIVAT	LGPVAVFRGG	KKFGESGYWG	ESLDVEASAE	KIAQLIKEGA
msa277662.2{330_A909}	~NKRVKIVAT	LGPVAVFRGG	KKFGESGYWG	ESLDVEASAE	KIAQLIKEGA
msa277662.2{330_CJB110}	~NKRVKIVAT	LGPVAVFRGG	KKFGESGYWG	ESLDVEASAE	KIAQLIKEGA
msa277662.2{330_H36B}	~NKRVKIVAT	LGPVAVFRGG	KKFGESGYWG	ESLDVEASAE	KIAQLIKEGA
msa277662.2{330_1169NT}	~NKRVKIVAT	LGPVAVFRGG	KKFGESGYWG	ESLDVEASAE	KIAQLIKEGA
msa277662.2{330_COH1}	~NKRVKIVAT	LGPVAVFRGG	KKFGESGYWG	ESLDVEASAE	KIAQLIKEGA
msa277662.2{330_M732}	~NKRVKIVAT	LGPVAVFRGG	KKFGESGYWG	ESLDVEASAE	KIAQLIKEGA
msa277662.2{330_M781}	~NKRVKIVAT	LGPVAVFRGG	KKFGESGYWG	ESLDVEASAE	KIAQLIKEGA
msa277662.2{330_JM9130013}	~NKRVKIVAT	LGPVAVFRGG	KKFGESGYWG	ESLDVEASAE	KIAQLIKEGA
msa277662.2{330_090}	~NKRVKIVAT	LGPVAVFRGG	KKFGESGYWG	ESLDVEASAE	KIAQLIKEGA
msa277662.2{330_2603}	mNKRVKIVAT	LGPVAVFRGG	KKFGESGYWG	ESLDVEASAE	KIAQLIKEGA
Consensus	*****	*****	*****	*****	*****
	51				100
msa277662.2{330_18RS21}	NVFRFNFSHG	DHAEQGARMA	TVRKAEEIAG	QKVGFLDLTK	GPEIRTELF
msa277662.2{330_A909}	NVFRFNFSHG	DHAEQGARMA	TVRKAEEIAG	QKVGFLDLTK	GPEIRTELF
msa277662.2{330_CJB110}	NVFRFNFSHG	DHAEQGARMA	TVRKAEEIAG	QKVGFLDLTK	GPEIRTELF
msa277662.2{330_H36B}	NVFRFNFSHG	DHAEQGARMA	TVRKAEEIAG	QKVGFLDLTK	GPEIRTELF
msa277662.2{330_1169NT}	NVFRFNFSHG	DHAEQGARMA	TVRKAEEIAG	QKVGFLDLTK	GPEIRTELF
msa277662.2{330_COH1}	NVFRFNFSHG	DHAEQGARMA	TVRKAEEIAG	QKVGFLDLTK	GPEIRTELF
msa277662.2{330_M732}	NVFRFNFSHG	DHAEQGARMA	TVRKAEEIAG	QKVGFLDLTK	GPEIRTELF
msa277662.2{330_M781}	NVFRFNFSHG	DHAEQGARMA	TVRKAEEIAG	QKVGFLDLTK	GPEIRTELF
msa277662.2{330_JM9130013}	NVFRFNFSHG	DHAEQGARMA	TVRKAEEIAG	QKVGFLDLTK	GPEIRTELF
msa277662.2{330_090}	NVFRFNFSHG	DHAEQGARMA	TVRKAEEIAG	QKVGFLDLTK	GPEIRTELF
msa277662.2{330_2603}	NVFRFNFSHG	DHAEQGARMA	TVRKAEEIAG	QKVGFLDLTK	GPEIRTELF
Consensus	*****	*****	*****	*****	*****
	101				150
msa277662.2{330_18RS21}	DGaDFHSYTT	GTLKRVATKQ	GIKSTPEVIA	LNAGGLDIF	DDVEVGKQIL
msa277662.2{330_A909}	DGaDFHSYTT	GTLKRVATKQ	GIKSTPEVIA	LNAGGLDIF	DDVEVGKQIL
msa277662.2{330_CJB110}	DGaDFHSYTT	GTLKRVATKQ	GIKSTPEVIA	LNAGGLDIF	DDVEVGKQIL
msa277662.2{330_H36B}	DGaDFHSYTT	GTLKRVATKQ	GIKSTPEVIA	LNAGGLDIF	DDVEVGKQIL
msa277662.2{330_1169NT}	DGaDFHSYTT	GTLKRVATKQ	GIKSTPEVIA	LNAGGLDIF	DDVEVGKQIL
msa277662.2{330_COH1}	DGaDFHSYTT	GTLKRVATKQ	GIKSTPEVIA	LNAGGLDIF	DDVEVGKQIL
msa277662.2{330_M732}	DGaDFHSYTT	GTLKRVATKQ	GIKSTPEVIA	LNAGGLDIF	DDVEVGKQIL
msa277662.2{330_M781}	DGaDFHSYTT	GTLKRVATKQ	GIKSTPEVIA	LNAGGLDIF	DDVEVGKQIL
msa277662.2{330_JM9130013}	DGsDFHSYTT	GTLKRVATKQ	GIKSTPEVIA	LNAGGLDIF	DDVEVGKQIL
msa277662.2{330_090}	DGsDFHSYTT	GTLKRVATKQ	GIKSTPEVIA	LNAGGLDIF	DDVEVGKQIL
msa277662.2{330_2603}	DGaDFHSYTT	GTLKRVATKQ	GIKSTPEVIA	LNAGGLDIF	DDVEVGKQIL
Consensus	**~*****	**~*****	*****	*****	*****
	151				200
msa277662.2{330_18RS21}	VDDGKLGTLV	FAKDKDTREF	EVVENDGLI	GKQKGVNIPY	TKIPFPALAE
msa277662.2{330_A909}	VDDGKLGTLV	FAKDKDTREF	EVVENDGLI	GKQKGVNIPY	TKIPFPALAE
msa277662.2{330_CJB110}	VDDGKLGTLV	FAKDKDTREF	EVVENDGLI	GKQKGVNIPY	TKIPFPALAE
msa277662.2{330_H36B}	VDDGKLGTLV	FAKDKDTREF	EVVENDGLI	GKQKGVNIPY	TKIPFPALAE
msa277662.2{330_1169NT}	VDDGKLGTLV	FAKDKDTREF	EVVENDGLI	GKQKGVNIPY	TKIPFPALAE
msa277662.2{330_COH1}	VDDGKLGTLV	FAKDKDTREF	EVVENDGLI	GKQKGVNIPY	TKIPFPALAE
msa277662.2{330_M732}	VDDGKLGTLV	FAKDKDTREF	EVVENDGLI	GKQKGVNIPY	TKIPFPALAE
msa277662.2{330_M781}	VDDGKLGTLV	FAKDKDTREF	EVVENDGLI	GKQKGVNIPY	TKIPFPALAE
msa277662.2{330_JM9130013}	VDDGKLGTLV	FAKDKDTREF	EVVENDGLI	GKQKGVNIPY	TKIPFPALAE
msa277662.2{330_090}	VDDGKLGTLV	FAKDKDTREF	EVVENDGLI	GKQKGVNIPY	TKIPFPALAE
msa277662.2{330_2603}	VDDGKLGTLV	FAKDKDTREF	EVVENDGLI	GKQKGVNIPY	TKIPFPALAE
Consensus	*****	*****	*****	*****	*****
	201				250
msa277662.2{330_18RS21}	RDNADIRFGL	EQGLNFIAIS	FVRTAKDVNE	VRAICEETGn	GHVKLFKIE
msa277662.2{330_A909}	RDNADIRFGL	EQGLNFIAIS	FVRTAKDVNE	VRAICEETGn	GHVKLFKIE
msa277662.2{330_CJB110}	RDNADIRFGL	EQGLNFIAIS	FVRTAKDVNE	VRAICEETGn	GHVKLFKIE
msa277662.2{330_H36B}	RDNADIRFGL	EQGLNFIAIS	FVRTAKDVNE	VRAICEETGn	GHVKLFKIE
msa277662.2{330_1169NT}	RDNADIRFGL	EQGLNFIAIS	FVRTAKDVNE	VRAICEETGn	GHVKLFKIE
msa277662.2{330_COH1}	RDNADIRFGL	EQGLNFIAIS	FVRTAKDVNE	VRAICEETGn	GHVKLFKIE
msa277662.2{330_M732}	RDNADIRFGL	EQGLNFIAIS	FVRTAKDVNE	VRAICEETGn	GHVKLFKIE
msa277662.2{330_M781}	RDNADIRFGL	EQGLNFIAIS	FVRTAKDVNE	VRAICEETGn	GHVKLFKIE
msa277662.2{330_JM9130013}	RDNADIRFGL	EQGLNFIAIS	FVRTAKDVNE	VRAICEETGn	GHVKLFKIE
msa277662.2{330_090}	RDNADIRFGL	EQGLNFIAIS	FVRTAKDVNE	VRAICEETGn	GHVKLFKIE
msa277662.2{330_2603}	RDNADIRFGL	EQGLNFIAIS	FVRTAKDVNE	VRAICEETGx	GHVKLFKIE
Consensus	*****	*****	*****	*****	*****

Table 72: Comparative Sequences relating to SAG0941

	251				300
msa277662.2{330_18RS21}	NQQGIDNIDE	IIEAADGIMI	ARGDMGIEVP	FEMVPVYQKM	IITKVNAAGK
msa277662.2{330_A909}	NQQGIDNIDE	IIEAADGIMI	ARGDMGIEVP	FEMVPVYQKM	IITKVNAAGK
msa277662.2{330_CJB110}	NQQGIDNIDE	IIEAADGIMI	ARGDMGIEVP	FEMVPVYQKM	IITKVNAAGK
msa277662.2{330_H36B}	NQQGIDNIDE	IIEAADGIMI	ARGDMGIEVP	FEMVPVYQKM	IITKVNAAGK
msa277662.2{330_1169NT}	NQQGIDNIDE	IIEAADGIMI	ARGDMGIEVP	FEMVPVYQKM	IITKVNAAGK
msa277662.2{330_COH1}	NQQGIDNIDE	IIEAADGIMI	ARGDMGIEVP	FEMVPVYQKM	IITKVNAAGK
msa277662.2{330_M732}	NQQGIDNIDE	IIEAADGIMI	ARGDMGIEVP	FEMVPVYQKM	IITKVNAAGK
msa277662.2{330_M781}	NQQGIDNIDE	IIEAADGIMI	ARGDMGIEVP	FEMVPVYQKM	IITKVNAAGK
msa277662.2{330_JM9130013}	NQQGIDNIDE	IIEAADGIMI	ARGDMGIEVP	FEMVPVYQKM	IITKVNAAGK
msa277662.2{330_090}	NQQGIDNIDE	IIEAADGIMI	ARGDMGIEVP	FEMVPVYQKM	IITKVNAAGK
msa277662.2{330_2603}	NQQGIDNIDE	IIEAADGIMI	ARGDMGIEVP	FEMVPVYQKM	IITKVNAAGK
Consensus	*****	*****	*****	*****	*****
	301				350
msa277662.2{330_18RS21}	AVITATNMLE	TMTDKPRATR	SEVSDVFNAV	IDGTDATMLS	GESANGKYPV
msa277662.2{330_A909}	AVITATNMLE	TMTDKPRATR	SEVSDVFNAV	IDGTDATMLS	GESANGKYPV
msa277662.2{330_CJB110}	AVITATNMLE	TMTDKPRATR	SEVSDVFNAV	IDGTDATMLS	GESANGKYPV
msa277662.2{330_H36B}	AVITATNMLE	TMTDKPRATR	SEVSDVFNAV	IDGTDATMLS	GESANGKYPV
msa277662.2{330_1169NT}	AVITATNMLE	TMTDKPRATR	SEVSDVFNAV	IDGTDATMLS	GESANGKYPV
msa277662.2{330_COH1}	AVITATNMLE	TMTDKPRATR	SEVSDVFNAV	IDGTDATMLS	GESANGKYPV
msa277662.2{330_M732}	AVITATNMLE	TMTDKPRATR	SEVSDVFNAV	IDGTDATMLS	GESANGKYPV
msa277662.2{330_M781}	AVITATNMLE	TMTDKPRATR	SEVSDVFNAV	IDGTDATMLS	GESANGKYPV
msa277662.2{330_JM9130013}	AVITATNMLE	TMTDKPRATR	SEVSDVFNAV	IDGTDATMLS	GESANGKYPV
msa277662.2{330_090}	AVITATNMLE	TMTDKPRATR	SEVSDVFNAV	IDGTDATMLS	GESANGKYPV
msa277662.2{330_2603}	AVITATNMLE	TMTDKPRATR	SEVSDVFNAV	IDGTDATMLS	GESANGKYPV
Consensus	*****	*****	*****	*****	*****
	351				400
msa277662.2{330_18RS21}	ESVRTMATID	KNAQTLLNEY	GRLDSSAFPR	NNKTDVIASA	VKDATHSMDI
msa277662.2{330_A909}	ESVRTMATID	KNAQTLLNEY	GRLDSSAFPR	NNKTDVIASA	VKDATHSMDI
msa277662.2{330_CJB110}	ESVRTMATID	KNAQTLLNEY	GRLDSSAFPR	NNKTDVIASA	VKDATHSMDI
msa277662.2{330_H36B}	ESVRTMATID	KNAQTLLNEY	GRLDSSAFPR	NNKTDVIASA	VKDATHSMDI
msa277662.2{330_1169NT}	ESVRTMATID	KNAQTLLNEY	GRLDSSAFPR	NNKTDVIASA	VKDATHSMDI
msa277662.2{330_COH1}	ESVRTMATID	KNAQTLLNEY	GRLDSSAFPR	NNKTDVIASA	VKDATHSMDI
msa277662.2{330_M732}	ESVRTMATID	KNAQTLLNEY	GRLDSSAFPR	NNKTDVIASA	VKDATHSMDI
msa277662.2{330_M781}	ESVRTMATID	KNAQTLLNEY	GRLDSSAFPR	NNKTDVIASA	VKDATHSMDI
msa277662.2{330_JM9130013}	ESVRTMATID	KNAQTLLNEY	GRLDSSAFPR	NNKTDVIASA	VKDATHSMDI
msa277662.2{330_090}	ESVRTMATID	KNAQTLLNEY	GRLDSSAFPR	NNKTDVIASA	VKDATHSMDI
msa277662.2{330_2603}	ESVRTMATID	KNAQTLLNEY	GRLDSSAFPR	NNKTDVIASA	VKDATHSMDI
Consensus	*****	*****	*****	*****	*****
	401				450
msa277662.2{330_18RS21}	KLVTITITETG	NTARAISKFR	PDADILAVTF	DEKVQRSLMI	NWGVIPLAD
msa277662.2{330_A909}	KLVTITITETG	NTARAISKFR	PDADILAVTF	DEKVQRSLMI	NWGVIPLAD
msa277662.2{330_CJB110}	KLVTITITETG	NTARAISKFR	PDADILAVTF	DEKVQRSLMI	NWGVIPLAD
msa277662.2{330_H36B}	KLVTITITETG	NTARAISKFR	PDADILAVTF	DEKVQRSLMI	NWGVIPLAD
msa277662.2{330_1169NT}	KLVTITITETG	NTARAISKFR	PDADILAVTF	DEKVQRSLMI	NWGVIPLAD
msa277662.2{330_COH1}	KLVTITITETG	NTARAISKFR	PDADILAVTF	DEKVQRSLMI	NWGVIPLAD
msa277662.2{330_M732}	KLVTITITETG	NTARAISKFR	PDADILAVTF	DEKVQRSLMI	NWGVIPLAD
msa277662.2{330_M781}	KLVTITITETG	NTARAISKFR	PDADILAVTF	DEKVQRSLMI	NWGVIPLAD
msa277662.2{330_JM9130013}	KLVTITITETG	NTARAISKFR	PDADILAVTF	DEKVQRSLMI	NWGVIPLAD
msa277662.2{330_090}	KLVTITITETG	NTARAISKFR	PDADILAVTF	DEKVQRSLMI	NWGVIPLAD
msa277662.2{330_2603}	KLVTITITETG	NTARAISKFR	PDADILAVTF	DEKVQRSLMI	NWGVIPLAD
Consensus	*****	*****	*****	*****	*****
	451				500
msa277662.2{330_18RS21}	KPASTDDMFE	VAERVALEAG	FVESGDNIVI	VAGVPVGTGG	TNTMRVRTVK
msa277662.2{330_A909}	KPASTDDMFE	VAERVALEAG	FVESGDNIVI	VAGVPVGTGG	TNTMRVRTVK
msa277662.2{330_CJB110}	KPASTDDMFE	VAERVALEAG	FVESGDNIVI	VAGVPVGTGG	TNTMRVRTVK
msa277662.2{330_H36B}	KPASTDDMFE	VAERVALEAG	FVESGDNIVI	VAGVPVGTGG	TNTMRVRTVK
msa277662.2{330_1169NT}	KPASTDDMFE	VAERVALEAG	FVESGDNIVI	VAGVPVGTGG	TNTMRVRTVK
msa277662.2{330_COH1}	KPASTDDMFE	VAERVALEAG	FVESGDNIVI	VAGVPVGTGG	TNTMRVRTVK
msa277662.2{330_M732}	KPASTDDMFE	VAERVALEAG	FVESGDNIVI	VAGVPVGTGG	TNTMRVRTVK
msa277662.2{330_M781}	KPASTDDMFE	VAERVALEAG	FVESGDNIVI	VAGVPVGTGG	TNTMRVRTVK
msa277662.2{330_JM9130013}	KPASTDDMFE	VAERVALEAG	FVESGDNIVI	VAGVPVGTGG	TNTMRVRTVK
msa277662.2{330_090}	KPASTDDMFE	VAERVALEAG	FVESGDNIVI	VAGVPVGTGG	TNTMRVRTVK
msa277662.2{330_2603}	KPASTDDMFE	VAERVALEAG	FVESGDNIVI	VAGVPVGTGG	TNTMRVRTVK
Consensus	*****	*****	*****	*****	*****

Table 73: Comparative Sequences relating to SAG0981

SEQ ID NO. 7301

STRAIN 2603

TTGTCTGCTATAATAGACAAAAAGGTGGTGATATTTATGTATTTAGCATTAAATCGGTGAT
 ATCATTAAATCAAAACAGATACTTGAACGTGAAACTTTCCAACAGTCTTTTCAGCAACTA
 ATGACCGAAGCTATCTGATGTATATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCT
 GGTGATGAATTTCAAGCTTTATTGAAACCATCAAAAAAGGTATTTCAAATTATTGACCAT
 ATTCAACTAGCTCTAAAACTGTTAATGTAAGGTTTCGGCCTCGGTACAGGAAACATTATA
 ACATCCATCAATTCAAATGAAAGTATCGGTGCTGATGGTCCTGCTACTGGCATGCTCGC
 TCAGCTATTAAATCATATACATGATAAAAAATGATTATGGAACAGTTCAAGTAGCTATTTGC
 CTTGATGATGAAGACCAAAACCTTGAATTAACACTAAATAGTCTCATTTAGCTGGTGAT
 TTTATCAAGTCAAAATGGACTACAAACCATTTTCAAATGCTTGAGCACTTAATACTTCAA
 GATAATTATCAAGAACAATTTCAACATCAAAAGTTAGCCCAACTGGAAAATATTGAACCT
 AGTGCCTGACTAAACGCTTAAAGCAAGCGGTCTGAAGATTACTTAAGAACGAGAACA
 CAGGCAGCCGATCTATTAGTTAAAGTTGCACTCAAACTAAAGGGGGAAGCTATGATTTTC

SEQ ID NO. 7302

STRAIN 090

TCTGCTATAATAGACAAAAAGGTGGTGATATTTATGTATTT
 AGCATTAAATCGGTGATATCATTAAATCAAAACAGATACTTGAACGTGAAA
 CTTTCCAACAGTCTTTTCAGCAACTAATGACCGAAGCTATCTGATGTATAT
 GGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGATGAATTTCA
 AGCTTTATTGAAACCATCAAAAAAGGTATTTCAAATTATTGACCATATTC
 AACTAGCTCTAAAACTGTTAATGTAAGGTTTCGGCCTCGGTACAGGAAAC
 ATTATAACATCCATCAATTTAAATGAAAGTATCGGTGCTGATGGTCCTGC
 CTACTGGCATGCTCGCTCAGCTATTAAATCATATACATGATAAAAAATGATT
 ATGGAACAGTTCAAGTAGCTATTTGCCTTGATGATGAAGACCAAAACCTT
 GAATTAACACTAAATAGTCTCATTTAGCTGGTGATTTTATCAAGTCAA
 ATGGACTACAAACCATTTTCAAATGCTTGAGCACTTAATACTTCAAGATA
 ATTATCAAGAACAATTTCAACATCAAAAGTTAGCCCAACTGGAAAATATT
 GAACCTAGTGCCTGACTAAACGCTTAAAGCAAGCGGTCTGAAGATTTA
 CTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAGTTGCACTC
 AAACCTAAAGGGGGAAGCTATGATTTTC

SEQ ID NO. 7303

STRAIN A909

TCTGCTATAATAGACAAAAAGGTGGTGATATTTATGTAT
 TTAGCATTAATCGGTGATATCATTAAATCAAAACAGATACTTGAACGTGA
 AACTTTCCAACAGTCTTTTCAGCAACTAATGACCGAAGCTATCTGATGTAT
 ATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGATGAATTT
 CAAGCTTTATTGAAACCATCAAAAAAGGTATTTCAAATTATTGACCATAT
 TCAACTAGCTCTAAAACTGTTAATGTAAGGTTTCGGCCTCGGTACAGGAA
 ACATTATAACATCCATCAATTCAAATGAAAGTATCGGTGCTGATGGTCCT
 GCCTACTGGCATGCTCGCTCAGCTATTAAATCATATACATGATAAAAAATGA
 TTATGGAACAGTTCAAGTAGCTATTTGCCTTGATGATGAAGACCAAAAC
 TTGAATTAACACTAAATAGTCTCATTTAGCTGGTGATTTTATCAAGTCA
 AATGGACTACAAACCATTTTCAAATGCTTGAGCACTTAATACTTCAAGA
 TAATTTATCAAGAACAATTTCAACATCAAAAGTTAGCCCAACTGGAAAATA
 TTGAACCTAGTGCCTGACTAAACGCTTAAAGCAAGCGGTCTGAAGATT
 TACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAGTTGCAC
 TCAAACTAAAGGGGGAAGCTATGATTTTC

SEQ ID NO. 7304

STRAIN H36B

TCTGCTATAATAGACAAAAAGGTGGTGATATTT
 ATGTATTTAGCATTAAATCGGTGATATCATTAAATCAAAACAGATACTTGA
 ACGTGAAACTTTCCAACAGTCTTTTCAGCAACTAATGACCGAAGCTATCTG
 ATGTATATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGAT
 GAATTTCAAGCTTTATTGAAACCATCAAAAAAGGTATTTCAAATTATTGA
 CCATATTCAACTAGCTCTAAAACTGTTAATGTAAGGTTTCGGCCTCGGTA
 CAGGAAACATTATAACATCCATCAATTCAAATGAAAGTATCGGTGCTGAT
 GGTCTGCTACTGGCATGCTCGCTCAGCTATTAAATCATATACATGATAA
 AAATGATTATGGAACAGTTCAAGTAGCTATTTGCCTTGATGATGAAGACC
 AAAACCTTGAATTAACACTAAATAGTCTCATTTAGCTGGTGATTTTATC
 AAGTCAAAATGGACTACAAACCATTTTCAAATGCTTGAGCACTTAATACT
 TCAAGATAATTATCAAGAACAATTTCAACATCAAAAGTTAGCCCAACTGG
 AAAATATTGAACCTAGTGCCTGACTAAACGCTTAAAGCAAGCGGTCTG
 AAGATTTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAG
 TTGCACTCAAACTAAAGGGGGAAGCTATGATTTTC

SEQ ID NO. 7305

STRAIN 18RS21

TCTGCTATAATAGACAAAAAGGTGGTGATATTT
 ATGTATTTAGCATTAAATCGGTGATATCATTAAATCAAAACAGATACTTGA
 ACGTGAAACTTTCCAACAGTCTTTTCAGCAACTAATGACCGAAGCTATCTG
 ATGTATATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGAT
 GAATTTCAAGCTTTATTGAAACCATCAAAAAAGGTATTTCAAATTATTGA
 CCATATTCAACTAGCTCTAAAACTGTTAATGTAAGGTTTCGGCCTCGGTA
 CAGGAAACATTATAACATCCATCAATTCAAATGAAAGTATCGGTGCTGAT
 GGTCTGCTACTGGCATGCTCGCTCAGCTATTAAATCATATACATGATAA
 AAATGATTATGGAACAGTTCAAGTAGCTATTTGCCTTGATGATGAAGACC
 AAAACCTTGAATTAACACTAAATAGTCTCATTTAGCTGGTGATTTTATC
 AAGTCAAAATGGACTACAAACCATTTTCAAATGCTTGAGCACTTAATACT
 TCAAGATAATTATCAAGAACAATTTCAACATCAAAAGTTAGCCCAACTGG
 AAAATATTGAACCTAGTGCCTGACTAAACGCTTAAAGCAAGCGGTCTG
 AAGATTTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAG
 TTGCACTCAAACTAAAGGGGGAAGCTATGATTTTC

Table 73: Comparative Sequences relating to SAG0981

TCAAGATAATTATCAAGAACAATTTCAACATCAAAAGTTAGCCCAACTGG
AAAATATTGAACCTAGTGCCTGACTAAACGCCTTAAAGCAAGCGGCTG
AAGATTTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAG
TTGCACTCAAACATAAGGGGAAGCTATGATTTTC

SEQ ID NO. 7306

STRAIN M732

TCTGCTATAATAGACAAAAAGGTGGTGATATT
TATGTATTTAGCATTAAATCGGTGATATCATTAAATCAAAACAGATACTTG
AACGTGAAACCTTTCCAACAGTCTTTTCAGCAACTAATGACCGAACTATCT
GATGTATATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGA
TGAATTTCAAGCTTTATTGAAACaATCAAAAAAGGTATTTCAAATTATTG
ACCATATTCAACTAGCTCTAAAACCTGTTAATGTAAGGTTCCGGCTCGGT
ACAGGAAACATTATAACATCCATCAATTCAAATGAAAGTATCGGTGCTGA
TGGTCCTGCCCTACTGGCATGCTCGCTCAGCTATTAATCATATACATGATA
AAAATGATTATGGAACAGTTCAAGTAGCTATTTGCCTTGATGATGAAGAC
CAAAACCTTGAATTAACACTAAATAGTCTCATTTTCAGCTGGTGATTTTAT
CAAGTCAAAATGGACTACAAACCATTTTCAAATGCTTGAGCACTTAATAC
TTCAAGATAATTATCAAGAACAATTTCAACATCAAAAGTTAGCCCAACTG
GAAAATATTGAACCTAGTGCCTGACTAAACGCCTTAAAGCAAGCGGCTCT
GAAGATTTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAG
GTTGCACTCAAACATAAGGGGAAGCTATGATTTTC

SEQ ID NO. 7307

STRAIN COH1

TCTGCTATAATAGACAAAAAGGTGGTGATATT
TATGTATTTAGCATTAAATCGGTGATATCATTAAATCAAAACAGATACTTG
AACGTGAAACCTTTCCAACAGTCTTTTCAGCAACTAATGACCGAACTATCT
GATGTATATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGA
TGAATTTCAAGCTTTATTGAAACaATCAAAAAAGGTATTTCAAATTATTG
ACCATATTCAACTAGCTCTAAAACCTGTTAATGTAAGGTTCCGGCTCGGT
ACAGGAAACATTATAACATCCATCAATTCAAATGAAAGTATCGGTGCTGA
TGGTCCTGCCCTACTGGCATGCTCGCTCAGCTATTAATCATATACATGATA
AAAATGATTATGGAACAGTTCAAGTAGCTATTTGCCTTGATGATGAAGAC
CAAAACCTTGAATTAACACTAAATAGTCTCATTTTCAGCTGGTGATTTTAT
CAAGTCAAAATGGACTACAAACCATTTTCAAATGCTTGAGCACTTAATAC
TTCAAGATAATTATCAAGAACAATTTCAACATCAAAAGTTAGCCCAACTG
GAAAATATTGAACCTAGTGCCTGACTAAACGCCTTAAAGCAAGCGGCTCT
GAAGATTTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAG
GTTGCACTCAAACATAAGGGGAAGCTATGATTTTC

SEQ ID NO. 7308

STRAIN M781

TCTGCTATAATAGACAAAAAGGTGGTGATATTT
ATGTATTTAGCATTAAATCGGTGATATCATTAAATCAAAACAGATACTTGA
ACGTGAAACCTTTCCAACAGTCTTTTCAGCAACTAATGACCGAACTATCTG
ATGTATATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGAT
GAATTTCAAGCTTTATTGAAACAATCAAAAAAGGTATTTCAAATTATTGA
CCATATTCAACTAGCTCTAAAACCTGTTAATGTAAGGTTCCGGCTCGGT
CAGGAAACATTATAACATCCATCAATTCAAATGAAAGTATCGGTGCTGAT
GGTCCTGCCCTACTGGCATGCTCGCTCAGCTATTAATCATATACATGATAA
AAATGATTATGGAACAGTTCAAGTAGCTATTTGCCTTGATGATGAAGACC
AAAACCTTGAATTAACACTAAATAGTCTCATTTTCAGCTGGTGATTTTATC
AAGTCAAAATGGACTACAAACCATTTTCAAATGCTTGAGCACTTAATACT
TCAAGATAATTATCAAGAACAATTTCAACATCAAAAGTTAGCCCAACTGG
AAAATATTGAACCTAGTGCCTGACTAAACGCCTTAAAGCAAGCGGCTCTG
AAGATTTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAG
TTGCACTCAAACATAAGGGGAAGCTATGATTTTC

SEQ ID NO. 7309

STRAIN CJB110

TCTGCTATAATAGACAAAAAGGTGGTGGA
TTTATGTATTTAGCATTAAATCGGTGATATCATTAAATCAAAACAGATACT
TGAACGTGAAACCTTTCCAACAGTCTTTTCAGCAACTAATGACCGAACTAT
CTGATGTATATGGTGAAGAGCTGATTTCTCTATTCACTATTACAGCTGGT
GATGAATTTCAAGCTTTATTGAAACCATCAAAAAAGGTATTTCAAATTAT
TGACCATATTCAACTAGCTCTAAAACCTGTTAATGTAAGGTTCCGGCTCG
GTACAGGAAACATTATAACATCCATCAATTCAAATGAAAGTATCGGTGCT
GATGGTCCTGCCCTACTGGCATGCTCGCTCAGCTATTAATCATATACATGA
TAAAAATGATTATGGAACAGTTCAAGTAGCTATTTGCCTTGATGATGAAG
ACCAAAACCTTGAATTAACACTAAATAGTCTCATTTTCAGCTGGTGATTTT
ATCAAGTCAAAATGGACTACTAACCATTTTCAAATGCTTGAGCACTTAAT
ACTTCAAGATAATTATCAAGAACAATTTCAACATCAAAAGTTAGCCCAAC
TGGAAAATATTGAACCTAGTGCCTGACTAAACGCCTTAAAGCAAGCGGT
CTGAAGATTTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAA
AAGTTGCACTCAAACATAAGGGGAAGCTATGATTTTC

SEQ ID NO. 7310

STRAIN JM9130013

TCTGCTATAATAGACAAAAAGGTGGTGATATTT
ATGTATTTAGCATTAAATCGGTGATATCATTAAATCAAAACAGATACTTGA
ACGTGAAACCTTTCCAACAGTCTTTTCAGCAACTAATGACCGAACTATCTG

Table 73: Comparative Sequences relating to SAG0981

ATGTATATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGAT
 GAATTTCAAGCTTTATTGAAACCATCAAAAAAGGTATTTCAAATTATTGA
 CCATATTCAACTAGCTCTAAAACCTGTTAATGTAAGGTTCCGGCTCGGTA
 CAGGAAACATTATAACATCCATCAATTCAAATGAAAGTATCGGTGCTGAT
 GGTCTGCTTACTGGCATGCTCGCTCAGCTATTAATCATATACATGATAA
 AAATGATTATGGAACAGTTCAAGTAGCTATTTGCCTTGATGATGAAGACC
 AAAACCTTGAATTAACACTAAATAGTCTCATTTCAGCTGGTGATTTTATC
 AAGTCAAAATGGACTACAAACCATTTTCAAATGCTTGAGCACTTAATACT
 TCAAGATAATTATCAAGAACAATTTCAACATCAAAAGTTAGCCCAACTGG
 AAAATATTGAACCTAGTGCCTGACTAAACGCCTTAAAGCAAGCGGTCTG
 AAGATTTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAAG
 TTGCACTCAAACCTAAAGGGGAAGCTATGATTTTC

PRETTY of: /biotmp/msa31912.2{*} February 18, 2003 08:19 ..

	1				50
msa31912.2{338_18RS21}	---TCTGCTA	TAATAGACAA	AAAGGTGGTG	aTATTTATGT	ATTAGCATT
msa31912.2{338_2603}	ttgTCTGCTA	TAATAGACAA	AAAGGTGGTG	aTATTTATGT	ATTAGCATT
msa31912.2{338_A909}	---TCTGCTA	TAATAGACAA	AAAGGTGGTG	aTATTTATGT	ATTAGCATT
msa31912.2{338_H36B}	---TCTGCTA	TAATAGACAA	AAAGGTGGTG	aTATTTATGT	ATTAGCATT
msa31912.2{338_JM9130013}	---TCTGCTA	TAATAGACAA	AAAGGTGGTG	aTATTTATGT	ATTAGCATT
msa31912.2{338_COH1}	---TCTGCTA	TAATAGACAA	AAAGGTGGTG	aTATTTATGT	ATTAGCATT
msa31912.2{338_M732}	---TCTGCTA	TAATAGACAA	AAAGGTGGTG	aTATTTATGT	ATTAGCATT
msa31912.2{338_M781}	---TCTGCTA	TAATAGACAA	AAAGGTGGTG	aTATTTATGT	ATTAGCATT
msa31912.2{338_090}	---TCTGCTA	TAATAGACAA	AAAGGTGGTG	aTATTTATGT	ATTAGCATT
msa31912.2{338_CJB110}	---TCTGCTA	TAATAGACAA	AAAGGTGGTG	gTATTTATGT	ATTAGCATT
Consensus	*****	*****	*****	*****	*****
	51				100
msa31912.2{338_18RS21}	AATCGGTGAT	ATCATTAATT	CAAAACAGAT	ACTTGAACGT	GAAACTTTCC
msa31912.2{338_2603}	AATCGGTGAT	ATCATTAATT	CAAAACAGAT	ACTTGAACGT	GAAACTTTCC
msa31912.2{338_A909}	AATCGGTGAT	ATCATTAATT	CAAAACAGAT	ACTTGAACGT	GAAACTTTCC
msa31912.2{338_H36B}	AATCGGTGAT	ATCATTAATT	CAAAACAGAT	ACTTGAACGT	GAAACTTTCC
msa31912.2{338_JM9130013}	AATCGGTGAT	ATCATTAATT	CAAAACAGAT	ACTTGAACGT	GAAACTTTCC
msa31912.2{338_COH1}	AATCGGTGAT	ATCATTAATT	CAAAACAGAT	ACTTGAACGT	GAAACTTTCC
msa31912.2{338_M732}	AATCGGTGAT	ATCATTAATT	CAAAACAGAT	ACTTGAACGT	GAAACTTTCC
msa31912.2{338_M781}	AATCGGTGAT	ATCATTAATT	CAAAACAGAT	ACTTGAACGT	GAAACTTTCC
msa31912.2{338_090}	AATCGGTGAT	ATCATTAATT	CAAAACAGAT	ACTTGAACGT	GAAACTTTCC
msa31912.2{338_CJB110}	AATCGGTGAT	ATCATTAATT	CAAAACAGAT	ACTTGAACGT	GAAACTTTCC
Consensus	*****	*****	*****	*****	*****
	101				150
msa31912.2{338_18RS21}	AACAGTCTTT	TCAGCAACTA	ATGACCGAAC	TATCTGATGT	ATATGGTGAA
msa31912.2{338_2603}	AACAGTCTTT	TCAGCAACTA	ATGACCGAAC	TATCTGATGT	ATATGGTGAA
msa31912.2{338_A909}	AACAGTCTTT	TCAGCAACTA	ATGACCGAAC	TATCTGATGT	ATATGGTGAA
msa31912.2{338_H36B}	AACAGTCTTT	TCAGCAACTA	ATGACCGAAC	TATCTGATGT	ATATGGTGAA
msa31912.2{338_JM9130013}	AACAGTCTTT	TCAGCAACTA	ATGACCGAAC	TATCTGATGT	ATATGGTGAA
msa31912.2{338_COH1}	AACAGTCTTT	TCAGCAACTA	ATGACCGAAC	TATCTGATGT	ATATGGTGAA
msa31912.2{338_M732}	AACAGTCTTT	TCAGCAACTA	ATGACCGAAC	TATCTGATGT	ATATGGTGAA
msa31912.2{338_M781}	AACAGTCTTT	TCAGCAACTA	ATGACCGAAC	TATCTGATGT	ATATGGTGAA
msa31912.2{338_090}	AACAGTCTTT	TCAGCAACTA	ATGACCGAAC	TATCTGATGT	ATATGGTGAA
msa31912.2{338_CJB110}	AACAGTCTTT	TCAGCAACTA	ATGACCGAAC	TATCTGATGT	ATATGGTGAA
Consensus	*****	*****	*****	*****	*****
	151				200
msa31912.2{338_18RS21}	GAGCTGATTT	CTCcATTAC	TATTACAGCT	GGTGATGAAT	TTCAAGCTTT
msa31912.2{338_2603}	GAGCTGATTT	CTCcATTAC	TATTACAGCT	GGTGATGAAT	TTCAAGCTTT
msa31912.2{338_A909}	GAGCTGATTT	CTCcATTAC	TATTACAGCT	GGTGATGAAT	TTCAAGCTTT
msa31912.2{338_H36B}	GAGCTGATTT	CTCcATTAC	TATTACAGCT	GGTGATGAAT	TTCAAGCTTT
msa31912.2{338_JM9130013}	GAGCTGATTT	CTCcATTAC	TATTACAGCT	GGTGATGAAT	TTCAAGCTTT
msa31912.2{338_COH1}	GAGCTGATTT	CTCcATTAC	TATTACAGCT	GGTGATGAAT	TTCAAGCTTT
msa31912.2{338_M732}	GAGCTGATTT	CTCcATTAC	TATTACAGCT	GGTGATGAAT	TTCAAGCTTT
msa31912.2{338_M781}	GAGCTGATTT	CTCcATTAC	TATTACAGCT	GGTGATGAAT	TTCAAGCTTT
msa31912.2{338_090}	GAGCTGATTT	CTCcATTAC	TATTACAGCT	GGTGATGAAT	TTCAAGCTTT
msa31912.2{338_CJB110}	GAGCTGATTT	CTCcATTAC	TATTACAGCT	GGTGATGAAT	TTCAAGCTTT
Consensus	*****	***-*****	*****	*****	*****
	201				250
msa31912.2{338_18RS21}	ATTGAAACcA	TCAAAAAAGG	TATTTCAAAT	TATTGACCAT	ATTCAACTAG
msa31912.2{338_2603}	ATTGAAACcA	TCAAAAAAGG	TATTTCAAAT	TATTGACCAT	ATTCAACTAG
msa31912.2{338_A909}	ATTGAAACcA	TCAAAAAAGG	TATTTCAAAT	TATTGACCAT	ATTCAACTAG
msa31912.2{338_H36B}	ATTGAAACcA	TCAAAAAAGG	TATTTCAAAT	TATTGACCAT	ATTCAACTAG
msa31912.2{338_JM9130013}	ATTGAAACcA	TCAAAAAAGG	TATTTCAAAT	TATTGACCAT	ATTCAACTAG
msa31912.2{338_COH1}	ATTGAAACcA	TCAAAAAAGG	TATTTCAAAT	TATTGACCAT	ATTCAACTAG
msa31912.2{338_M732}	ATTGAAACcA	TCAAAAAAGG	TATTTCAAAT	TATTGACCAT	ATTCAACTAG
msa31912.2{338_M781}	ATTGAAACcA	TCAAAAAAGG	TATTTCAAAT	TATTGACCAT	ATTCAACTAG
msa31912.2{338_090}	ATTGAAACcA	TCAAAAAAGG	TATTTCAAAT	TATTGACCAT	ATTCAACTAG
msa31912.2{338_CJB110}	ATTGAAACcA	TCAAAAAAGG	TATTTCAAAT	TATTGACCAT	ATTCAACTAG
Consensus	*****-*	*****	*****	*****	*****
	251				300
msa31912.2{338_18RS21}	CTCTAAAAACC	TGTTAATGTA	AGGTTCCGGCC	TCGGTACAGG	AAACATTATA
msa31912.2{338_2603}	CTCTAAAAACC	TGTTAATGTA	AGGTTCCGGCC	TCGGTACAGG	AAACATTATA

Table 73: Comparative Sequences relating to SAG0981

msa31912.2{338_A909}	CTCTAAAACC	TGTTAATGTA	AGGTTTCGGCC	TCGGTACAGG	AAACATTATA
msa31912.2{338_H36B}	CTCTAAAACC	TGTTAATGTA	AGGTTTCGGCC	TCGGTACAGG	AAACATTATA
msa31912.2{338_JM9130013}	CTCTAAAACC	TGTTAATGTA	AGGTTTCGGCC	TCGGTACAGG	AAACATTATA
msa31912.2{338_COH1}	CTCTAAAACC	TGTTAATGTA	AGGTTTCGGCC	TCGGTACAGG	AAACATTATA
msa31912.2{338_M732}	CTCTAAAACC	TGTTAATGTA	AGGTTTCGGCC	TCGGTACAGG	AAACATTATA
msa31912.2{338_M781}	CTCTAAAACC	TGTTAATGTA	AGGTTTCGGCC	TCGGTACAGG	AAACATTATA
msa31912.2{338_090}	CTCTAAAACC	TGTTAATGTA	AGGTTTCGGCC	TCGGTACAGG	AAACATTATA
msa31912.2{338_CJB110}	CTCTAAAACC	TGTTAATGTA	AGGTTTCGGCC	TCGGTACAGG	AAACATTATA
Consensus	*****	*****	*****	*****	*****
msa31912.2{338_18RS21}	ACATCCATCA	ATTcAAATGA	AAGTATCGGT	GCTGATGGTC	CTGCCTACTG
msa31912.2{338_2603}	ACATCCATCA	ATTcAAATGA	AAGTATCGGT	GCTGATGGTC	CTGCCTACTG
msa31912.2{338_A909}	ACATCCATCA	ATTcAAATGA	AAGTATCGGT	GCTGATGGTC	CTGCCTACTG
msa31912.2{338_H36B}	ACATCCATCA	ATTcAAATGA	AAGTATCGGT	GCTGATGGTC	CTGCCTACTG
msa31912.2{338_JM9130013}	ACATCCATCA	ATTcAAATGA	AAGTATCGGT	GCTGATGGTC	CTGCCTACTG
msa31912.2{338_COH1}	ACATCCATCA	ATTcAAATGA	AAGTATCGGT	GCTGATGGTC	CTGCCTACTG
msa31912.2{338_M732}	ACATCCATCA	ATTcAAATGA	AAGTATCGGT	GCTGATGGTC	CTGCCTACTG
msa31912.2{338_M781}	ACATCCATCA	ATTcAAATGA	AAGTATCGGT	GCTGATGGTC	CTGCCTACTG
msa31912.2{338_090}	ACATCCATCA	ATTcAAATGA	AAGTATCGGT	GCTGATGGTC	CTGCCTACTG
msa31912.2{338_CJB110}	ACATCCATCA	ATTcAAATGA	AAGTATCGGT	GCTGATGGTC	CTGCCTACTG
Consensus	*****	***-*****	*****	*****	*****
msa31912.2{338_18RS21}	GCATGCTCGC	TCAGCTATTA	ATCATATACA	TGATAAAAAAT	GATTATGGAA
msa31912.2{338_2603}	GCATGCTCGC	TCAGCTATTA	ATCATATACA	TGATAAAAAAT	GATTATGGAA
msa31912.2{338_A909}	GCATGCTCGC	TCAGCTATTA	ATCATATACA	TGATAAAAAAT	GATTATGGAA
msa31912.2{338_H36B}	GCATGCTCGC	TCAGCTATTA	ATCATATACA	TGATAAAAAAT	GATTATGGAA
msa31912.2{338_JM9130013}	GCATGCTCGC	TCAGCTATTA	ATCATATACA	TGATAAAAAAT	GATTATGGAA
msa31912.2{338_COH1}	GCATGCTCGC	TCAGCTATTA	ATCATATACA	TGATAAAAAAT	GATTATGGAA
msa31912.2{338_M732}	GCATGCTCGC	TCAGCTATTA	ATCATATACA	TGATAAAAAAT	GATTATGGAA
msa31912.2{338_M781}	GCATGCTCGC	TCAGCTATTA	ATCATATACA	TGATAAAAAAT	GATTATGGAA
msa31912.2{338_090}	GCATGCTCGC	TCAGCTATTA	ATCATATACA	TGATAAAAAAT	GATTATGGAA
msa31912.2{338_CJB110}	GCATGCTCGC	TCAGCTATTA	ATCATATACA	TGATAAAAAAT	GATTATGGAA
Consensus	*****	*****	*****	*****	*****
msa31912.2{338_18RS21}	CAGTTCAAGT	AGCTATTTGC	CTTGATGATG	AAGACCAAAA	CCTTGAATTA
msa31912.2{338_2603}	CAGTTCAAGT	AGCTATTTGC	CTTGATGATG	AAGACCAAAA	CCTTGAATTA
msa31912.2{338_A909}	CAGTTCAAGT	AGCTATTTGC	CTTGATGATG	AAGACCAAAA	CCTTGAATTA
msa31912.2{338_H36B}	CAGTTCAAGT	AGCTATTTGC	CTTGATGATG	AAGACCAAAA	CCTTGAATTA
msa31912.2{338_JM9130013}	CAGTTCAAGT	AGCTATTTGC	CTTGATGATG	AAGACCAAAA	CCTTGAATTA
msa31912.2{338_COH1}	CAGTTCAAGT	AGCTATTTGC	CTTGATGATG	AAGACCAAAA	CCTTGAATTA
msa31912.2{338_M732}	CAGTTCAAGT	AGCTATTTGC	CTTGATGATG	AAGACCAAAA	CCTTGAATTA
msa31912.2{338_M781}	CAGTTCAAGT	AGCTATTTGC	CTTGATGATG	AAGACCAAAA	CCTTGAATTA
msa31912.2{338_090}	CAGTTCAAGT	AGCTATTTGC	CTTGATGATG	AAGACCAAAA	CCTTGAATTA
msa31912.2{338_CJB110}	CAGTTCAAGT	AGCTATTTGC	CTTGATGATG	AAGACCAAAA	CCTTGAATTA
Consensus	*****	*****	*****	*****	*****
msa31912.2{338_18RS21}	ACACTAAATA	GTCTCATTTT	AGCTGGTGAT	TTTATCAAGT	CAAAATGGAC
msa31912.2{338_2603}	ACACTAAATA	GTCTCATTTT	AGCTGGTGAT	TTTATCAAGT	CAAAATGGAC
msa31912.2{338_A909}	ACACTAAATA	GTCTCATTTT	AGCTGGTGAT	TTTATCAAGT	CAAAATGGAC
msa31912.2{338_H36B}	ACACTAAATA	GTCTCATTTT	AGCTGGTGAT	TTTATCAAGT	CAAAATGGAC
msa31912.2{338_JM9130013}	ACACTAAATA	GTCTCATTTT	AGCTGGTGAT	TTTATCAAGT	CAAAATGGAC
msa31912.2{338_COH1}	ACACTAAATA	GTCTCATTTT	AGCTGGTGAT	TTTATCAAGT	CAAAATGGAC
msa31912.2{338_M732}	ACACTAAATA	GTCTCATTTT	AGCTGGTGAT	TTTATCAAGT	CAAAATGGAC
msa31912.2{338_M781}	ACACTAAATA	GTCTCATTTT	AGCTGGTGAT	TTTATCAAGT	CAAAATGGAC
msa31912.2{338_090}	ACACTAAATA	GTCTCATTTT	AGCTGGTGAT	TTTATCAAGT	CAAAATGGAC
msa31912.2{338_CJB110}	ACACTAAATA	GTCTCATTTT	AGCTGGTGAT	TTTATCAAGT	CAAAATGGAC
Consensus	*****	*****	*****	*****	*****
msa31912.2{338_18RS21}	TACaAACCAT	TTTCAAATGC	TTGAGCACTT	AATACTTCAA	GATAATTATC
msa31912.2{338_2603}	TACaAACCAT	TTTCAAATGC	TTGAGCACTT	AATACTTCAA	GATAATTATC
msa31912.2{338_A909}	TACaAACCAT	TTTCAAATGC	TTGAGCACTT	AATACTTCAA	GATAATTATC
msa31912.2{338_H36B}	TACaAACCAT	TTTCAAATGC	TTGAGCACTT	AATACTTCAA	GATAATTATC
msa31912.2{338_JM9130013}	TACaAACCAT	TTTCAAATGC	TTGAGCACTT	AATACTTCAA	GATAATTATC
msa31912.2{338_COH1}	TACaAACCAT	TTTCAAATGC	TTGAGCACTT	AATACTTCAA	GATAATTATC
msa31912.2{338_M732}	TACaAACCAT	TTTCAAATGC	TTGAGCACTT	AATACTTCAA	GATAATTATC
msa31912.2{338_M781}	TACaAACCAT	TTTCAAATGC	TTGAGCACTT	AATACTTCAA	GATAATTATC
msa31912.2{338_090}	TACaAACCAT	TTTCAAATGC	TTGAGCACTT	AATACTTCAA	GATAATTATC
msa31912.2{338_CJB110}	TACaAACCAT	TTTCAAATGC	TTGAGCACTT	AATACTTCAA	GATAATTATC
Consensus	***-*****	*****	*****	*****	*****
msa31912.2{338_18RS21}	AAGAACAATT	TCAACATCAA	AAGTTAGCCC	AACTGGAAAA	TATTGAACCT
msa31912.2{338_2603}	AAGAACAATT	TCAACATCAA	AAGTTAGCCC	AACTGGAAAA	TATTGAACCT
msa31912.2{338_A909}	AAGAACAATT	TCAACATCAA	AAGTTAGCCC	AACTGGAAAA	TATTGAACCT
msa31912.2{338_H36B}	AAGAACAATT	TCAACATCAA	AAGTTAGCCC	AACTGGAAAA	TATTGAACCT
msa31912.2{338_JM9130013}	AAGAACAATT	TCAACATCAA	AAGTTAGCCC	AACTGGAAAA	TATTGAACCT
msa31912.2{338_COH1}	AAGAACAATT	TCAACATCAA	AAGTTAGCCC	AACTGGAAAA	TATTGAACCT
msa31912.2{338_M732}	AAGAACAATT	TCAACATCAA	AAGTTAGCCC	AACTGGAAAA	TATTGAACCT

Table 73: Comparative Sequences relating to SAG0981

msa31912.2{338_M781}	AAGAACAATT	TCAACATCAA	AAGTTAGCCC	AACTGGAAAA	TATTGAACCT
msa31912.2{338_090}	AAGAACAATT	TCAACATCAA	AAGTTAGCCC	AACTGGAAAA	TATTGAACCT
msa31912.2{338_CJB110}	AAGAACAATT	TCAACATCAA	AAGTTAGCCC	AACTGGAAAA	TATTGAACCT
Consensus	*****	*****	*****	*****	*****
msa31912.2{338_18RS21}	AGTGCGCTGA	CTAAACGCCT	TAAAGCAAGC	GGTCTGAAGA	TTTACTTAAG
msa31912.2{338_2603}	AGTGCGCTGA	CTAAACGCCT	TAAAGCAAGC	GGTCTGAAGA	TTTACTTAAG
msa31912.2{338_A909}	AGTGCGCTGA	CTAAACGCCT	TAAAGCAAGC	GGTCTGAAGA	TTTACTTAAG
msa31912.2{338_H36B}	AGTGCGCTGA	CTAAACGCCT	TAAAGCAAGC	GGTCTGAAGA	TTTACTTAAG
msa31912.2{338_JM9130013}	AGTGCGCTGA	CTAAACGCCT	TAAAGCAAGC	GGTCTGAAGA	TTTACTTAAG
msa31912.2{338_COH1}	AGTGCGCTGA	CTAAACGCCT	TAAAGCAAGC	GGTCTGAAGA	TTTACTTAAG
msa31912.2{338_M732}	AGTGCGCTGA	CTAAACGCCT	TAAAGCAAGC	GGTCTGAAGA	TTTACTTAAG
msa31912.2{338_M781}	AGTGCGCTGA	CTAAACGCCT	TAAAGCAAGC	GGTCTGAAGA	TTTACTTAAG
msa31912.2{338_090}	AGTGCGCTGA	CTAAACGCCT	TAAAGCAAGC	GGTCTGAAGA	TTTACTTAAG
msa31912.2{338_CJB110}	AGTGCGCTGA	CTAAACGCCT	TAAAGCAAGC	GGTCTGAAGA	TTTACTTAAG
Consensus	*****	*****	*****	*****	*****
msa31912.2{338_18RS21}	AACGAGAACA	CAGGCAGCCG	ATCTATTAGT	TAAAAGTTGC	ACTCAAACCTA
msa31912.2{338_2603}	AACGAGAACA	CAGGCAGCCG	ATCTATTAGT	TAAAAGTTGC	ACTCAAACCTA
msa31912.2{338_A909}	AACGAGAACA	CAGGCAGCCG	ATCTATTAGT	TAAAAGTTGC	ACTCAAACCTA
msa31912.2{338_H36B}	AACGAGAACA	CAGGCAGCCG	ATCTATTAGT	TAAAAGTTGC	ACTCAAACCTA
msa31912.2{338_JM9130013}	AACGAGAACA	CAGGCAGCCG	ATCTATTAGT	TAAAAGTTGC	ACTCAAACCTA
msa31912.2{338_COH1}	AACGAGAACA	CAGGCAGCCG	ATCTATTAGT	TAAAAGTTGC	ACTCAAACCTA
msa31912.2{338_M732}	AACGAGAACA	CAGGCAGCCG	ATCTATTAGT	TAAAAGTTGC	ACTCAAACCTA
msa31912.2{338_M781}	AACGAGAACA	CAGGCAGCCG	ATCTATTAGT	TAAAAGTTGC	ACTCAAACCTA
msa31912.2{338_090}	AACGAGAACA	CAGGCAGCCG	ATCTATTAGT	TAAAAGTTGC	ACTCAAACCTA
msa31912.2{338_CJB110}	AACGAGAACA	CAGGCAGCCG	ATCTATTAGT	TAAAAGTTGC	ACTCAAACCTA
Consensus	*****	*****	*****	*****	*****
msa31912.2{338_18RS21}	AAGGGGGAAG	CTATGATTTC			
msa31912.2{338_2603}	AAGGGGGAAG	CTATGATTTC			
msa31912.2{338_A909}	AAGGGGGAAG	CTATGATTTC			
msa31912.2{338_H36B}	AAGGGGGAAG	CTATGATTTC			
msa31912.2{338_JM9130013}	AAGGGGGAAG	CTATGATTTC			
msa31912.2{338_COH1}	AAGGGGGAAG	CTATGATTTC			
msa31912.2{338_M732}	AAGGGGGAAG	CTATGATTTC			
msa31912.2{338_M781}	AAGGGGGAAG	CTATGATTTC			
msa31912.2{338_090}	AAGGGGGAAG	CTATGATTTC			
msa31912.2{338_CJB110}	AAGGGGGAAG	CTATGATTTC			
Consensus	*****	*****			
SEQ ID NO. 7311					
STRAIN 2603 frame: 1					
LSAIDKKVVFMYLALIGDIINSKQILERETFQQS FQQLMTELSDVYGEELISPFTITA					
GDEFQALLKPSKKVFQIIDHIQLALKPVNVRFG LGTGNIIITSINSNESIGADGPAYWHAR					
SAINHIHDKNNDYGT VQVAICLDDEDQNL ETLNLSISAGDFIKSKWTTNHFQMLEHLILQ					
DNYQE QFQHQLAQL ENIEPSALT KRLKASGLKIYLRTRTQAADLLVKSC TQTKGGSYDF					
SEQ ID NO. 7312					
STRAIN 090 frame: 1					
SAIDKKVVFMYLALIGDIINSKQILERETFQQS FQQLMTELSDVYGEELISPFTITAG					
DEFQALLKPSKKVFQIIDHIQLALKPVNVRFG LGTGNIIITSINL NESIGADGPAYWHARS					
AINHIHDKNNDYGT VQVAICLDDEDQNL ETLNLSISAGDFIKSKWTTNHFQMLEHLILQD					
NYQE QFQHQLAQL ENIEPSALT KRLKASGLKIYLRTRTQAADLLVKSC TQTKGGSYDF					
SEQ ID NO. 7313					
STRAIN A909 frame: 1					
SAIDKKVVFMYLALIGDIINSKQILERETFQQS FQQLMTELSDVYGEELISPFTITAG					
DEFQALLKPSKKVFQIIDHIQLALKPVNVRFG LGTGNIIITSINSNESIGADGPAYWHARS					
AINHIHDKNNDYGT VQVAICLDDEDQNL ETLNLSISAGDFIKSKWTTNHFQMLEHLILQD					
NYQE QFQHQLAQL ENIEPSALT KRLKASGLKIYLRTRTQAADLLVKSC TQTKGGSYDF					
SEQ ID NO. 7314					
STRAIN H36B frame: 1					
SAIDKKVVFMYLALIGDIINSKQILERETFQQS FQQLMTELSDVYGEELISPFTITAG					
DEFQALLKPSKKVFQIIDHIQLALKPVNVRFG LGTGNIIITSINSNESIGADGPAYWHARS					
AINHIHDKNNDYGT VQVAICLDDEDQNL ETLNLSISAGDFIKSKWTTNHFQMLEHLILQD					
NYQE QFQHQLAQL ENIEPSALT KRLKASGLKIYLRTRTQAADLLVKSC TQTKGGSYDF					
SEQ ID NO. 7315					
STRAIN 18RS21 frame: 1					
SAIDKKVVFMYLALIGDIINSKQILERETFQQS FQQLMTELSDVYGEELISPFTITAG					
DEFQALLKPSKKVFQIIDHIQLALKPVNVRFG LGTGNIIITSINSNESIGADGPAYWHARS					
AINHIHDKNNDYGT VQVAICLDDEDQNL ETLNLSISAGDFIKSKWTTNHFQMLEHLILQD					
NYQE QFQHQLAQL ENIEPSALT KRLKASGLKIYLRTRTQAADLLVKSC TQTKGGSYDF					
SEQ ID NO. 7316					
STRAIN M732 frame: 1					
SAIDKKVVFMYLALIGDIINSKQILERETFQQS FQQLMTELSDVYGEELISPFTITAG					

Table 73: Comparative Sequences relating to SAG0981

DEFQALLKQSKKVFQIIDHIQLALKPVNVRFGGLGTGNIITSINSNESIGADGPAYWHARS
 AINHIHDKNDYGTQVQVAICLDDQNLLELTLSLISAGDFIKSKWTTNHFQMLEHLILQD
 NYQEQQFQHQKLAQLENIEPSALTKRLKASGLKIYLRTRTQAADLLVKSCQTQKGGSYDF

SEQ ID NO. 7317

STRAIN COH1 frame: 1

SAIIDKKVVFMYLALIGDIINSKQILERETFQOSFQQLMTELSDVYGEELISPFTITAG
 DEFQALLKQSKKVFQIIDHIQLALKPVNVRFGGLGTGNIITSINSNESIGADGPAYWHARS
 AINHIHDKNDYGTQVQVAICLDDQNLLELTLSLISAGDFIKSKWTTNHFQMLEHLILQD
 NYQEQQFQHQKLAQLENIEPSALTKRLKASGLKIYLRTRTQAADLLVKSCQTQKGGSYDF

SEQ ID NO. 7318

STRAIN M781 frame: 1

SAIIDKKVVFMYLALIGDIINSKQILERETFQOSFQQLMTELSDVYGEELISPFTITAG
 DEFQALLKQSKKVFQIIDHIQLALKPVNVRFGGLGTGNIITSINSNESIGADGPAYWHARS
 AINHIHDKNDYGTQVQVAICLDDQNLLELTLSLISAGDFIKSKWTTNHFQMLEHLILQD
 NYQEQQFQHQKLAQLENIEPSALTKRLKASGLKIYLRTRTQAADLLVKSCQTQKGGSYDF

SEQ ID NO. 7319

STRAIN CJB110 frame: 1

SAIIDKKVVFMYLALIGDIINSKQILERETFQOSFQQLMTELSDVYGEELISLFTITAG
 DEFQALLKPSKKVFQIIDHIQLALKPVNVRFGGLGTGNIITSINSNESIGADGPAYWHARS
 AINHIHDKNDYGTQVQVAICLDDQNLLELTLSLISAGDFIKSKWTTNHFQMLEHLILQD
 NYQEQQFQHQKLAQLENIEPSALTKRLKASGLKIYLRTRTQAADLLVKSCQTQKGGSYDF

SEQ ID NO. 7320

STRAIN JM9130013 frame: 1

SAIIDKKVVFMYLALIGDIINSKQILERETFQOSFQQLMTELSDVYGEELISPFTITAG
 DEFQALLKPSKKVFQIIDHIQLALKPVNVRFGGLGTGNIITSINSNESIGADGPAYWHARS
 AINHIHDKNDYGTQVQVAICLDDQNLLELTLSLISAGDFIKSKWTTNHFQMLEHLILQD
 NYQEQQFQHQKLAQLENIEPSALTKRLKASGLKIYLRTRTQAADLLVKSCQTQKGGSYDF

PRETTY of: /biotmp/msa32053.2{*} February 18, 2003 08:25 ..

	1		50
msa32053.2{338_18RS21}	~SAIIDKKVV iFMYLALIGD IINSKQILER	ETFQOSFQQL MTELSDVYGE	
msa32053.2{338_2603}	lSAIIDKKVV iFMYLALIGD IINSKQILER	ETFQOSFQQL MTELSDVYGE	
msa32053.2{338_A909}	~SAIIDKKVV iFMYLALIGD IINSKQILER	ETFQOSFQQL MTELSDVYGE	
msa32053.2{338_CJB110}	~SAIIDKKVV vFMYLALIGD IINSKQILER	ETFQOSFQQL MTELSDVYGE	
msa32053.2{338_COH1}	~SAIIDKKVV iFMYLALIGD IINSKQILER	ETFQOSFQQL MTELSDVYGE	
msa32053.2{338_H36B}	~SAIIDKKVV iFMYLALIGD IINSKQILER	ETFQOSFQQL MTELSDVYGE	
msa32053.2{338_JM9130013}	~SAIIDKKVV iFMYLALIGD IINSKQILER	ETFQOSFQQL MTELSDVYGE	
msa32053.2{338_M732}	~SAIIDKKVV iFMYLALIGD IINSKQILER	ETFQOSFQQL MTELSDVYGE	
msa32053.2{338_M781}	~SAIIDKKVV iFMYLALIGD IINSKQILER	ETFQOSFQQL MTELSDVYGE	
msa32053.2{338_090}	~SAIIDKKVV iFMYLALIGD IINSKQILER	ETFQOSFQQL MTELSDVYGE	
Consensus	***** -***** *****	***** *****	
	51		100
msa32053.2{338_18RS21}	ELISpFTITA GDEFQALLKp SKKVFQIIDH IQLALKPVNV	RFGLGTGNI I	
msa32053.2{338_2603}	ELISpFTITA GDEFQALLKp SKKVFQIIDH IQLALKPVNV	RFGLGTGNI I	
msa32053.2{338_A909}	ELISpFTITA GDEFQALLKp SKKVFQIIDH IQLALKPVNV	RFGLGTGNI I	
msa32053.2{338_CJB110}	ELISlFTITA GDEFQALLKp SKKVFQIIDH IQLALKPVNV	RFGLGTGNI I	
msa32053.2{338_COH1}	ELISpFTITA GDEFQALLKq SKKVFQIIDH IQLALKPVNV	RFGLGTGNI I	
msa32053.2{338_H36B}	ELISpFTITA GDEFQALLKp SKKVFQIIDH IQLALKPVNV	RFGLGTGNI I	
msa32053.2{338_JM9130013}	ELISpFTITA GDEFQALLKp SKKVFQIIDH IQLALKPVNV	RFGLGTGNI I	
msa32053.2{338_M732}	ELISpFTITA GDEFQALLKq SKKVFQIIDH IQLALKPVNV	RFGLGTGNI I	
msa32053.2{338_M781}	ELISpFTITA GDEFQALLKq SKKVFQIIDH IQLALKPVNV	RFGLGTGNI I	
msa32053.2{338_090}	ELISpFTITA GDEFQALLKp SKKVFQIIDH IQLALKPVNV	RFGLGTGNI I	
Consensus	****-***** *****- *****	***** *****	
	101		150
msa32053.2{338_18RS21}	TSINsNESIG ADGPAYWHAR SAINHIHDKN	DYGTQVQVAIC LDDQNLLEL	
msa32053.2{338_2603}	TSINsNESIG ADGPAYWHAR SAINHIHDKN	DYGTQVQVAIC LDDQNLLEL	
msa32053.2{338_A909}	TSINsNESIG ADGPAYWHAR SAINHIHDKN	DYGTQVQVAIC LDDQNLLEL	
msa32053.2{338_CJB110}	TSINsNESIG ADGPAYWHAR SAINHIHDKN	DYGTQVQVAIC LDDQNLLEL	
msa32053.2{338_COH1}	TSINsNESIG ADGPAYWHAR SAINHIHDKN	DYGTQVQVAIC LDDQNLLEL	
msa32053.2{338_H36B}	TSINsNESIG ADGPAYWHAR SAINHIHDKN	DYGTQVQVAIC LDDQNLLEL	
msa32053.2{338_JM9130013}	TSINsNESIG ADGPAYWHAR SAINHIHDKN	DYGTQVQVAIC LDDQNLLEL	
msa32053.2{338_M732}	TSINsNESIG ADGPAYWHAR SAINHIHDKN	DYGTQVQVAIC LDDQNLLEL	
msa32053.2{338_M781}	TSINsNESIG ADGPAYWHAR SAINHIHDKN	DYGTQVQVAIC LDDQNLLEL	
msa32053.2{338_090}	TSINlNESIG ADGPAYWHAR SAINHIHDKN	DYGTQVQVAIC LDDQNLLEL	
Consensus	****-***** *****	***** *****	
	151		200
msa32053.2{338_18RS21}	TLNSLISAGD FIKSKWTTNH FQMLEHLILQ	DNYQEQQFQHQ KLAQLENIEP	
msa32053.2{338_2603}	TLNSLISAGD FIKSKWTTNH FQMLEHLILQ	DNYQEQQFQHQ KLAQLENIEP	
msa32053.2{338_A909}	TLNSLISAGD FIKSKWTTNH FQMLEHLILQ	DNYQEQQFQHQ KLAQLENIEP	
msa32053.2{338_CJB110}	TLNSLISAGD FIKSKWTTNH FQMLEHLILQ	DNYQEQQFQHQ KLAQLENIEP	
msa32053.2{338_COH1}	TLNSLISAGD FIKSKWTTNH FQMLEHLILQ	DNYQEQQFQHQ KLAQLENIEP	
msa32053.2{338_H36B}	TLNSLISAGD FIKSKWTTNH FQMLEHLILQ	DNYQEQQFQHQ KLAQLENIEP	
msa32053.2{338_JM9130013}	TLNSLISAGD FIKSKWTTNH FQMLEHLILQ	DNYQEQQFQHQ KLAQLENIEP	
msa32053.2{338_M732}	TLNSLISAGD FIKSKWTTNH FQMLEHLILQ	DNYQEQQFQHQ KLAQLENIEP	
msa32053.2{338_M781}	TLNSLISAGD FIKSKWTTNH FQMLEHLILQ	DNYQEQQFQHQ KLAQLENIEP	

Table 73: Comparative Sequences relating to SAG0981

msa32053.2{338_090}	TLNSLISAGD	FIKSKWTTNH	FQMLEHLILQ	DNYQEQFQHQ	KLAQLENIEP
Consensus	*****	*****	*****	*****	*****
	201			240	
msa32053.2{338_18RS21}	SALTKRLKAS	GLKIYLRTRT	QAADLLVKSC	TQTKGGSYDF	
msa32053.2{338_2603}	SALTKRLKAS	GLKIYLRTRT	QAADLLVKSC	TQTKGGSYDF	
msa32053.2{338_A909}	SALTKRLKAS	GLKIYLRTRT	QAADLLVKSC	TQTKGGSYDF	
msa32053.2{338_CJB110}	SALTKRLKAS	GLKIYLRTRT	QAADLLVKSC	TQTKGGSYDF	
msa32053.2{338_COH1}	SALTKRLKAS	GLKIYLRTRT	QAADLLVKSC	TQTKGGSYDF	
msa32053.2{338_H36B}	SALTKRLKAS	GLKIYLRTRT	QAADLLVKSC	TQTKGGSYDF	
msa32053.2{338_JM9130013}	SALTKRLKAS	GLKIYLRTRT	QAADLLVKSC	TQTKGGSYDF	
msa32053.2{338_M732}	SALTKRLKAS	GLKIYLRTRT	QAADLLVKSC	TQTKGGSYDF	
msa32053.2{338_M781}	SALTKRLKAS	GLKIYLRTRT	QAADLLVKSC	TQTKGGSYDF	
msa32053.2{338_090}	SALTKRLKAS	GLKIYLRTRT	QAADLLVKSC	TQTKGGSYDF	
Consensus	*****	*****	*****	*****	

Table 74: Comparative Sequences relating to SAG1572

SEQ ID NO. 7401

STRAIN 2603

ATGGAAATGCAAGTTCAAAAAAGTTTTAAATCAAATATACATTACGGAACACTCTAT
CTAGTCCCAACTCCAATTGGTAATCTAGATGATATGACTTTTCGTGCCATTAGGATTTTA
AGAGAAGTTGATTTTATTTGTGCAGAGGATACACGAAATACGGGACTTTTACTCAAGCAC
TTTGATATTACTACTAAACAAATTAGTTTTCACGAACACAATGCTTACGATAAAATCTCT
GGGTTAATTGATTTGTTAAAAGAAGGGAAATCTTTAGCCCAAGTATCTGATGCAGGAATG
CCCTCTATTTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAAGGGGATATCCCA
GTTGTATCTATACCAGGAGCTAGCGCTGGTATTACTGCTCTCATCGCTTCAGGTTTAGCT
CCACAACCTCATATTTTTATGGCTTCTTACCTCGTAAGAAAGGTCAACAAATAACTTTC
TTTGAAACAAAGCAAGATTACCCTGAAACACAAATCTTTTATGAGTCACCGTTTCGAGTC
TCTGATACGCTAAAACACATGAAAGAGATTTACGAGAGATCGCCAAGTTGTTTTAGTACGC
GAATTGACGAAACTCTATGAAGAGTATCAAAGAGGAACCAITTAGTCAACTTTTAGAGCAT
ATTGAAAGGTCCCTCTCAAAGGTGAATGCTTAATTATTGTTGATGGTAAGAGAGATACC
GAGCGAGTGAAAGACAGTAGCCAACAAGATCCACTAGTATTAGTAAAAGAATATATCGCT
AATGGTGATAAACTAATCAAGCGATAAAAAAGTAGCAAAAGAATTTAATCTCAATAGA
CAAGAACTCTATGCTAGTTTCCATGATTTA

SEQ ID NO. 7402

STRAIN 090

GAAATGCAAGTTCAAAAAAGTTTTAAATCAAATACACATTACGGGACACT
CTATCTAGTCCCAACTCCAATTGGTAATCTAGATGATATGACTTTTCGTG
CCATTAGGATTTTAAGAGAAGTTGATTTTATTTGTGCAGAGGATACACGA
AATACGGGACTTTTACTCAAGCACTTTGATATTACTACTAAACAAATTAG
TTTTTCACGAACACAATGCTTACGATAAAATCTCTGGGTTAATTGATTTGT
TAAAAGAAGGGAGATCTTTAGCCCAAGTATCTGATGCAGGAATGCCCTCT
ATTTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAAGGGGGGAT
CCCGGTCTGATCTATACCAGGAGCTAGCGCTGGTATTACTGCTCTCATCG
CTTCAGGTTTAGCTCCACAACCTCATATTTTTATGGCTTCTTACCGCGT
AAGAAAGGTCAACAAATAACTTTTTTTGAAACAAAGAAAGATTACCCTGa
AACACAAATCTTTTATGAGTCACCGTTCGAGTCTCTGATACGCTAAAAC
ACATGAAAGAGATTTACGGAGATCGCCAAGTTGTTTAGTACGCGAATTG
ACGAAaCTCTATGAAGAGTATCAAAGAGGAACCAITTAGTCAACTTTTAGG
GCATATTGAAAAAGTCCCTCTCAAAGGTGAATGCTTAATTATTGTTGATG
GTAAGAGAGATACCGAGCGAGTGAAAGACAGTAGCCAACAAGATCCACTA
GTATTAGTAA

SEQ ID NO. 7403

STRAIN A909

AGTTCAAAAAAGTTTTAAATCAAATATACATTACGGAACACTCTATCTAG
TCCCAACTCCAATTGGTAATCTAGATGATATGACTTTTCGTGCCATTAGG
ATTTTAAGAGAAGTTGATTTTATTTGTGCAGAGGATACACGAAATACGGG
ACTTTTACTCAAGCACTTTGATATTACTACTAAACAAATTAGTTTTACG
AACACAATGCTTACGATAAAATCTCTGGGTTAATTGATTTGTTAAAAGAA
GGGAAATCTTTAGCCCAAGTATCTGATGCAGGAATGCCCTCTATTTCTGA
CCCGAGACATGACCTTGTCAAGGCTGCTATTGAAGGGGATATCCAGTTG
TATCTATACCAGGAGCTAGCGCTGGTATTACTGCTCTCATCGCTTCAGGT
TTAGCTCCACAACCTCATATTTTTATGGCTTCTTACCACGTAAGAAAGG
TCAACAAATAACTTTCTTTGAAACAAAGCAAGATTACCCTGAAACACAAA
TCTTTTATGAGTCACCGTTTCGAGTCTCTGATACGCTAAAACACATGAAA
GAGATTTACGGAGATCGCCAAGTTGTTTAGTACGCGAATTGACGAAACT
CTATGAAGAGTATCAAAGAGGAACCAITTAGTCAACTTTTAGAGCATAITG
AAAAGGTCCCTCTCAAAGGTGAATGCTTAATTATTGTTGATGGTAAGAGA
GATACCGAGCGAGTGAAAGACAGTAGCCAACAAGATCCACTAGTATTAGT
AA

SEQ ID NO. 7404

STRAIN H36B

GAAATGCAAGTTCAAAAAAGTTTTAAATCAAATACACATT
ACGGGACACTCTATCTAGTCCCAACTCCAATTGGTAATCTAGATGATATG
ACTTTTCGTGCCATTAGGATTTTAAGAGAAGTTGATTTTATTTGTGCAGA
GGATACACGAAATAACGGGACTTTTACTCAAGCACTTTGATATTACTACTA
AACAAATTAGTTTTCACGAACACAATGCTTATGATAAAATCTCTGGGTTA
ATTGATTTGTTAAAAGAAGGGAGATCTTTAGCCCAAGTATCTGATGCAGG
AATGCCCTCTATTTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTG
AAGGGGATATCCCGGTCTGATCTATACCAGGAGCTAGCGCTGGTATTACT
GCTCTCATCGCTTCAGGTTTAGCTCCACAACCTCATATTTTTATGGCTT
CTTACCGCGTAAGCAAGGTCAACAAATAACTTTTTTTGAAACAAAGAAAG
ATTACCCTGAAACACAAATCTTTTATGAGTCACCGTTCGAGTCTCTGAT
ACGCTAAAACACATGAAAGAGATTTATGGAGATCGCCAAGTTGTTTAGT
ACGCGAATTGACGAAACTCTATGAAGAGTATCAAAGAGGAACCAITTAGTC
AACTTTTAGGGCATATTGAAAAGGTCCCTCTCAAAGGTGAATGCTTAATT
ATTGTTGATGGTAAGAGAGATAGTACGAGAGTGAAAGACAGTAGCCAACA
AGATCCACTAGTATTAGTAA

SEQ ID NO. 7405

STRAIN 18RS21

GAAATGCAAGTTCAAAAAAGTTTTAAATCAAATATACATT
ACGGAACACTCTATCTAGTCCCAACTCCAATTGGTAATCTAGATGATATG
ACTTTTCGTGCCATTAGGATTTTAAGAGAAGTTGATTTTATTTGTGCAGA
GGATACACGAAATAACGGGACTTTTACTCAAGCACTTTGATATTACTACTA
AACAAATTAGTTTTCACGAACACAATGCTTACGATAAAATCTCTGGGTTA
ATTGATTTGTTAAAAGAAGGGAAATCTTTAGCCCAAGTATCTGATGCAGG

Table 74: Comparative Sequences relating to SAG1572

AATGCCCTCTATTTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTG
 AAGGGGATATCCAGTTGTATCTATACCAGGAGCTAGCGCTGGTATTACT
 GCTCTCATCGCTTCAGGTTTAGCTCCACAACCTCATATTTTTATGGCTT
 CTTACCACGTAAGAAAGGTCAACAAATAACTTTCTTGAACAAAGCAAG
 ATTACCCTGAAACACAAATCTTTTATGAGTCACCGTTTCGAGTCTCTGAT
 ACGCTAAAACACATGAAAGAGATTTACGGAGATCGCCAAGTTGTTTAGT
 ACGCGAATTGACGAACTCTATGAAGAGTATCAAAGAGGAACCATTAGTC
 AACTTTTAGAGCATATTGAAAAGGTCCCTCTCAAAGGTGAATGCTTAATT
 ATTGTTGATGGTAAGAGAGATACCGAGCGAGTGAAAGACAGTAGCCAACA
 AGATCCACTAGTATTAGTAA

SEQ ID NO. 7406

STRAIN M732

GAAATGCAAGTTCAAAAAAGTTTTAAATCAAAT
 ATACATTACGGAACACTCTATCTAGTCCCAACTCCAATTGGTAATCTAGA
 TGATATGACTTTTCGTGCCATTAGGATTTTAAGAGAAGTTGATTTTATTT
 GTGCAGAGGATACACGAAATACGGGACTTTTACTCAAGCACTTTGATATT
 ACTACTAAACAAATTAGTTTTTACGAACACAATGCTTACGATAAAATCTC
 TGGGTTAATTGATTTGTTAAAAGAAGGGAAATCTTTAGCCCAAGTATCTG
 ATGCAGGAATGCCCTCTATTTCTGACCCAGGACATGACCTTGTCAAGGCT
 GCTATTGAAGGGGATATCCAGTTGTATCTATACCAGGAGCTAGCGCTGG
 TATTACTGCTCTCATCGCTTCAGGTTTAGCTCCACAACCTCATATTTTTT
 ATGGCTTCTTACCACGTAAGAAAGGTCAACAAATAACTTTCTTTGAAACA
 AAGCAAGATTACCCTGAAACACAAATCTTTTATGAGTCACCGTTTCGAGT
 CTCTGATACGCTAAAACACATGAAAGAGATTTACGGAGATCGCCAAGTTG
 TTTTAGTACGCGAATTGACGAACTCTATGAAGAGTATCAAAGAGGAACC
 ATTAGTCAACTTTTAGAGCATATTGAAAAGGTCCCTCTCAAAGGTGAATG
 CTTAATTATTGTTGATGGTAAGAGAGATACCGAGCGAGTGAAAGACAGTA
 GCCAACAAGATCCACTAGTATTAGTAA

SEQ ID NO. 7407

STRAIN COH1

GAAATGCAAGTTCAAAAAAGTTTTAAATCAAATATACATTAC
 GGAACACTCTATCTAGTCCCAACTCCAATTGGTAATCTAGATGATATGAC
 TTTTCGTGCCATTAGGATTTTAAGAGAAGTTGATTTTATTTGTGCAGAGG
 ATACACGAAATACGGGACTTTTACTCAAGCACTTTGATATTACTACTAAA
 CAAATTAGTTTTTACGAACACAATGCTTACGATAAAATCTCTGGGTTAAT
 TGATTTGTTAAAAGAAGGGAAATCTTTAGCCCAAGTATCTGATGCAGGAA
 TGCCCTCTATTTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAA
 GGGGATATCCAGTTGTATCTATACCAGGAGCTAGCGCTGGTATTACTGC
 TCTCATCGCTTCAGGTTTAGCTCCACAACCTCATATTTTTTATGGCTTCT
 TACCACGTAAGAAAGGTCAACAAATAACTTTCTTTGAAACAAAGCAAGAT
 TACCCTGAAACACAAATCTTTTATGAGTCACCGTTTCGAGTCTCTGATAC
 GCTAAAACACATGAAAGAGATTTACGGAGATCGCCAAGTTGTTTATGATAC
 GCGAATTGACGAACTCTATGAAGAGTATCAAAGAGGAACCATTAGTCAA
 CTTTTAGAGCATATTGAAAAGGTCCCTCTCAAAGGTGAATGCTTAATTAT
 TGTGATGGTAAGAGAGATACCGAGCGAGTGAAAGACAGTAGCCAACAAG
 ATCCACTAGTATTAGTAA

SEQ ID NO. 7408

STRAIN M781

AAATGCAAGTTCAAAAAAGTTTTAAATCAAATATACATTACGGAACACTC
 TATCTAGTCCCAACTCCAATTGGTAATCTAGATGATATGACTTTTCGTGC
 CATTAGGATTTTAAGAGAAGTTGATTTTATTTGTGCAGAGGATACACGAA
 ATACGGGACTTTTACTCAAGCACTTTGATATTACTACTAAACAAATTAGT
 TTTACGAACACAATGCTTACGATAAAATCTCTGGGTTAATTGATTTGTT
 AAAAGAAGGGAAATCTTTAGCCCAAGTATCTGATGCAGGAATGCCCTCTA
 TTTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAAGGGGATATC
 CCAGTTGTATCTATACCAGGAGCTAGCGCTGGTATTACTGCTCTCATCGC
 TTCAGGTTTAGCTCCACAACCTCATATTTTTTATGGCTTCTTACCACGTA
 AGAAAGGTCAACAAATAACTTTCTTTGAAACAAAGCAAGATTACCCTGAA
 ACACAAATCTTTTATGAGTCACCGTTTCGAGTCTCTGATACGCTAAAACA
 CATGAAAGAGATTTACGGAGATCGCCAAGTTGTTTATGATACGCGAATTGA
 CGAAACTCTATGAAGAGTATCAAAGAGGAACCATTAGTCAACTTTTAGAG
 CATATTGAAAAGGTCCCTCTCAAAGGTGAATGCTTAATTATTGTTGATGG
 TAAGAGAGATACCGAGCGAGTGAAAGACAGTAGCCAACAAGATCCACTAG
 TATTAGTAA

A

SEQ ID NO. 7409

STRAIN CJB110

GAAATGCAAGTTCAAAAAAGTTTTAAATCAAATACACATTACGGGACAC
 TCTATCTAGTCCCAACTCCAATTGGTAATCTAGATGATATGACTTTTCGT
 GCCATTAGGATTTTAAGAGAAGTTGATTTTATTTGTGCAGAGGATACACG
 AAATACGGGACTTTTACTCAAGCACTTTGATATTACTACTAAACAAATTA
 GTTTTCACGAACACAATGCTTACGATAAAATCTCTGGGTTAATTGATTTG
 TTAAAAGAAGGGAGATCTTTAGCCCAAGTATCTGATGCAGGAATGCCCTC
 TATTTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAAGGGGGGA
 TCCCGGTCGTATCTATACCAGGAGCTAGCGCTGGTATTACTGCTCTCATC
 GCTTCAGGTTTAGCTCCACAACCTCATATTTTTTATGGCTTCTTACCGCG
 TAAGAAAGGTCAACAAATAACTTTTCTTGAACAAAGAAAGATTACCCTG
 AAACACAAATCTTTTATGAGTCACCGTTTCGAGTCTCTGATACGCTAAAA
 CACATGAAAGAGATTTACGGAGATCGCCAAGTTGTTTATGATACGCGAATT

Table 74: Comparative Sequences relating to SAG1572

GACGAACTCTATGAAGAGTATCAAAGAGGAACCATTAGTCAACTTTTAG
GGCATATTGAAAAAGTCCCTCTCAAAGGTGAATGCTTAATTATTGTTGAT
GGTAAGAGAGATACCGAGCGAGTGAAAGACAGTAGCCAACAAGATCCACT
AGTATTAGTAA

SEQ ID NO. 7410

STRAIN 1169NT

TGCAAGTTCAAAAAAGTTTAAATCAAATACACATTATGGGACACTCTAT
CTAGTCCCAACTCCAATTGGTAATCTAGATGATATGACTTTTCGTGCCAT
TAGGATTTTAAGAGAAAGTTGaTTTATTTGTGCAGAGGATACACGAAATA
CGGGACTTTTACTCAAGCACTTTTGATaTTACTACTAAACAAATTAGtTTT
cACGAACACAATGCTTACGATAAAATCTCTGGGTAAATTGATTtGTTAAA
AGAAGGGAAATCTTTAGCCCAAGTATCTGATGCAGGAATGCCCTCTATTT
CTGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAAGGGGATATCCCA
GTTGTATCTATACCAGGAGCTAGCGCTGGTATTACTGCTCTCATCGCTTC
AGGTTTAGCTCCACAACCTCATATTTTATGGCTTCTTACCACGTAAGA
AAGGTCAACAAATAACTTTTGTGAAACAAGCAAGATTATCTGAAACA
CAAATCTTTTATGAGTCACCGtTTCGAGTCTCTGATACGCTAAACACAT
GAAAGAGATTTACGAGATFCGCCAAGTTGTTTATGACGGAATTGACgA
AACTCTATGAAGAGTATCAAAGAGGAACCATTaGTCAACTTTTAGAGCAT
ATTGAAAAGGTCCCTCTCAAAGGTGAATGCTTAATTATTGtTGATGGTAA
GAGAGAtaCCGAGCGAGTGAAAGACAGTAGCCAACAAGATCCACTAGTAT
TAGTAA

SEQ ID NO. 7411

STRAIN JM9130013

GAAATGCAAGTTCAAAAAAGTTTAAATCAAATACACATTACGGGA
CACTCTATCTAGTCCCAACTCCAATTGGTAATCTAGATGATATGACTTTT
CGTGCCATTAGGATTTTAAGAGAAGTTGATTTTATTTGTGCAGAGGATAC
ACGAAATACGGGACTTTTACTCAAGCACTTTGATATTACTACTAAACAA
TTAGTTTTCACGAACACAATGCTTATGATAAAATCTCTGGGTAAATTGAT
TTGTTAAAAGAAGGGAGATCTTTAGCCCAAGTATCTGATGCAGGAATGCC
CTCTATTTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAAGGGG
ATATCCCGTCTGATCTATACCAGGAGCTAGCGCTGGTATTACTGCTCTC
ATCGCTTCAGGTTTAGCTCCACAACCTCATATTTTATGGCTTCTTACC
GCGTAAGCAAGGTCAACAAATAACTTTTTTGTGAAACAAGAAAGATTACC
CTGAAACACAAATCTTTTATGAGTCACCGTTTCGAGTCTCTGATACGCTA
AAACACATGAAAGAGATTTATGGAGATCGCCAAGTTGTTTATGACGGA
ATTGACGAAACTCTATGAAGAGTATCAAAGAGGAACCATTAGTCAACTTT
TAGGGCATATTGaAAAGGTCCCTCTCAAAGGTGAATGCTTAATTATTGTT
GATGGTAAGAGAGATACTGAGCGAGTGAAAGACAGTAGCCAACAAGATCC
AGTAGTATTAGTAA

PRETTY of: /biotmp/msa323014.2{*} March 28, 2003 02:40 ..

	1		50
msa323014.2{343_18RS21}	---gaaatgc	aAGTTCAAAA	AAGTTTTAAA TCAAATAtAC ATTAcGGaAC
msa323014.2{343_A909}	-----	-AGTTCAAAA	AAGTTTTAAA TCAAATAtAC ATTAcGGaAC
msa323014.2{343_COH1}	---gaaatgc	aAGTTCAAAA	AAGTTTTAAA TCAAATAtAC ATTAcGGaAC
msa323014.2{343_M732}	---gaaatgc	aAGTTCAAAA	AAGTTTTAAA TCAAATAtAC ATTAcGGaAC
msa323014.2{343_M781}	----aaatgc	aAGTTCAAAA	AAGTTTTAAA TCAAATAtAC ATTAcGGaAC
msa323014.2{343_2603}	atggaaatgc	aAGTTCAAAA	AAGTTTTAAA TCAAATAtAC ATTAcGGaAC
msa323014.2{343_1169NT}	-----tgc	aAGTTCAAAA	AAGTTTTAAA TCAAATAcAC ATTAtGGgAC
msa323014.2{343_090}	---gaaatgc	aAGTTCAAAA	AAGTTTTAAA TCAAATAcAC ATTAcGGgAC
msa323014.2{343_CJB110}	---gaaatgc	aAGTTCAAAA	AAGTTTTAAA TCAAATAcAC ATTAcGGgAC
msa323014.2{343_H36B}	---gaaatgc	aAGTTCAAAA	AAGTTTTAAA TCAAATAcAC ATTAcGGgAC
msa323014.2{343_JM9130013}	---gaaatgc	aAGTTCAAAA	AAGTTTTAAA TCAAATAcAC ATTAcGGgAC
Consensus	***-----	-*****	*****-** ****-**-**
	51		100
msa323014.2{343_18RS21}	ACTCTATCTA	GTCCCAACTC	CAATTGGTAA TCTAGATGAT ATGACTTTTC
msa323014.2{343_A909}	ACTCTATCTA	GTCCCAACTC	CAATTGGTAA TCTAGATGAT ATGACTTTTC
msa323014.2{343_COH1}	ACTCTATCTA	GTCCCAACTC	CAATTGGTAA TCTAGATGAT ATGACTTTTC
msa323014.2{343_M732}	ACTCTATCTA	GTCCCAACTC	CAATTGGTAA TCTAGATGAT ATGACTTTTC
msa323014.2{343_M781}	ACTCTATCTA	GTCCCAACTC	CAATTGGTAA TCTAGATGAT ATGACTTTTC
msa323014.2{343_2603}	ACTCTATCTA	GTCCCAACTC	CAATTGGTAA TCTAGATGAT ATGACTTTTC
msa323014.2{343_1169NT}	ACTCTATCTA	GTCCCAACTC	CAATTGGTAA TCTAGATGAT ATGACTTTTC
msa323014.2{343_090}	ACTCTATCTA	GTCCCAACTC	CAATTGGTAA TCTAGATGAT ATGACTTTTC
msa323014.2{343_CJB110}	ACTCTATCTA	GTCCCAACTC	CAATTGGTAA TCTAGATGAT ATGACTTTTC
msa323014.2{343_H36B}	ACTCTATCTA	GTCCCAACTC	CAATTGGTAA TCTAGATGAT ATGACTTTTC
msa323014.2{343_JM9130013}	ACTCTATCTA	GTCCCAACTC	CAATTGGTAA TCTAGATGAT ATGACTTTTC
Consensus	*****	*****	*****
	101		150
msa323014.2{343_18RS21}	GTGCCATTAG	GATTTTAAGA	GAAGTTGATT TTATTTGTGC AGAGGATACA
msa323014.2{343_A909}	GTGCCATTAG	GATTTTAAGA	GAAGTTGATT TTATTTGTGC AGAGGATACA
msa323014.2{343_COH1}	GTGCCATTAG	GATTTTAAGA	GAAGTTGATT TTATTTGTGC AGAGGATACA
msa323014.2{343_M732}	GTGCCATTAG	GATTTTAAGA	GAAGTTGATT TTATTTGTGC AGAGGATACA
msa323014.2{343_M781}	GTGCCATTAG	GATTTTAAGA	GAAGTTGATT TTATTTGTGC AGAGGATACA
msa323014.2{343_2603}	GTGCCATTAG	GATTTTAAGA	GAAGTTGATT TTATTTGTGC AGAGGATACA
msa323014.2{343_1169NT}	GTGCCATTAG	GATTTTAAGA	GAAGTTGATT TTATTTGTGC AGAGGATACA
msa323014.2{343_090}	GTGCCATTAG	GATTTTAAGA	GAAGTTGATT TTATTTGTGC AGAGGATACA

Table 74: Comparative Sequences relating to SAG1572

msa323014.2{343_CJB110}	GTGCCATTAG	GATTTTAAAGA	GAAGTTGATT	TTATTTGTGC	AGAGGATACA
msa323014.2{343_H36B}	GTGCCATTAG	GATTTTAAAGA	GAAGTTGATT	TTATTTGTGC	AGAGGATACA
msa323014.2{343_JM9130013}	GTGCCATTAG	GATTTTAAAGA	GAAGTTGATT	TTATTTGTGC	AGAGGATACA
Consensus	*****	*****	*****	*****	*****
msa323014.2{343_18RS21}	CGAAATACGG	GACTTTTACT	CAAGCACTTT	GATATTACTA	CTAAACAAAT
msa323014.2{343_A909}	CGAAATACGG	GACTTTTACT	CAAGCACTTT	GATATTACTA	CTAAACAAAT
msa323014.2{343_COH1}	CGAAATACGG	GACTTTTACT	CAAGCACTTT	GATATTACTA	CTAAACAAAT
msa323014.2{343_M732}	CGAAATACGG	GACTTTTACT	CAAGCACTTT	GATATTACTA	CTAAACAAAT
msa323014.2{343_M781}	CGAAATACGG	GACTTTTACT	CAAGCACTTT	GATATTACTA	CTAAACAAAT
msa323014.2{343_2603}	CGAAATACGG	GACTTTTACT	CAAGCACTTT	GATATTACTA	CTAAACAAAT
msa323014.2{343_1169NT}	CGAAATACGG	GACTTTTACT	CAAGCACTTT	GATATTACTA	CTAAACAAAT
msa323014.2{343_090}	CGAAATACGG	GACTTTTACT	CAAGCACTTT	GATATTACTA	CTAAACAAAT
msa323014.2{343_CJB110}	CGAAATACGG	GACTTTTACT	CAAGCACTTT	GATATTACTA	CTAAACAAAT
msa323014.2{343_H36B}	CGAAATACGG	GACTTTTACT	CAAGCACTTT	GATATTACTA	CTAAACAAAT
msa323014.2{343_JM9130013}	CGAAATACGG	GACTTTTACT	CAAGCACTTT	GATATTACTA	CTAAACAAAT
Consensus	*****	*****	*****	*****	*****
msa323014.2{343_18RS21}	TAGTTTTTCAC	GAACACAATG	CTTAcGATAA	AATCTCTGGG	TTAATTGATT
msa323014.2{343_A909}	TAGTTTTTCAC	GAACACAATG	CTTAcGATAA	AATCTCTGGG	TTAATTGATT
msa323014.2{343_COH1}	TAGTTTTTCAC	GAACACAATG	CTTAcGATAA	AATCTCTGGG	TTAATTGATT
msa323014.2{343_M732}	TAGTTTTTCAC	GAACACAATG	CTTAcGATAA	AATCTCTGGG	TTAATTGATT
msa323014.2{343_M781}	TAGTTTTTCAC	GAACACAATG	CTTAcGATAA	AATCTCTGGG	TTAATTGATT
msa323014.2{343_2603}	TAGTTTTTCAC	GAACACAATG	CTTAcGATAA	AATCTCTGGG	TTAATTGATT
msa323014.2{343_1169NT}	TAGTTTTTCAC	GAACACAATG	CTTAcGATAA	AATCTCTGGG	TTAATTGATT
msa323014.2{343_090}	TAGTTTTTCAC	GAACACAATG	CTTAcGATAA	AATCTCTGGG	TTAATTGATT
msa323014.2{343_CJB110}	TAGTTTTTCAC	GAACACAATG	CTTAcGATAA	AATCTCTGGG	TTAATTGATT
msa323014.2{343_H36B}	TAGTTTTTCAC	GAACACAATG	CTTAcGATAA	AATCTCTGGG	TTAATTGATT
msa323014.2{343_JM9130013}	TAGTTTTTCAC	GAACACAATG	CTTAcGATAA	AATCTCTGGG	TTAATTGATT
Consensus	*****	*****	*****	*****	*****
msa323014.2{343_18RS21}	TGTTAAAAGA	AGGGAAATCT	TTAGCCCAAG	TATCTGATGC	AGGAATGCCC
msa323014.2{343_A909}	TGTTAAAAGA	AGGGAAATCT	TTAGCCCAAG	TATCTGATGC	AGGAATGCCC
msa323014.2{343_COH1}	TGTTAAAAGA	AGGGAAATCT	TTAGCCCAAG	TATCTGATGC	AGGAATGCCC
msa323014.2{343_M732}	TGTTAAAAGA	AGGGAAATCT	TTAGCCCAAG	TATCTGATGC	AGGAATGCCC
msa323014.2{343_M781}	TGTTAAAAGA	AGGGAAATCT	TTAGCCCAAG	TATCTGATGC	AGGAATGCCC
msa323014.2{343_2603}	TGTTAAAAGA	AGGGAAATCT	TTAGCCCAAG	TATCTGATGC	AGGAATGCCC
msa323014.2{343_1169NT}	TGTTAAAAGA	AGGGAAATCT	TTAGCCCAAG	TATCTGATGC	AGGAATGCCC
msa323014.2{343_090}	TGTTAAAAGA	AGGGAAATCT	TTAGCCCAAG	TATCTGATGC	AGGAATGCCC
msa323014.2{343_CJB110}	TGTTAAAAGA	AGGGAAATCT	TTAGCCCAAG	TATCTGATGC	AGGAATGCCC
msa323014.2{343_H36B}	TGTTAAAAGA	AGGGAAATCT	TTAGCCCAAG	TATCTGATGC	AGGAATGCCC
msa323014.2{343_JM9130013}	TGTTAAAAGA	AGGGAAATCT	TTAGCCCAAG	TATCTGATGC	AGGAATGCCC
Consensus	*****	*****	*****	*****	*****
msa323014.2{343_18RS21}	TCTATTTCTG	ACCCAGGACA	TGACCTTGTC	AAGGCTGCTA	TTGAAGGGGa
msa323014.2{343_A909}	TCTATTTCTG	ACCCAGGACA	TGACCTTGTC	AAGGCTGCTA	TTGAAGGGGa
msa323014.2{343_COH1}	TCTATTTCTG	ACCCAGGACA	TGACCTTGTC	AAGGCTGCTA	TTGAAGGGGa
msa323014.2{343_M732}	TCTATTTCTG	ACCCAGGACA	TGACCTTGTC	AAGGCTGCTA	TTGAAGGGGa
msa323014.2{343_M781}	TCTATTTCTG	ACCCAGGACA	TGACCTTGTC	AAGGCTGCTA	TTGAAGGGGa
msa323014.2{343_2603}	TCTATTTCTG	ACCCAGGACA	TGACCTTGTC	AAGGCTGCTA	TTGAAGGGGa
msa323014.2{343_1169NT}	TCTATTTCTG	ACCCAGGACA	TGACCTTGTC	AAGGCTGCTA	TTGAAGGGGa
msa323014.2{343_090}	TCTATTTCTG	ACCCAGGACA	TGACCTTGTC	AAGGCTGCTA	TTGAAGGGGg
msa323014.2{343_CJB110}	TCTATTTCTG	ACCCAGGACA	TGACCTTGTC	AAGGCTGCTA	TTGAAGGGGg
msa323014.2{343_H36B}	TCTATTTCTG	ACCCAGGACA	TGACCTTGTC	AAGGCTGCTA	TTGAAGGGGa
msa323014.2{343_JM9130013}	TCTATTTCTG	ACCCAGGACA	TGACCTTGTC	AAGGCTGCTA	TTGAAGGGGa
Consensus	*****	*****	*****	*****	*****
msa323014.2{343_18RS21}	tATCCCaGt	GTATCTATAC	CAGGAGCTAG	CGCTGGTATT	ACTGCTCTCA
msa323014.2{343_A909}	tATCCCaGt	GTATCTATAC	CAGGAGCTAG	CGCTGGTATT	ACTGCTCTCA
msa323014.2{343_COH1}	tATCCCaGt	GTATCTATAC	CAGGAGCTAG	CGCTGGTATT	ACTGCTCTCA
msa323014.2{343_M732}	tATCCCaGt	GTATCTATAC	CAGGAGCTAG	CGCTGGTATT	ACTGCTCTCA
msa323014.2{343_M781}	tATCCCaGt	GTATCTATAC	CAGGAGCTAG	CGCTGGTATT	ACTGCTCTCA
msa323014.2{343_2603}	tATCCCaGt	GTATCTATAC	CAGGAGCTAG	CGCTGGTATT	ACTGCTCTCA
msa323014.2{343_1169NT}	tATCCCaGt	GTATCTATAC	CAGGAGCTAG	CGCTGGTATT	ACTGCTCTCA
msa323014.2{343_090}	gATCCCGt	GTATCTATAC	CAGGAGCTAG	CGCTGGTATT	ACTGCTCTCA
msa323014.2{343_CJB110}	gATCCCGt	GTATCTATAC	CAGGAGCTAG	CGCTGGTATT	ACTGCTCTCA
msa323014.2{343_H36B}	tATCCCGt	GTATCTATAC	CAGGAGCTAG	CGCTGGTATT	ACTGCTCTCA
msa323014.2{343_JM9130013}	tATCCCGt	GTATCTATAC	CAGGAGCTAG	CGCTGGTATT	ACTGCTCTCA
Consensus	-*****-	*****	*****	*****	*****
msa323014.2{343_18RS21}	TCGCTTCAGG	TTTAGCTCCA	CAACCTCATA	TTTTTTATGG	CTTCTTACCa
msa323014.2{343_A909}	TCGCTTCAGG	TTTAGCTCCA	CAACCTCATA	TTTTTTATGG	CTTCTTACCa
msa323014.2{343_COH1}	TCGCTTCAGG	TTTAGCTCCA	CAACCTCATA	TTTTTTATGG	CTTCTTACCa
msa323014.2{343_M732}	TCGCTTCAGG	TTTAGCTCCA	CAACCTCATA	TTTTTTATGG	CTTCTTACCa
msa323014.2{343_M781}	TCGCTTCAGG	TTTAGCTCCA	CAACCTCATA	TTTTTTATGG	CTTCTTACCa
msa323014.2{343_2603}	TCGCTTCAGG	TTTAGCTCCA	CAACCTCATA	TTTTTTATGG	CTTCTTACCa
msa323014.2{343_1169NT}	TCGCTTCAGG	TTTAGCTCCA	CAACCTCATA	TTTTTTATGG	CTTCTTACCa

Table 74: Comparative Sequences relating to SAG1572

msa323014.2{343_090}	TCGCTTCAGG	TTTAGCTCCA	CAACCTCATA	TTTTTTATGG	CTTCTTACCg
msa323014.2{343_CJB110}	TCGCTTCAGG	TTTAGCTCCA	CAACCTCATA	TTTTTTATGG	CTTCTTACCg
msa323014.2{343_H36B}	TCGCTTCAGG	TTTAGCTCCA	CAACCTCATA	TTTTTTATGG	CTTCTTACCg
msa323014.2{343_JM9130013}	TCGCTTCAGG	TTTAGCTCCA	CAACCTCATA	TTTTTTATGG	CTTCTTACCg
Consensus	*****	*****	*****	*****	*****-
msa323014.2{343_18RS21}	CGTAAGaAAG	GTCAACAAAT	AACTTTcTTT	GAAACAAAGc	AAGATTAcCC
msa323014.2{343_A909}	CGTAAGaAAG	GTCAACAAAT	AACTTTcTTT	GAAACAAAGc	AAGATTAcCC
msa323014.2{343_COH1}	CGTAAGaAAG	GTCAACAAAT	AACTTTcTTT	GAAACAAAGc	AAGATTAcCC
msa323014.2{343_M732}	CGTAAGaAAG	GTCAACAAAT	AACTTTcTTT	GAAACAAAGc	AAGATTAcCC
msa323014.2{343_M781}	CGTAAGaAAG	GTCAACAAAT	AACTTTcTTT	GAAACAAAGc	AAGATTAcCC
msa323014.2{343_2603}	CGTAAGaAAG	GTCAACAAAT	AACTTTcTTT	GAAACAAAGc	AAGATTAcCC
msa323014.2{343_1169NT}	CGTAAGaAAG	GTCAACAAAT	AACTTTtTTT	GAAACAAAGc	AAGATTAcCC
msa323014.2{343_090}	CGTAAGaAAG	GTCAACAAAT	AACTTTtTTT	GAAACAAAGa	AAGATTAcCC
msa323014.2{343_CJB110}	CGTAAGaAAG	GTCAACAAAT	AACTTTtTTT	GAAACAAAGa	AAGATTAcCC
msa323014.2{343_H36B}	CGTAAGcAAG	GTCAACAAAT	AACTTTtTTT	GAAACAAAGa	AAGATTAcCC
msa323014.2{343_JM9130013}	CGTAAGcAAG	GTCAACAAAT	AACTTTtTTT	GAAACAAAGa	AAGATTAcCC
Consensus	*****-***	*****	*****-***	*****-*	*****-**
msa323014.2{343_18RS21}	TGAAACACAA	ATCTTTTATG	AGTCACCGTT	TCGAGTCTCT	GATACGCTAA
msa323014.2{343_A909}	TGAAACACAA	ATCTTTTATG	AGTCACCGTT	TCGAGTCTCT	GATACGCTAA
msa323014.2{343_COH1}	TGAAACACAA	ATCTTTTATG	AGTCACCGTT	TCGAGTCTCT	GATACGCTAA
msa323014.2{343_M732}	TGAAACACAA	ATCTTTTATG	AGTCACCGTT	TCGAGTCTCT	GATACGCTAA
msa323014.2{343_M781}	TGAAACACAA	ATCTTTTATG	AGTCACCGTT	TCGAGTCTCT	GATACGCTAA
msa323014.2{343_2603}	TGAAACACAA	ATCTTTTATG	AGTCACCGTT	TCGAGTCTCT	GATACGCTAA
msa323014.2{343_1169NT}	TGAAACACAA	ATCTTTTATG	AGTCACCGTT	TCGAGTCTCT	GATACGCTAA
msa323014.2{343_090}	TGAAACACAA	ATCTTTTATG	AGTCACCGTT	TCGAGTCTCT	GATACGCTAA
msa323014.2{343_CJB110}	TGAAACACAA	ATCTTTTATG	AGTCACCGTT	TCGAGTCTCT	GATACGCTAA
msa323014.2{343_H36B}	TGAAACACAA	ATCTTTTATG	AGTCACCGTT	TCGAGTCTCT	GATACGCTAA
msa323014.2{343_JM9130013}	TGAAACACAA	ATCTTTTATG	AGTCACCGTT	TCGAGTCTCT	GATACGCTAA
Consensus	*****	*****	*****	*****	*****
msa323014.2{343_18RS21}	AACACATGAA	AGAGATTTAc	GGAGATCGCC	AAGTTGTTTT	AGTACGCGAA
msa323014.2{343_A909}	AACACATGAA	AGAGATTTAc	GGAGATCGCC	AAGTTGTTTT	AGTACGCGAA
msa323014.2{343_COH1}	AACACATGAA	AGAGATTTAc	GGAGATCGCC	AAGTTGTTTT	AGTACGCGAA
msa323014.2{343_M732}	AACACATGAA	AGAGATTTAc	GGAGATCGCC	AAGTTGTTTT	AGTACGCGAA
msa323014.2{343_M781}	AACACATGAA	AGAGATTTAc	GGAGATCGCC	AAGTTGTTTT	AGTACGCGAA
msa323014.2{343_2603}	AACACATGAA	AGAGATTTAc	GGAGATCGCC	AAGTTGTTTT	AGTACGCGAA
msa323014.2{343_1169NT}	AACACATGAA	AGAGATTTAc	GGAGATCGCC	AAGTTGTTTT	AGTACGCGAA
msa323014.2{343_090}	AACACATGAA	AGAGATTTAc	GGAGATCGCC	AAGTTGTTTT	AGTACGCGAA
msa323014.2{343_CJB110}	AACACATGAA	AGAGATTTAc	GGAGATCGCC	AAGTTGTTTT	AGTACGCGAA
msa323014.2{343_H36B}	AACACATGAA	AGAGATTTAc	GGAGATCGCC	AAGTTGTTTT	AGTACGCGAA
msa323014.2{343_JM9130013}	AACACATGAA	AGAGATTTAc	GGAGATCGCC	AAGTTGTTTT	AGTACGCGAA
Consensus	*****	*****	*****	*****	*****
msa323014.2{343_18RS21}	TTGACGAAAC	TCTATGAAGA	GTATCAAAGA	GGAACCATTA	GTCAACTTTT
msa323014.2{343_A909}	TTGACGAAAC	TCTATGAAGA	GTATCAAAGA	GGAACCATTA	GTCAACTTTT
msa323014.2{343_COH1}	TTGACGAAAC	TCTATGAAGA	GTATCAAAGA	GGAACCATTA	GTCAACTTTT
msa323014.2{343_M732}	TTGACGAAAC	TCTATGAAGA	GTATCAAAGA	GGAACCATTA	GTCAACTTTT
msa323014.2{343_M781}	TTGACGAAAC	TCTATGAAGA	GTATCAAAGA	GGAACCATTA	GTCAACTTTT
msa323014.2{343_2603}	TTGACGAAAC	TCTATGAAGA	GTATCAAAGA	GGAACCATTA	GTCAACTTTT
msa323014.2{343_1169NT}	TTGACGAAAC	TCTATGAAGA	GTATCAAAGA	GGAACCATTA	GTCAACTTTT
msa323014.2{343_090}	TTGACGAAAC	TCTATGAAGA	GTATCAAAGA	GGAACCATTA	GTCAACTTTT
msa323014.2{343_CJB110}	TTGACGAAAC	TCTATGAAGA	GTATCAAAGA	GGAACCATTA	GTCAACTTTT
msa323014.2{343_H36B}	TTGACGAAAC	TCTATGAAGA	GTATCAAAGA	GGAACCATTA	GTCAACTTTT
msa323014.2{343_JM9130013}	TTGACGAAAC	TCTATGAAGA	GTATCAAAGA	GGAACCATTA	GTCAACTTTT
Consensus	*****	*****	*****	*****	*****
msa323014.2{343_18RS21}	AGaGCATATT	GAAAAgGTCC	CTCTCAAAGG	TGAATGCTTA	ATTATTGTTG
msa323014.2{343_A909}	AGaGCATATT	GAAAAgGTCC	CTCTCAAAGG	TGAATGCTTA	ATTATTGTTG
msa323014.2{343_COH1}	AGaGCATATT	GAAAAgGTCC	CTCTCAAAGG	TGAATGCTTA	ATTATTGTTG
msa323014.2{343_M732}	AGaGCATATT	GAAAAgGTCC	CTCTCAAAGG	TGAATGCTTA	ATTATTGTTG
msa323014.2{343_M781}	AGaGCATATT	GAAAAgGTCC	CTCTCAAAGG	TGAATGCTTA	ATTATTGTTG
msa323014.2{343_2603}	AGaGCATATT	GAAAAgGTCC	CTCTCAAAGG	TGAATGCTTA	ATTATTGTTG
msa323014.2{343_1169NT}	AGaGCATATT	GAAAAgGTCC	CTCTCAAAGG	TGAATGCTTA	ATTATTGTTG
msa323014.2{343_090}	AGgGCATATT	GAAAAaGTCC	CTCTCAAAGG	TGAATGCTTA	ATTATTGTTG
msa323014.2{343_CJB110}	AGgGCATATT	GAAAAaGTCC	CTCTCAAAGG	TGAATGCTTA	ATTATTGTTG
msa323014.2{343_H36B}	AGgGCATATT	GAAAAgGTCC	CTCTCAAAGG	TGAATGCTTA	ATTATTGTTG
msa323014.2{343_JM9130013}	AGgGCATATT	GAAAAgGTCC	CTCTCAAAGG	TGAATGCTTA	ATTATTGTTG
Consensus	**-*****	*****-****	*****	*****	*****
msa323014.2{343_18RS21}	ATGGTAAGAG	AGATACcGAG	CGAGTGAAAG	ACAGTAGCCA	ACAAGATCCA
msa323014.2{343_A909}	ATGGTAAGAG	AGATACcGAG	CGAGTGAAAG	ACAGTAGCCA	ACAAGATCCA
msa323014.2{343_COH1}	ATGGTAAGAG	AGATACcGAG	CGAGTGAAAG	ACAGTAGCCA	ACAAGATCCA
msa323014.2{343_M732}	ATGGTAAGAG	AGATACcGAG	CGAGTGAAAG	ACAGTAGCCA	ACAAGATCCA
msa323014.2{343_M781}	ATGGTAAGAG	AGATACcGAG	CGAGTGAAAG	ACAGTAGCCA	ACAAGATCCA
msa323014.2{343_2603}	ATGGTAAGAG	AGATACcGAG	CGAGTGAAAG	ACAGTAGCCA	ACAAGATCCA

Table 74: Comparative Sequences relating to SAG1572

msa323014.2{343_1169NT}	ATGGTAAGAG	AGATACcGAG	CGAGTGAAAG	ACAGTAGCCA	ACAAGATCCA
msa323014.2{343_090}	ATGGTAAGAG	AGATACcGAG	CGAGTGAAAG	ACAGTAGCCA	ACAAGATCCA
msa323014.2{343_CJB110}	ATGGTAAGAG	AGATACcGAG	CGAGTGAAAG	ACAGTAGCCA	ACAAGATCCA
msa323014.2{343_H36B}	ATGGTAAGAG	AGATACTGAG	CGAGTGAAAG	ACAGTAGCCA	ACAAGATCCA
msa323014.2{343_JM9130013}	ATGGTAAGAG	AGATACTGAG	CGAGTGAAAG	ACAGTAGCCA	ACAAGATCCA
Consensus	*****	*****-***	*****	*****	*****
751					
msa323014.2{343_18RS21}	cTAGTATTAG	TAA-----	-----	-----	-----
msa323014.2{343_A909}	cTAGTATTAG	TAA-----	-----	-----	-----
msa323014.2{343_COH1}	cTAGTATTAG	TAA-----	-----	-----	-----
msa323014.2{343_M732}	cTAGTATTAG	TAA-----	-----	-----	-----
msa323014.2{343_M781}	cTAGTATTAG	TAAA-----	-----	-----	-----
msa323014.2{343_2603}	cTAGTATTAG	TAAagaata	tatcgcta	ggtgataaaa	ctaatacaagc
msa323014.2{343_1169NT}	cTAGTATTAG	TAA-----	-----	-----	-----
msa323014.2{343_090}	cTAGTATTAG	TAA-----	-----	-----	-----
msa323014.2{343_CJB110}	cTAGTATTAG	TAA-----	-----	-----	-----
msa323014.2{343_H36B}	cTAGTATTAG	TAA-----	-----	-----	-----
msa323014.2{343_JM9130013}	gTAGTATTAG	TAA-----	-----	-----	-----
Consensus	-*****	*****	*****	*****	*****
801					
msa323014.2{343_18RS21}	-----	-----	-----	-----	-----
msa323014.2{343_A909}	-----	-----	-----	-----	-----
msa323014.2{343_COH1}	-----	-----	-----	-----	-----
msa323014.2{343_M732}	-----	-----	-----	-----	-----
msa323014.2{343_M781}	-----	-----	-----	-----	-----
msa323014.2{343_2603}	gataaaaaaa	gtagcaaaag	aatttaatact	caatagacaa	gaactctatg
msa323014.2{343_1169NT}	-----	-----	-----	-----	-----
msa323014.2{343_090}	-----	-----	-----	-----	-----
msa323014.2{343_CJB110}	-----	-----	-----	-----	-----
msa323014.2{343_H36B}	-----	-----	-----	-----	-----
msa323014.2{343_JM9130013}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
851					
msa323014.2{343_18RS21}	-----	-----	-----	-----	-----
msa323014.2{343_A909}	-----	-----	-----	-----	-----
msa323014.2{343_COH1}	-----	-----	-----	-----	-----
msa323014.2{343_M732}	-----	-----	-----	-----	-----
msa323014.2{343_M781}	-----	-----	-----	-----	-----
msa323014.2{343_2603}	ctagtttcca	tgattta	-----	-----	-----
msa323014.2{343_1169NT}	-----	-----	-----	-----	-----
msa323014.2{343_090}	-----	-----	-----	-----	-----
msa323014.2{343_CJB110}	-----	-----	-----	-----	-----
msa323014.2{343_H36B}	-----	-----	-----	-----	-----
msa323014.2{343_JM9130013}	-----	-----	-----	-----	-----
Consensus	*****	*****	-----	-----	-----
867					

SEQ ID NO. 7412

STRAIN 2603 frame: 1

MEMQVQKSFKSNHYGTLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFD
 DITTKQISFHEHNAYDKISGLIDLLKEGKSLAQVSDAGMPSISDPGHDLVKAAIEGDIPV
 VSIPGASAGITALIASGLAPQPHIFYGFLPRKKGQQITFFETKQDYPETQIFYESPFRVS
 DTLKHMKEIYGDRQVVLVRELTKLYEYQRTISQLLEHIEKVPLKGECLIIVDGKRDT
 RVKDSQQDPLVLVKEYIANGDKTNQAIKKVAKFNLNRQELYASFHDL

SEQ ID NO. 7413

STRAIN 090 frame: 1

EMQVQKSFKSNHYGTLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFD
 ITTKQISFHEHNAYDKISGLIDLLKEGRSLAQVSDAGMPSISDPGHDLVKAAIEGGIPV
 SIPGASAGITALIASGLAPQPHIFYGFLPRKKGQQITFFETKQDYPETQIFYESPFRVSD
 TLKHMKEIYGDRQVVLVRELTKLYEYQRTISQLLEHIEKVPLKGECLIIVDGKRDT
 VKDSQQDPLVLV

SEQ ID NO. 7414

STRAIN A909 frame: 2

VQKSFKSNHYGTLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFDIT
 KQISFHEHNAYDKISGLIDLLKEGRSLAQVSDAGMPSISDPGHDLVKAAIEGDIPVVSIP
 GASAGITALIASGLAPQPHIFYGFLPRKKGQQITFFETKQDYPETQIFYESPFRVSDTLK
 HMKEIYGDRQVVLVRELTKLYEYQRTISQLLEHIEKVPLKGECLIIVDGKRDT
 SSQQDPLVLV

SEQ ID NO. 7415

STRAIN H36B frame: 1

EMQVQKSFKSNHYGTLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFD
 ITTKQISFHEHNAYDKISGLIDLLKEGRSLAQVSDAGMPSISDPGHDLVKAAIEGDIPV
 SIPGASAGITALIASGLAPQPHIFYGFLPRKKGQQITFFETKQDYPETQIFYESPFRVSD
 TLKHMKEIYGDRQVVLVRELTKLYEYQRTISQLLEHIEKVPLKGECLIIVDGKRDT
 VKDSQQDPLVLV

SEQ ID NO. 7416

Table 74: Comparative Sequences relating to SAG1572

STRAIN 18RS21 frame: 1
 EMQVQKSFKSNIHYGTLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHF
 ITTKQISFHEHNAYDKISGLIDLLKEGKSLAQVSDAGMPSISDPGHDLVKAIEGDI PVV
 SIPGASAGITALIASGLAPQPHIFYGFLPRKKGQQITFFETKQDYPETQIFYESPFRVSD
 TLKHMKEIYGDRQVVLVRELTKLYEYQRTISQLLEHIEKVPLKGECLIIDGKRDTER
 VKDSSQQDPLVLV

SEQ ID NO. 7417

STRAIN M732 frame: 1
 EMQVQKSFKSNIHYGTLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHF
 ITTKQISFHEHNAYDKISGLIDLLKEGKSLAQVSDAGMPSISDPGHDLVKAIEGDI PVV
 SIPGASAGITALIASGLAPQPHIFYGFLPRKKGQQITFFETKQDYPETQIFYESPFRVSD
 TLKHMKEIYGDRQVVLVRELTKLYEYQRTISQLLEHIEKVPLKGECLIIDGKRDTER
 VKDSSQQDPLVLV

SEQ ID NO. 7418

STRAIN COH1 frame: 1
 EMQVQKSFKSNIHYGTLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHF
 ITTKQISFHEHNAYDKISGLIDLLKEGKSLAQVSDAGMPSISDPGHDLVKAIEGDI PVV
 SIPGASAGITALIASGLAPQPHIFYGFLPRKKGQQITFFETKQDYPETQIFYESPFRVSD
 TLKHMKEIYGDRQVVLVRELTKLYEYQRTISQLLEHIEKVPLKGECLIIDGKRDTER
 VKDSSQQDPLVLV

SEQ ID NO. 7419

STRAIN M781 frame: 3
 MQVQKSFKSNIHYGTLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHF
 ITTKQISFHEHNAYDKISGLIDLLKEGKSLAQVSDAGMPSISDPGHDLVKAIEGDI PVV
 IPGASAGITALIASGLAPQPHIFYGFLPRKKGQQITFFETKQDYPETQIFYESPFRVSD
 LKHMKEIYGDRQVVLVRELTKLYEYQRTISQLLEHIEKVPLKGECLIIDGKRDTER
 KDSSQQDPLVLV

SEQ ID NO. 7420

STRAIN CJB110 frame: 1
 EMQVQKSFKSNIHYGTLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHF
 ITTKQISFHEHNAYDKISGLIDLLKEGKSLAQVSDAGMPSISDPGHDLVKAIEGDI PVV
 SIPGASAGITALIASGLAPQPHIFYGFLPRKKGQQITFFETKQDYPETQIFYESPFRVSD
 TLKHMKEIYGDRQVVLVRELTKLYEYQRTISQLLGHIEKVPLKGECLIIDGKRDTER
 VKDSSQQDPLVLV

SEQ ID NO. 7421

STRAIN 1169NT frame: 3
 QVQKSFKSNIHYGTLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHF
 ITTKQISFHEHNAYDKISGLIDLLKEGKSLAQVSDAGMPSISDPGHDLVKAIEGDI PVV
 SIPGASAGITALIASGLAPQPHIFYGFLPRKKGQQITFFETKQDYPETQIFYESPFRVSD
 TLKHMKEIYGDRQVVLVRELTKLYEYQRTISQLLEHIEKVPLKGECLIIDGKRDTER
 DSSQQDPLVLV

SEQ ID NO. 7422

STRAIN JM9130013 frame: 1
 EMQVQKSFKSNIHYGTLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHF
 ITTKQISFHEHNAYDKISGLIDLLKEGKSLAQVSDAGMPSISDPGHDLVKAIEGDI PVV
 SIPGASAGITALIASGLAPQPHIFYGFLPRKKGQQITFFETKQDYPETQIFYESPFRVSD
 TLKHMKEIYGDRQVVLVRELTKLYEYQRTISQLLGHIEKVPLKGECLIIDGKRDTER
 VKDSSQQDPVVLV

	1				50
msa324064.2{343_18RS21}	~emqVQKSFK	SNiHYGTLYL	VPTPIGNLDD	MTFRAIRILR	EVDFICAEDT
msa324064.2{343_A909}	----VQKSFK	SNiHYGTLYL	VPTPIGNLDD	MTFRAIRILR	EVDFICAEDT
msa324064.2{343_M781}	--mqVQKSFK	SNiHYGTLYL	VPTPIGNLDD	MTFRAIRILR	EVDFICAEDT
msa324064.2{343_2603}	memqVQKSFK	SNiHYGTLYL	VPTPIGNLDD	MTFRAIRILR	EVDFICAEDT
msa324064.2{343_COH1}	~emqVQKSFK	SNiHYGTLYL	VPTPIGNLDD	MTFRAIRILR	EVDFICAEDT
msa324064.2{343_M732}	~emqVQKSFK	SNiHYGTLYL	VPTPIGNLDD	MTFRAIRILR	EVDFICAEDT
msa324064.2{343_1169NT}	---qVQKSFK	SNtHYGTLYL	VPTPIGNLDD	MTFRAIRILR	EVDFICAEDT
msa324064.2{343_090}	~emqVQKSFK	SNtHYGTLYL	VPTPIGNLDD	MTFRAIRILR	EVDFICAEDT
msa324064.2{343_CJB110}	~emqVQKSFK	SNtHYGTLYL	VPTPIGNLDD	MTFRAIRILR	EVDFICAEDT
msa324064.2{343_H36B}	~emqVQKSFK	SNtHYGTLYL	VPTPIGNLDD	MTFRAIRILR	EVDFICAEDT
msa324064.2{343_JM9130013}	~emqVQKSFK	SNtHYGTLYL	VPTPIGNLDD	MTFRAIRILR	EVDFICAEDT
Consensus	*--*****	***-*****	*****	*****	*****
	51				100
msa324064.2{343_18RS21}	RNTGLLLKHF	DITTKQISFH	EHNAYDKISG	LIDLLKEGks	LAQVSDAGMP
msa324064.2{343_A909}	RNTGLLLKHF	DITTKQISFH	EHNAYDKISG	LIDLLKEGks	LAQVSDAGMP
msa324064.2{343_M781}	RNTGLLLKHF	DITTKQISFH	EHNAYDKISG	LIDLLKEGks	LAQVSDAGMP
msa324064.2{343_2603}	RNTGLLLKHF	DITTKQISFH	EHNAYDKISG	LIDLLKEGks	LAQVSDAGMP
msa324064.2{343_COH1}	RNTGLLLKHF	DITTKQISFH	EHNAYDKISG	LIDLLKEGks	LAQVSDAGMP
msa324064.2{343_M732}	RNTGLLLKHF	DITTKQISFH	EHNAYDKISG	LIDLLKEGks	LAQVSDAGMP
msa324064.2{343_1169NT}	RNTGLLLKHF	DITTKQISFH	EHNAYDKISG	LIDLLKEGks	LAQVSDAGMP
msa324064.2{343_090}	RNTGLLLKHF	DITTKQISFH	EHNAYDKISG	LIDLLKEGrs	LAQVSDAGMP
msa324064.2{343_CJB110}	RNTGLLLKHF	DITTKQISFH	EHNAYDKISG	LIDLLKEGrs	LAQVSDAGMP
msa324064.2{343_H36B}	RNTGLLLKHF	DITTKQISFH	EHNAYDKISG	LIDLLKEGrs	LAQVSDAGMP
msa324064.2{343_JM9130013}	RNTGLLLKHF	DITTKQISFH	EHNAYDKISG	LIDLLKEGrs	LAQVSDAGMP
Consensus	*****	*****	*****	*****-*	*****

Table 74: Comparative Sequences relating to SAG1572

	101				150
msa324064.2{343_18RS21}	SISDPGHDLV	KAAIEGdIPV	VSIPGASAGI	TALIASGLAP	QPHIFYGFLP
msa324064.2{343_A909}	SISDPGHDLV	KAAIEGdIPV	VSIPGASAGI	TALIASGLAP	QPHIFYGFLP
msa324064.2{343_M781}	SISDPGHDLV	KAAIEGdIPV	VSIPGASAGI	TALIASGLAP	QPHIFYGFLP
msa324064.2{343_2603}	SISDPGHDLV	KAAIEGdIPV	VSIPGASAGI	TALIASGLAP	QPHIFYGFLP
msa324064.2{343_COH1}	SISDPGHDLV	KAAIEGdIPV	VSIPGASAGI	TALIASGLAP	QPHIFYGFLP
msa324064.2{343_M732}	SISDPGHDLV	KAAIEGdIPV	VSIPGASAGI	TALIASGLAP	QPHIFYGFLP
msa324064.2{343_1169NT}	SISDPGHDLV	KAAIEGdIPV	VSIPGASAGI	TALIASGLAP	QPHIFYGFLP
msa324064.2{343_090}	SISDPGHDLV	KAAIEGgIPV	VSIPGASAGI	TALIASGLAP	QPHIFYGFLP
msa324064.2{343_CJB110}	SISDPGHDLV	KAAIEGgIPV	VSIPGASAGI	TALIASGLAP	QPHIFYGFLP
msa324064.2{343_H36B}	SISDPGHDLV	KAAIEGdIPV	VSIPGASAGI	TALIASGLAP	QPHIFYGFLP
msa324064.2{343_JM9130013}	SISDPGHDLV	KAAIEGdIPV	VSIPGASAGI	TALIASGLAP	QPHIFYGFLP
Consensus	*****	*****-***	*****	*****	*****
	151				200
msa324064.2{343_18RS21}	RKkGQQITFF	ETKqDYPETQ	IFYESPFRVS	DTLKHMKEIY	GDRQVVLVRE
msa324064.2{343_A909}	RKkGQQITFF	ETKqDYPETQ	IFYESPFRVS	DTLKHMKEIY	GDRQVVLVRE
msa324064.2{343_M781}	RKkGQQITFF	ETKqDYPETQ	IFYESPFRVS	DTLKHMKEIY	GDRQVVLVRE
msa324064.2{343_2603}	RKkGQQITFF	ETKqDYPETQ	IFYESPFRVS	DTLKHMKEIY	GDRQVVLVRE
msa324064.2{343_COH1}	RKkGQQITFF	ETKqDYPETQ	IFYESPFRVS	DTLKHMKEIY	GDRQVVLVRE
msa324064.2{343_M732}	RKkGQQITFF	ETKqDYPETQ	IFYESPFRVS	DTLKHMKEIY	GDRQVVLVRE
msa324064.2{343_1169NT}	RKkGQQITFF	ETKqDYPETQ	IFYESPFRVS	DTLKHMKEIY	GDRQVVLVRE
msa324064.2{343_090}	RKkGQQITFF	ETKkDYPETQ	IFYESPFRVS	DTLKHMKEIY	GDRQVVLVRE
msa324064.2{343_CJB110}	RKkGQQITFF	ETKkDYPETQ	IFYESPFRVS	DTLKHMKEIY	GDRQVVLVRE
msa324064.2{343_H36B}	RKkGQQITFF	ETKkDYPETQ	IFYESPFRVS	DTLKHMKEIY	GDRQVVLVRE
msa324064.2{343_JM9130013}	RKkGQQITFF	ETKkDYPETQ	IFYESPFRVS	DTLKHMKEIY	GDRQVVLVRE
Consensus	**-*	*****	*****	*****	*****
	201				250
msa324064.2{343_18RS21}	LTKLYEEYQR	GTISQLLeHI	EKVPLKGECL	IIVDGKRDTE	RVKDSSQQDP
msa324064.2{343_A909}	LTKLYEEYQR	GTISQLLeHI	EKVPLKGECL	IIVDGKRDTE	RVKDSSQQDP
msa324064.2{343_M781}	LTKLYEEYQR	GTISQLLeHI	EKVPLKGECL	IIVDGKRDTE	RVKDSSQQDP
msa324064.2{343_2603}	LTKLYEEYQR	GTISQLLeHI	EKVPLKGECL	IIVDGKRDTE	RVKDSSQQDP
msa324064.2{343_COH1}	LTKLYEEYQR	GTISQLLeHI	EKVPLKGECL	IIVDGKRDTE	RVKDSSQQDP
msa324064.2{343_M732}	LTKLYEEYQR	GTISQLLeHI	EKVPLKGECL	IIVDGKRDTE	RVKDSSQQDP
msa324064.2{343_1169NT}	LTKLYEEYQR	GTISQLLeHI	EKVPLKGECL	IIVDGKRDTE	RVKDSSQQDP
msa324064.2{343_090}	LTKLYEEYQR	GTISQLLgHI	EKVPLKGECL	IIVDGKRDTE	RVKDSSQQDP
msa324064.2{343_CJB110}	LTKLYEEYQR	GTISQLLgHI	EKVPLKGECL	IIVDGKRDTE	RVKDSSQQDP
msa324064.2{343_H36B}	LTKLYEEYQR	GTISQLLgHI	EKVPLKGECL	IIVDGKRDTE	RVKDSSQQDP
msa324064.2{343_JM9130013}	LTKLYEEYQR	GTISQLLgHI	EKVPLKGECL	IIVDGKRDTE	RVKDSSQQDP
Consensus	*****	*****-***	*****	*****	*****
	251				289
msa324064.2{343_18RS21}	lVLV-----	-----	-----	-----	-----
msa324064.2{343_A909}	lVLV-----	-----	-----	-----	-----
msa324064.2{343_M781}	lVLV-----	-----	-----	-----	-----
msa324064.2{343_2603}	lVLVkeyian	gdktqnaiikk	vakefnlnrq	elyasfhd1	-----
msa324064.2{343_COH1}	lVLV-----	-----	-----	-----	-----
msa324064.2{343_M732}	lVLV-----	-----	-----	-----	-----
msa324064.2{343_1169NT}	lVLV-----	-----	-----	-----	-----
msa324064.2{343_090}	lVLV-----	-----	-----	-----	-----
msa324064.2{343_CJB110}	lVLV-----	-----	-----	-----	-----
msa324064.2{343_H36B}	lVLV-----	-----	-----	-----	-----
msa324064.2{343_JM9130013}	vVLV-----	-----	-----	-----	-----
Consensus	-*****	*****	*****	*****	*****

Table 75: Comparative Sequences relating to SAG0671

SEQ ID NO. 7501

STRAIN 2603

ATGAGCGTATATGTTAGTGGAATAGGAATTATT
 TCTTCTTTGGGAAAGAAATTATAGCGAGCATAAACAGCATCTCTTCGACTTAAAAGAAGGA
 ATTTCTAAACATTTATATAAAAAATCACGACTCTATTTTAGAATCTTATACAGGAAGCATA
 ACTAGTGACCCAGAGGTTCCCTGAGCAATACAAAGATGAGACACGTAATTTTAAATTTGCT
 TTTACCGCTTTTGAAGAGGGCTCTTGCTTCTTCAGGTGTTAATTTAAAAGCTTATCATAAT
 ATTGCTGTGTGTTTAGGGACCTCACTTGGGGGAAAGAGTGCTGGTCAAATGCCTTGAT
 CAATTTGAAGAAGGAGAGCGTCAAGTAGATGCTAGTTTATTAGAAAAAGCATCTGTTTAC
 CATATTGCTGATGAATTGATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTTCA
 ACCGCTGTTCTGCAAGTAATAATGCCGTAATATTAGGAACACAATTACTTCAAGATGGC
 GATTGTGATTTAGCTATTTGTGGTGGCTGTGATGAGTTAAGTGATATTTCTTTAGCAGGC
 TTCACATCACTAGGAGCTATTAATACAGAAATGGCATGTGAGCCCTATTCTTCTGGAAAA
 GGAATCAATTTGGGTGAGGGCGCTGGTTTTGTGTTCTTGTCAAAGATCAGTCCTTAGCT
 AAATATGGAAAAATTTATCGGTGGTCTTATTACTTCAGATGGTTATCATATAACAGCACCT
 AAGCCAACAGGTGAAGGGGCGGCACAGATTGCAAAGCAGCTAGTGACTCAAGCAGGTATT
 GACTACAGTGAGATTGACTATATTAACGGTCACGGTACAGGTACTCAAGCTAATGATAAA
 ATGGAAAAAATATGTATGGTAAGTTTTCGCGACAACGACATTGATCAGCAGTACCAAG
 GGGCAAACGGGTCTACTCTAGGGGCTGCAGGTATTATCGAATTGATTAATTGTTTAGCG
 GCAATAGAGGAACAGACTGTACCAGCACTAAAAATGAGATTGGGATAGAAGGTTTCCA
 GAAAAATTTGTCTATCATCAAAAGAGAGAATACCCAATAAGAAATGCTTTAAATTTTTCG
 TTGCTTTTGGTGGAAATAATAGTGGTGTCTTATTGTCTATTTAGATTACCTCTAGAA
 ACATTACCTGCTAGAGAAAATCTTAAATGGCTATCTTATCATCTGTTGCTTCCATTTCT
 AAGAATGAATCACTTTCTATAACCTATGAAAAAGTTGCTAGTAATTTCAACGACTTTGAA
 GCATTTACGCTTTTAAAGGGGCTAGACCACCCAAAACTGTCAACCCAGCACAATTTAGGAAA
 ATGGATGATTTTCCAAAATGGTTGCCGTAACAACAGCTCAAGCACTAATAGAAAGCAAT
 ATTAATCTAAAAAACAAGATACTTCAAAAGTAGGAATTGTATTTACAACACTTTCTGGA
 CCAGTTGAGGTTGTTGAAGGTATTGAAAAGCAAATCACAACAGAAGGATATGCACATGTT
 TCTGCTTCACGATTCCCGTTTACAGTAATGAATGCAGCAGCTGGTATGCTTTCTATCATT
 TTTAAAAATAACAGGTCTTTTATCTGTCTATTTTCGACAAATAGTGGAGCGCTTGATGGTATA
 CAATATGCCAAGGAATGATGCGTAACGATAATCTAGACTATGTGATTCTTGTTTCTGCT
 AATCAGTGGACAGACATGAGTTTTATGTGGTGGCAACAATTAACTATGATAGTCAAATG
 TTTGTGCGTTCTGATTATTGTTTCAACAGTCTCTCTCGTCAAGCATTGGATAATTCT
 CCTATAATATTAGGTAGTAAACAATTAAAAATATAGCCATAAAACATTACAGATGTGATG
 ACTATTTTGTGCTGCGCTTCAAAATTTATTATCAGACTTAGGACTAACCATAAAAGAT
 ATCAAAGGTTTTCGTTTGGAAATGAGCGGAAGGAGGAGTTAGTTTCAAGATTATGATTTCTTA
 GCGAAGCTTGTCTGAGTATTATAATATGCCAAACCTTGCTTCTGGTCAGTTTGGATTTTCA
 TCTAATGGTGTGCTGGTGAAGAACTGGACTATACTGTTAATGAAAGTATAGAAAAGGGCTAT
 TATTTAGTCTCTATCTTATTCGATCTTCGGTGGTATCTCTTTTGCTATTATTGAAAAAAGG

SEQ ID NO. 7502

STRAIN 090

ATGTTAGTGGAATAGGAATTATTTCTTCTTTGGGAAAGaATTAT
 AGCGAGCATAAACAGCATCTCTTCGACTTAAAAGAAGGAATTTCTAAACA
 TTTATATAAAAAATCACGACTCTATTTTAGAATCTTATACAGGAAGCATAA
 CTAGTGACCCAGAGGTTCCCTGAGCAATACAAAGATGAGACACGTAATTTT
 AAATTTGCTTTTACCGCTTTTGAAGAGGGCTCTTGCTTCTTCAGGTGTTAA
 TTTAAAAGCTTATCATAATATTGCTGTGTGTTTAGGGACCTCACTTGGGG
 GAAAGAGTGCTGGTCAAATGCCTTGTATCAATTTGAAGAAGGAGAGCGT
 CAAGTAGATGCTAGTTTATTAGAAAAAGCATCTGTTTACCATATTGCTGA
 TGAATTGATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTTCAA
 CCGCTGTTCTGCAAGTAATAATGCCGTAATATTAGGAACACAATTACTT
 CAAGATGGCGATTGTGATTTAGCTATTTGTGGTGGCTGTGATGAGTTAAG
 TGATATTTCTTTAGCAGGCTTACATCACTAGGAGCTATTAAATACAGAAA
 TGGCATGTGAGCCCTATTCTTCTGGAAAAGGAATCAATTTGGGTGAGGGC
 GCTGGTTTTGTGTTCTTGTCAAAGATCAGTCCTTAGCTAAATATGGAAA
 AATTATCGGTGGTCTTATTACTTCAGATGGTTATCATATAACAGCACCTA
 AGCCAACAGGTGAAGGGGCGGCACAGATTGCAAAGCAGCTAGTGACTCAA
 GCAGGTATTGACTACAGTGAGATTGACTATATTAACGGTCACGGTACAGG
 TACTCAAGCTAATGATAAAATGGAAAAAATATGTATGGTAAGTTTTC
 CGACAACGACATTGATCAGCAGTACCAAGGGGCAAACGGGTCTACTCTA
 GGGGCTGCAGGTATTATCGAATTGATTAATTGTTTAGCGGCAATAGAGGA
 ACAGACTGTACCAGCACTAAAAATGAGATTGGGATAGAAGGTTTTCAG
 AAAATTTTGTCTATCATCAAAAGAGAGAATACCCAATAAGAAATGCTTTA
 AATTTTTCGTTTGTCTTTGGTGGAAATAATAGTGGTATCTTATTGTCTATC
 TTTAGATTACCTCTAGAAACATTACCTGCTAGAGAAAATCTTAAATGG
 CTATCTTATCATCTGTTGCTTCCATTTCTAAGAATGAATCACTTTCTATA
 ACCTATGAAAAAGTTGCTAGTAATTTCAACGACTTTGAAGCATTACGCTT
 TAAAGGGGCTAGACCACCCAAACTGTCAACCCAGCACAATTTAGGAAAA
 TGGATGATTTTCCAAAATGGTTGCCGTAACAACAGCTCAAGCACTAATA
 GAAAGCAATATTAATCTAAAAAACAAGATACTTCAAAAGTAGGAATTGT
 ATTTACAACACTTTCTGGACAGTTGAGGTTGTTGAAGGTATTGAAAAGC
 AAATCACAACAGAAGGATATGCACATGTTTCTGCTTACGATTCCCGTTT
 ACAGTAATGAATGCAGCAGCTGGTATGCTTTCTATCATTTTAAAATAAC
 AGGTCTTTTATCTGTCTATTTGACAAATAGTGGAGCGCTTGATGGTATAC
 AATATGCCAAGGAATGATGCGTAACGATAATCTAGACTATGTGATTCTT
 GTTTCTGCTAATCAGTGGACAGACATGAGTTTATGTGGTGGCAACAATT
 AAATATGATAGTCAAATGTTTGTGCGTTCTGATTATTGTTTCAACAGCAG
 TCCTCTCTCGTCAAGCATTGGATAATTCTCCTATAATATTAGGTAGTAAA
 CAATTAATAATATAGCCATAAAACATTACAGATGTGATGACTATTTTGA
 TGCTGCGCTTCAAAATTTATTATCAGACTTAGGACTAACCATAAAAGATA
 TCAAAGGTTTTCGTTTGGAAATGAGCGGAAGGAGGAGTTAGTTTCAAGATTAT
 GATTTCTTAGCGAAGTTGTCTGAGTATTATAATATGCCAAACCTTGCTTC

Table 75: Comparative Sequences relating to SAG0671

TGGTCAGTTTGGATTTCATCTAATGGTGCTGGTGAAGAACTGGACTATA
CTGTTAATGAAAGTATAGAAAAGGGCTATTATTTAGTCCTATCTTATTCG
ATCTTTGGTGGTATCTCTTTTGCTATTATTGAAAAAAGG

SEQ ID NO. 7503**STRAIN A909**

ATGTTAGTGGAATAGGAATTATTTCTTCTTTGGGAAAGAATT
ATAGCGAGCATAAACAGCATCTCTTCGACTTAAAAGAAGGAATTTCTAAA
CATTATATATAAAAATCACGACTCTATTTTAGAATCTTATACAGGAAGCAT
AACTAGTGACCCAGAGGTTCTGAGCAATACAAAGATGAGACACGTAATT
TTAAATTTGCTTTTACCGCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTT
AATTTAAAAGCTTATCATAATATTGCTGTGTGTTTAGGGACCTCACTTGG
GGGAAAGAGTGGTGGTCAAAATGCCCTTGATCAATTTGAAGAAGGAGAGC
GTCAAGTAGATGCTAGTTTATTAGAAAAAGCATCTGTTTACCATATTGCT
GATGAATTGATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTTT
AACCCTGCTGTTCTGCAAGTAATAATGCCGTAATATTAGGAACACAATTAC
TTCAAGATGGCGATTGTGATTTAGCTATTTGTGGTGGCTGTGATGAGTTA
AGTGATATTTCTTTAGCAGGCTTCACATCACTAGGAGCTATTAATACAGA
AATGGCATGTGAGCCCTATTCTTCTGGAAAAGGAATCAATTTGGGTGAGG
GCGCTGGTTTTGTGTTCTTGTCAAAGATCAGTCCTTAGCTAAATATGGA
AAAATTATCGGTGGTCTTATTACTTCAGATGGTTATCATATAACAGCACC
TAAGCCAACAGGTGAAGGGGCGGCACAGATTGCAAAGCAGCTAGTGACTC
AAGCAGGTATTGACTACAGTGAGATTGACTATATTAACGGTCACGGTACA
GGTACTCAAGCTAATGATAAAATGGAATAATATGTATGGTAAGTTTTT
CCCGACAACGACATTGATCAGCAGTACCAAGGGGCAAACGGGTCACTC
TAGGGGCTGCAGGTATTATCGAATTGATTAATTGTTTAGCGGCAATAGAG
GAACAGACTGTACCAGCAACTAAAATGAGATTGGGATAGAAGGTTTTCC
AGAAAATTTGTCTATCATCAAAGAGAGAATACCCAATAAGAAATGCTT
TAAATTTTTCTGTTTTGCTTTTGGTGGAAATAATAGTGGTGTCTTATTGTCA
TCTTTAGATTACCTCTAGAAACATTACCTGCTAGAGAAAATCTTAAAT
GGCTATCTTATCATCTGTTGCTTCCATTTCTAAGAATGAATCACTTTCTA
TAACCTATGAAAAAGTTGCTAGTAATTTCAACGACTTTGAAGCATTACGC
TTTAAAGGGGCTAGACCACCCAAACTGTCAACCCAGCACAAATTTAGGAA
AATGGATGATTTTTCCAAAATGGTTGCCGTAACAACAGCTCAAGCACTAA
TAGAAAGCAATATTAATCTAAAAAACAAGATACTTCAAAAGTAGGAAT
GTATTTACAACACTTTCTGGACCAGTTGAGGTTGTTGAAGGTATTGAAAA
GCAATCACAAACAGAAGGATATGCACATGTTTCTGCTTCACGATTTCCCGT
TTACAGTAATGAATGCAGCAGCTGGTATGCTTTCTATCATTTTTAAAATA
ACAGGTCCTTTATCTGTCAATTCGACAAATAGTGGAGCGCTTGATGGTAT
ACAATATGCCAAGGAAATGATGCGTAACGATAATCTAGACTATGTGATTC
TTGTTTTCTGCTAATCAGTGGACAGACATGAGTTTTATGTGGTGGCAACAA
TTAAACTATGATAGTCAAATGTTTTGTCGGTTCTGATTATTGTTTCAGCACA
AGTCCTCTCTCGTCAAGCATTGGATAATTCTCCTATAATATTAGGTAGTA
AACAATTAAAATATAGCCATAAAACATTACAGATGTGATGACTATTTTT
GATGCTGCGCTTCAAATTTATTATCAGACTTAGGACTAACCATAAAAGA
TATCAAAGGTTTTGTTTTGGAATGAGCGGAAGAAGGCAGTTAGTTTCAGATT
ATGATTTCTTAGCGAATTTGTCTGAGTATTATAATATGCCAAACCTTGCT
TCTGGTCAGTTTGGATTTTCATCTAATGGTGCTGGTGAAGAACTGGACTA
TACTGTTAATGAAAGTATAGAAAAGGGCTATTATTTAGTCCTATCTTATT
CGATCTTCGGTGGTATCTCTTTTGCTATTATTGAAAAAAGG

SEQ ID NO. 7504**STRAIN H36B**

ATGTTAGTGGAATAGGAATTATTTCTTCTTTGGGAAAGAATTATAGCGA
GCATAAACAGCATCTCTTCGACTTAAAAGAAGGAATTTCTAAACATTTAT
ATAAAAATCACGACTCTATTTTAGAATCTTATACAGGAAGCATAACTAGT
GACCCAGAGGTTCTGAGCAATACAAAGATGAGACACGTAATTTTAAATT
TGCTTTTACCGCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTTAATTTAA
AAGCTTATCATAATATTGCTGTGTGTTTAGGGACCTCACTTGGGGGAAAG
AGTGCTGGTCAAAATGCCCTTGATCAATTTGAAGAAGGAGAGCGTCAAGT
AGATGCTAGTTTATTAGAAAAAGCATCTGTTTACCATATTGCTGATGAAT
TGATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTTCAACCGCC
TGTTCTGCAAGTAATAATGCCGTAATATTAGGAACACAATTTACTTCAAGA
TGGCGATTGTGATTTAGCTATTTGTGGTGGCTGTGATGAGTTAAGTGATA
TTTCTTTAGCAGGCTTCACATCACTAGGAGCTATTAATACAGAAATGGCA
TGTCAGCCCTATTCTTCTGGAAAAGGAATCAATTTGGGTGAGGGCGCTGG
TTTTGTTGTTCTTGTCAAAGATCAGTCCTTAGCTAAATATGGAAAAATTA
TCGGTGGTCTTATTACTTCAGATGGTTATCATATAACAGCACCTAAGCCA
ACAGGTGAAGGGGCGGCACAGATTGCAAAGCAGCTAGTGACTCAAGCAGG
TATTGACTACAGTGAGATTGACTATATTAACGGTCACGGTACAGGTACTC
AAGCTAATGATAAAATGGAATAATATGTATGGTAAGTTTTTCCCGACA
ACGACATTGATCAGCAGTACCAAGGGGCAAACGGGTCACTACTAGGGGC
TGCAGGTATTATCGAATTGATTAATTTGTTTACGGGCAATAGAGGAACAGA
CTGTACCAGCAACTAAAAATGAGATTGGGATAGAAGGTTTTCCAGAAAAAT
TTTGTCTATCATCAAAGAGAGAATACCCAATAAGAAATGCTTTAAATTT
TTCGTTTGCTTTTGGTGGAAATAATAGTGGTGTCTTATTGTCTATCTTTAG
ATTACCTCTAGAAAATTACCTGCTAGAGAAAATCTTAAATGGCTATC
TTATCATCTGTTGCTTCCATTTCTAAGAATGAATCACTTTCTATAACCTA
TGAAAAAGTTGCTAGTAATTTCAACGACTTTGAAGCATTAACGCTTTAAAG
GGGCTAGACCACCCAAAATGTCAACCCAGCACAAATTTAGGAAAAATGGAT
GATTTTTCCAAAATGGTTGCCGTAACAACAGCTCAAGCACTAATAGAAAG
CAATATTAATCTAAAAAACAAGATACTTCAAAAGTAGGAATTTGTATTTA
CAACACTTTCTGGACCAGTTGAGGTTGTTGAAGGTATTGAAAAGCAAATC

Table 75: Comparative Sequences relating to SAG0671

ACAACAGAAGGATATGCACATGTTTCTGCTTCACGATTCCCGTTTACAGT
 AATGAATGCAGCAGCTGGTATGCTTTCTATCATTTTTTAAATAACAGGTC
 CTTTATCTGTCAATTCGACAAATAGTGGAGCGCTTGATGGTATACAATAT
 GCCAAGGAAATGATGCGTAACGATAATCTAGACTATGTGATTCTTGTTTC
 TGCTAATCAGTGGACAGACATGAGTTTTATGTGGTGGCAACAATTAACT
 ATGATAGTCAAATGTTTTGTGCGTTCTGATTATTGTTTACGACACAAGTCCTC
 TCTCGTCAAGCATTGGATAATTCTCCTATAATATTAGGTAGTAAACAATT
 AAAATATAGCCATAAAACATTACAGATGTGATGACTATTTTTGATGCTG
 CGCTTCAAATTTATTATCAGACTTAGGACTAACCATAAAAGATATCAAA
 GGTTTCGTTTGGAAATGAGCGGAAGAAGGCAGTTAGTTTCAAGATTATGATT
 CTAGCGAACTTGTCTGAGTATTATAATATGCCAAACCTTGCTTCTGGTC
 AGTTTGGATTTCATCTAATGGTGTCTGGTGAAGAAGTGGACTATACTGTT
 AATGAAAGTATAGAAAAGGGCTATTATTAGTCTTATTCGATCTT
 CGGTGGTATCTCTTTTGCTATTATTGAAAAAAGG

SEQ ID NO. 7505**STRAIN 18RS21**

ATGTTAGTGGAAATAGGAATTATTTCTTCTTTGGGAAAGAATTATAGC
 GAGCATAAACAGCATCTCTTCGACTTAAAGAAGGAATTTCTAAACATTT
 ATATAAAAATCACGACTCTATTTTAGAATCTTATACAGGAAGCATAACTA
 GTGACCCAGAGGTTCTGAGCAATACAAAGATGAGACACGTAATTTTAAA
 TTTGCTTTTACCGCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTTAATTT
 AAAAGCTTATCATAATATTGCTGTGTGTTTAGGGACCTCACTTGGGGGAA
 AGAGTGTGGTCAAATGCCTTGTATCAATTTGAAGAAGGAGAGCGTCAA
 GTAGATGCTAGTTTATTAGAAAAGCATCTGTTTACCATATTGCTGATGA
 ATTGATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTTCAACCG
 CCTGTTCTGCAAGTAATAATGCCGTAATATTAGGAACACAATTACTTCAA
 GATGGCGATTGTGATTTAGCTATTTGTGGTGGCTGTGATGAGTTAAGTGA
 TATTTCTTTAGCAGGCTTCACATCACTAGGAGCTATTAATACAGAAATGG
 CATGTCAGCCCTATTCTTCTGGAAAAGGAATCAATTTGGGTGAGGGCGCT
 GGTTTTGTTGTTCTTGTCAAAGATCAGTCTTAGCTAAATATGGAAAAAT
 TATCGGTGGTCTTATTACTTCAGATGGTTATCATATAACAGCACCTAAGC
 CAACAGGTGAAGGGGCGGCACAGATTGCAAAGCAGCTAGTGACTCAAGCA
 GGTATTGACTACAGTGAGATTGACTATATTAACGGTCACGGTACAGGTAC
 TCAAGCTAATGATAAAATGGAAAAAATATGTATGGTAAGTTTTTCCCGA
 CAACGACATTGATCAGCAGTACCAAGGGGCAAACGGGTCTACTCTAGGG
 GCTGCAAGGTATTATCGAATTGATTAAATTGTTTAGCGGCAATAGAGGAACA
 GACTGTACCAGCAACTAAAAATGAGATTGGGATAGAAGGTTTTCCAGAAA
 ATTTTGTCTATCATCAAAAGAGAGAATACCAATAAGAAATGCTTTAAAT
 TTTTCGTTTGCTTTTGGTGGAAATAATAGTGGTGTCTTATTGTCATCTTT
 AGATTCACCTCTAGAAACATTACCTGCTAGAGAAAATCTTAAATGGCTA
 TCTTATCATCTGTTGCTTCCATTTCTAAGAATGAATCACTTTCTATAACC
 TATGAAAAAGTTGCTAGTAATTTCAACGACTTTGAAGCATTACGCTTTAA
 AGGGGCTAGACCACCCAAAATGTCAACCCAGCACAAATTTAGGAAAAATGG
 ATGATTTTTTCAAATGGTTGCCGTAACAACAGCTCAAGCACTAATAGAA
 AGCAATATTAATCTAAAAAACAAGATACTTCAAAAGTAGGAATTGTATT
 TACAACACTTTCTGGACCAGTTGAGGTTGTTGAAGGTATTGAAAAGCAAA
 TCACAACAGAAGGATATGCACATGTTTCTGCTTCACGATTCCCGTTTACA
 GTAATGAATGCAGCAGCTGGTATGCTTTCTATCATTTTTTAAATAACAGG
 TCCTTTATCTGTCAATTCGACAAATAGTGGAGCGCTTGATGGTATACAAT
 ATGCCAAGGAAATGATGCGTAACGATAATCTAGACTATGTGATTCTTGTT
 TCTGCTAATCAGTGGACAGACATGAGTTTTATGTGGTGGCAACAATTAAA
 CTATGATAGTCAAATGTTTGTGCGTTCTGATTATTGTTTACGACAAAGTCC
 TCTCTCGTCAAGCATTGGATAATTCTCCTATAATATTAGGTAGTAAACAA
 TTAAATATATAGCCATAAAACATTACAGATGTGATGACTATTTTTGATGC
 TGCGCTTCAAATTTATTATCAGACTTAGGACTAACCATAAAAGATATCA
 AAGGTTTTCGTTTGGAAATGAGCGGAAGAAGGCAGTTAGTTTCAAGTTATGAT
 TTCTTAGCGAACTTGTCTGAGTATTATAATATGCCAAACCTTGCTTCTGG
 TCAGTTTGGATTTCATCTAATGGTGTCTGGTGAAGAAGTGGACTATACTG
 TTAATGAAAGTATAGAAAAGGGCTATTATTAGTCTTATCTTATTCGATC
 TTCGGTGGTATCTCTTTTGCTATTATTGAAAAAAGG

SEQ ID NO. 7506**STRAIN M732**

ATGTTAGTGGAAATAGGAATTATTTCTTCTTTGGGAAAGAATTATAGC
 CGAGCATAAACAGCATCTCTTCGACTTAAAGAAGGAATTTCTAAACATT
 TATATAAAAATCACGACTCTATTTTAGAATCTTATACAGGAAGCATAACT
 AGTGACCCAGAGGTTCTGAGCAATACAAAGATGAGACACGTAATTTTAA
 ATTTGCTTTTACCGCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTTAATT
 TAAAAGCTTATCATAATATTGCTGTGTGTTTAGGGACCTCACTTGGGGGA
 AAGAGTGTGGTCAAATGCCTTGTATCAATTTGAAGAAGGAGAGCGTCA
 AGTAGATGCTAGTTTATTAGAAAAAGCATCTGTTTACCATATTGCTGATG
 AATTGATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTTCAACC
 GCCTGTTCTGCAAGTAATAATGCCGTAATATTAGGAACACAATTACTTCA
 AGATGGCGATTGTGATTTAGCTATTTGTGGTGGCTGTGATGAGTTAAGTG
 ATATTTCTTTAGCAGGCTTCACATCACTAGGAGCTATTAAATACAGAAATG
 GCATGTCAGCCCTATTCTTCTGGAAAAGGAATCAATTTGGGTGAGGGCGC
 TGGTTTTGTTGTTCTTGTCAAAGATCAGTCCCTAGCTAAATATGGAAAAA
 TTATCGGTGGTCTTATTACTTCAGATGGTTATCATATAACAGCACCTAAG
 CCAACAGGTGAAGGGGCGGCACAGATTGCAAAGCAGCTAGTGACTCAAGC
 AGGTATTGACTACAGTGAGATTGACTATATTAACGGTCACGGTACAGGTA
 CTCAAGCTAATGATAAAATGGAAAAAATATGTATGGTAAGTTTTTCCCG
 ACAACGACATTGATCAGCAGTACCAAGGGGCAAACGGGTCTACTCTAGG

Table 75: Comparative Sequences relating to SAG0671

GGCTGCAGGTATTATCGAATTGATTAAATTGTTTAGCGGCAATAGAGGAAC
 AGACTGTACCAGCAACTAAAAATGAGATTGGGATAGAAGGTTTTCCAGAA
 AATTTTGTCTATCATCAAAAGAGAGAATACCCAATAAGAAATGCTTTAAA
 TTTTTCGTTTGCTTTTGGTGGAAATAATAGTGGTGTCTTATGTCTATCTT
 TAGATTACCTCTAGAAACATTACCTGCTAGAGAAAATCTTAAAAATGGCT
 ATCTTATCATCTGTTGCTTCCATTTCTAAGAATGAATCACTTTCTATAAC
 CTATGAAAAAGTTGCTAGTAATTTCAACGACTTTGAAGCATTACGCTTTA
 AAGGGGCTAGACCACCCAAAACGTCAACCCAGCACAAATTTAGGAAAATG
 GATGATTTTTCCAAAATGGTTGCCGTAACAACAGCTCAAGCACTAATAGA
 AAGCAATATTAATCTAAAAAACAAGATACTTCAAAAGTAGGAATTGTAT
 TTACAACACTTTCTGGACCAGTTGAGGTTGTTGAAGGTATTGAAAAGCAA
 ATCACAACAGAAGGATATGCACATGTTTCTGCTTCACGATTTCCCGTTTAC
 AGTAATGAATGACGAGCTGGTATGCTTTCTATCATTTTAAAAAACAAG
 GTCCTTTATCTGTCTTTTCGACAAATAGTGGAGCGCTTGATGGTATACAA
 TATGCCAAGGAAATGATGCGTAACGATAATCTAGACTATGTGATTCTTGT
 TTCTGCTAATCAGTGGACAGACATGAGTTTATGTGGTGGCAACAATTAA
 ACTATGATAGTCAAATGTTTGTGCGTTCTGATTATTGTTTCAAGCACAAGTC
 CTCTCTCGTCAAGCATTGGATAATTCTCTATAATATTAGGTAGTAAACA
 ATTAAAAATATAGCCATAAAACATTACAGATGTGATGACTATTTTGTATG
 CTGCGCTTCAAAATTTATTATCAGACTTAGGACTAACCATAAAAAGATATC
 AAAGGTTTTCGTTTGAATGAGCGGAAGAAGGCAGTTAGTTTCAAGATTATGA
 TTTCTTAGCGAAGTTGTCTGAGTATTATAATATGCCAAACCTTGCTTCTG
 GTCAGTTTGGATTTTCTAATGGTGTGCTGGTGAAGAACTGGACTATaCT
 GTTAATGAAAGTATAGAAAAGGGCTATTATTTAGTCTCTATCTATTTCGAT
 CTTCCGTGGTATCTCTTTTGCTATTATTGAAAAAAGG

SEQ ID NO. 7507

STRAIN COH1

ATGTTAGTGGAATAGGAATTATTTCTTCTTTGGGAAAGAATTATAGC
 GAGCATAAACAGCATCTCTTCGACTTAAAAGAAGGAATTTCTAAACATTT
 ATATAAAAATCAGACTCTATTTTAGAATCTTATACAGGAAGCATAACTA
 GTGACCCAGAGGTTCTTGAGCAATACAAAGATGAGACACGTAATTTTAAA
 TTTGCTTTTACCGCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTTAATTT
 AAAAGCTTATCATAATATTGCTGTGTGTTTAGGGACCTCACTTGGGGGAA
 AGAGTGCTGGTCAAAATGCCCTTGATCAATTTGAAGAAGGAGAGCGTCAA
 GTAGATGCTAGTTTATTAGAAAAAGCATCTGTTTACCATAATTGCTGATGA
 ATTGATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTTCAACCG
 CCTGTTCTGCAAGTAATAATGCCGTAATATTAGGAACACAATTACTTCAA
 GATGGCGATTGTGATTTAGCTATTTGTGGTGGCTGTGATGAGTTAAGTGA
 TATTTCTTTAGCAGGCTTCACATCACTAGGAGCTATTAATACAGAAATGG
 CATGTGAGCCCTATTCTTCTGGAAAAGGAATCAATTTGGGTGAGGGCGCT
 GGTTTTGTGTTCTTGTCAAAGATCAGTCCCTAGCTAAATATGGAAAAAT
 TATCCGTGGTCTTATTACTTCAGATGGTTATCATATAACAGCACCTAAGC
 CAACAGGTGAAGGGGCGGCACAGATTGCAAGCAGCTAGTGACTCAAGCA
 GGTATTGACTACAGTGAGATTGACTATATTAAACGGTCACGGTACAGGTAC
 TCAAGCTAATGATAAAATGGAAAAAATATGTATGGTAAGTTTTTCCCGA
 CAACGACATTGATCAGCAGTACCAAGGGGCAACGGGTCTACTCTAGGG
 GCTGCAAGTATTATCGAATTGATTAATTTGTTTAGCGGCAATAGAGGAACA
 GACTGTACCAGCAACTAAAAATGAGATTGGGATAGAAGGTTTTCCAGAAA
 ATTTTGTCTATCATCAAAAGAGAGAATAACCCAATAAGAAATGCTTTAAAT
 TTTTCGTTTGCTTTTGGTGGAAATAATAGTGGTGTCTTATTGTCTATCTT
 AGATTACCTCTAGAAACATTACCTGCTAGAGAAAATCTTAAAAATGGCTA
 TCTTATCATCTGTTGCTTCCATTTCTAAGAATGAATCACTTTCTATAACC
 TATGAAAAAGTTGCTAGTAATTTCAACGACTTTGAAGCATTACGCTTTAA
 AGGGGCTAGACCACCCAAAACGTGTCAACCCAGCACAAATTTAGGAAAATGG
 ATGATTTTTCAAAATGGTTGCCGTAACAACAGCTCAAGCACTAATAGAA
 AGCAATATTAATCTAAAAAACAAGATACTTCAAAAGTAGGAATTGTATT
 TACAACACTTTCTGGACCAGTTGAGGTTGTTGAAGGTATTGAAAAGCAAA
 TCACAACAGAAGGATATGCACATGTTTCTGCTTCACGATTCCCGTTTACA
 GTAATGAATGCAGCAGCTGGTATGCTTTCTATCATTTTAAAAATAACAGG
 TCCTTTTATCTGTCTATTTGACAAATAGTGGAGCGCTTGATGGTATACAAT
 ATGCCAAGGAAATGATGCGTAACGATAATCTAGACTATGTGATTCTTGT
 TCTGCTAATCAGTGGACAGACATGAGTTTATGTGGTGGCAACAATTAAA
 CTATGATAGTCAAATGTTTGTGCGTTCTGATTATTGTTTCAAGCACAAGTCC
 TCTCTCGTCAAGCATTGATAATTTCTCCTATAATATTAGGTAGTAAACAA
 TTAAAAATATAGCCATAAAACATTACAGATGTGATGACTATTTTGTATGC
 TCGCTTCAAAATTTATTATCAGACTTAGGACTAACCATAAAAAGATATCA
 AAGGTTTTCGTTTGAATGAGCGGAAGAAGGCAGTTAGTTTCAAGATTATGAT
 TTCTTAGCGAAGTTGTCTGAGTATTATAATATGCCAAACCTTGCTTCTGG
 TCAGTTTGGATTTTCTAATGGTGTGCTGGTGAAGAACTGGACTATACTG
 TTAATGAAAGTATAGAAAAGGGCTATTATTTAGTCTCTATCTATTTCGATC
 TTCGGTGGTATCTCTTTTGCTATTATTGAAAAAAGG

SEQ ID NO. 7508

STRAIN M781

ATGTTAGTGGAATAGGAATTATTTCTTCTTTGGGAAAGAATTATAGC
 GAGCATAAACAGCATCTCTTCGACTTAAAAGAAGGAATTTCTAAACATTT
 ATATAAAAATCAGACTCTATTTTAGAATCTTATACAGGAAGCATAACTA
 GTGACCCAGAGGTTCTTGAGCAATACAAAGATGAGACACGTAATTTTAAA
 TTTGCTTTTACCGCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTTAATTT
 AAAAGCTTATCATAATATTGCTGTGTGTTTAGGGACCTCACTTGGGGGAA
 AGAGTGCTGGTCAAAATGCCCTTGATCAATTTGAAGAAGGAGAGCGTCAA
 GTAGATGCTAGTTTATTAGAAAAAGCATCTGTTTACCATAATTGCTGATGA

Table 75: Comparative Sequences relating to SAG0671

ATTGATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTTCAACCG
 CCTGTTCTGCAAGTAATAATGCCGTAATATTAGGAACACAATTACTTCAA
 GATGGCGATTGTGATTTAGCTATTTGTGGTGGCTGTGATGAGTTAAGTGA
 TATTTCTTTAGCAGGCTTCACATCACTAGGAGCTATTAATACAGAAATGG
 CATGTCAGCCCTATTCTTCTGGAAAAGGAATCAATTTGGGTGAGGGCGCT
 GGTTTTGTGTGTTCTTGTCAAAGATCAGTCCTTAGCTAAATATGGAAAAAT
 TATCGGTGGTCTTATTACTTCAGATGGTTATCATATAACAGCACCTAAGC
 CAACAGGTGAAGGGGCGGCACAGATTGCAAAGCAGCTAGTGACTCAAGCA
 GGTATTGACTACAGTGAGATTGACTATATTAATGGTCACGGTACAGGTAC
 TCAAGCTAATGATAAAATGGAAAAAAATATGTATGGTAAGTTTTTCCCGA
 CAACGACATTGATCAGCAGTACCAAGGGGCAAACGGGTCTACTCTAGGG
 GCTGCAGGTATTATCGAATTGATTAATTGTTTAGCGGCAATAGAGGAACA
 GACTGTACCAGCAACTAAAAATGAGATTGGGATAGAAGGTTTTCCAGAAA
 ATTTTGTCTATCATCAAAAGAGAGAATACCCAATAAGAAATGCTTTAAAT
 TTTTCGTTTGTCTTTGGTGGAAATAATAGTGGTATCTTATTGTCATCTTT
 AGATTACCTCTAGAAACATTACCTGCTAGAGAAAATCTTAAATGGCTA
 TCTTATCATCTGTGCTTCCATTTCTAAGAATGAATCACTTTCTATAACC
 TATGAAAAAGTTGCTAGTAATTTCAACGACTTTGAAGCATTACGCTTTAA
 AGGGGCTAGACCACCCAAAACCTGTCAACCCAGCACAAATTTAGGAAAATGG
 ATGATTTTCCAAAATGGTTGCCGTAACAACAGCTCAAGCACTAATAGAA
 AGCAATATTAAATCTAAAAAAACAAGATACTTCAAAAGTAGGAATTGTATT
 TACAACACTTTCTGGACCAGTTGAGGTTGTTGAAGGTATTGAAAAGCAAA
 TCACAACAGAAGGATATGCACATGTTTCTGCTTCACGATTCCCGTTTACA
 GTAATGAATGCAGCAGCTGGTATGCTTTCTATCATTTTTTAAATAACAGG
 TCCTTTATCTGTCTTTTCGACAAATAGTGGAGCGCTTGATGGTATACAAT
 ATGCCAAGGAAATGATGCGTAACGATAATCTAGACTATGTGATTCTTGTT
 TCTGCTAATCAGTGGACAGACATGAGTTTTATGTGGTGGCAACAATTAAA
 CTATGATAGTCAAAATGTTTGTGCGTTCTGATTATTGTTTCAACAGTCC
 TCTCTCGTCAAGCATTGGATAATTCTCCTATAATATTAGGTAGTAAACAA
 TTAAAAATATAGCCATAAAACATTACAGATGTGATGACTATTTTTGATGC
 TGCGCTTCAAAATTTATTATCAGACTTAGGACTAACCATAAAAGATATCA
 AAGGTTTCGTTTGGAAATGAGCGGAAGAAGGCAGTTAGTTTCAAGATTATGAT
 TTCTTAGCGAATCTGTCTGAGTATTATAATATGCCAAACCTTGCTTCTGG
 TCAGTTTGGATTTCATCTAATGGTGTGGTGAAGAACTGGACTATACTG
 TTAATGAAAGTATAGAAAAGGGCTATTATTTAGTCCTATCTTATTGATC
 TTTGGTGGTATCTCTTTTGCTATTATTGAAAAAAGG

SEQ ID NO. 7509

STRAIN CJB110

ATGTTAGTGGAAATAGGAATTATTTCTTCTTTGGGAAAGAATTATAGC
 GAGCATAAACAGCATCTCTTCGACTTAAAAGAAGGAATTTCTAAACATTT
 ATATAAAATCAGCACTCTATTTTAGAATCTTATACAGGAAGCATAACTA
 GTGACCCAGAGGTTCTGAGCAATACAAAGATGAGACACGTAATTTTAAA
 TTTGCTTTTACCGCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTTAATTT
 AAAAGCTTATCATAATATTGCTGTGTGTTTAGGGACCTCACTTGGGGGAA
 AGAGTGCTGGTCAAATGCCTTGTATCAATTTGAAGAAGGAGAGCGTCAA
 GTAGATGCTAGTTTATTAGAAAAAGCATCTGTTTACCATATTGCTGATGA
 ATTGATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTTCAACCG
 CCTGTTCTGCAAGTAATAATGCCGTAATATTAGGAACACAATTACTTCAA
 GATGGCGATTGTGATTTAGCTATTTGTGGTGGCTGTGATGAGTTAAGTGA
 TATTTCTTTAGCAGGCTTCACATCACTAGGAGCTATTAATACAGAAATGG
 CATGTCAGCCCTATTCTTCTGGAAAAGGAATCAATTTGGGTGAGGGCGCT
 GGTTTTGTGTTCTTGTCAAAGATCAGTCCTTAGCTAAATATGGAAAAAT
 TATCGGTGGTCTTATTACTTCAGATGGTTATCATATAACAGCACCTAAGC
 CAACAGGTGAAGGGGCGGCACAGATTGCAAAGCAGCTAGTGACTCAAGCA
 GGTATTGACTACAGTGAGATTGACTATATTAATGGTCACGGTACAGGTAC
 TCAAGCTAATGATAAAATGGAAAAAAATATGTATGGTAAGTTTTTCCCGA
 CAACGACATTGATCAGCAGTACCAAGGGGCAAACGGGTCTACTCTAGGG
 GCTGCAGGTATTATCGAATTGATTAATTGTTTAGCGGCAATAGAGGAACA
 GACTGTACCAGCAACTAAAAATGAGATTGGGATAGAAGGTTTTCCAGAAA
 ATTTTGTCTATCATCAAAAGAGAGAATACCCAATAAGAAATGCTTTAAAT
 TTTTCGTTTGTCTTTTGGTGGAAATAATAGTGGTATCTTATTGTCATCTTT
 AGATTACCTCTAGAAACATTACCTGCTAGAGAAAATCTTAAATGGCTA
 TCTTATCATCTGTTGCTTCCATTTCTAAGAATGAATCACTTTCTATAACC
 TATGAAAAAGTTGCTAGTAATTTCAACGACTTTGAAGCATTACGCTTTAA
 AGGGGCTAGACCACCCAAAACCTGTCAACCCAGCACAAATTTAGGAAAATGG
 ATGATTTTCCAAAATGGTTGCCGTAACAACAGCTCAAGCACTAATAGAA
 AGCAATATTAAATCTAAAAAAACAAGATACTTCAAAAGTAGGAATTGTATT
 TACAACACTTTCTGGACCAGTTGAGGTTGTTGAAGGTATTGAAAAGCAAA
 TCACAACAGAAGGATATGCACATGTTTCTGCTTCACGATTCCCGTTTACA
 GTAATGAATGCAGCAGCTGGTATGCTTTCTATCATTTTTTAAATAACAGG
 TCCTTTATCTGTCTTTTCGACAAATAGTGGAGCGCTTGATGGTATACAAT
 ATGCCAAGGAAATGATGCGTAACGATAATCTAGACTATGTGATTCTTGTT
 TCTGCTAATCAGTGGACAGACATGAGTTTATGTGGTGGCAACAATTAAA
 CTATGATAGTCAAATGTTTGTGCGTTCTGATTATTGTTTCAACAGTCC
 TCTCTCGTCAAGCATTGGATAATTCTCCTATAATATTAGGTAGTAAACAA
 TTAAAAATATAGCCATAAAACATTACAGATGTGATGACTATTTTTGATGC
 TGCGCTTCAAAATTTATTATCAGACTTAGGACTAACCATAAAAGATATCA
 AAGGTTTTCGTTTGGAAATGAGCGGAAGAAGGCAGTTAGTTTCAAGATTATGAT
 TTCTTAGCGAATCTGTCTGAGTATTATAATATGCCAAACCTTGCTTCTGG
 TCAGTTTGGATTTCATCTAATGGTGTGGTGAAGAACTGGACTATACTG
 TTAATGAAAGTATAGAAAAGGGCTATTATTTAGTCCTATCTTATTGATC
 TTTGGTGGTATCTCTTTTGCTATTATTGAAAAAAGG

Table 75: Comparative Sequences relating to SAG0671

SEQ ID NO. 7510

STRAIN 1169NT

ATGTTAGTGGGAATAGGAATTATTTCTTCTTTGGGAAAGAATTATAG
 CGAGCATAAACAGCATCTCTTCGACTTAAAAGAAGGAATTTCTAAACATT
 TATATAAAAATCAGCACTCTATTTTAGAATCTTATACAGGAAGCATAACT
 AGTGACCCAGAGGTTCTTGAGCAATACAAAGATGAGACACGTAATTTTAA
 ATTTGCTTTTACCGCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTTAATT
 TAAAAGCTTATCATAATATTGCTGTGTGTTTAGGGACCTCAGTTGGGGGA
 AAGAGTGCCTGGTCAAAATGCCTTGTATCAATTTGAAGAAGGAGAGCGTCA
 AGTAGATGCTAGTTTATTAGAAAAAGCATCTGTTTACCATATTGCTGATG
 AATTGATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTTCAACC
 GCCTGTTCTGCAAGTAATAATGCCGTAATATTAGGAACACAATTACTTCA
 AGATGGCGATTGTGATTTAGCTATTTGTGGTGGCTGTGATGAGTTAAGTG
 ATATTTCTTTAGCAGGCTTCACATCACTAGGAGCTATTAATACAGAAATG
 GCATGTCAGCCCTATTCTTCTGGAAAAGGAATCAATTTGGGTGAGGGCGC
 TGGTTTGTGTTCTTGTCAAAGATCAGTCCTTAGCTAAATATGGAAAAA
 TTATCGGTGGTCTTATTACTTCAGATGGTTATCATATAACAGCACCTAAG
 CCAACAGGTGAAGGGCGGCACAGATTGCAAAGCAGCTAGTGACTCAAGC
 AGGTATTGACTACAGTGAGATTGACTATATTAACGGTCACGGTACAGGTA
 CTCAGCTAATGATAAAAATGGAAAAAATATGTATGGTAAGTTTTTCCCG
 ACAACGACATTGATCAGCAGTACCAAGGGGCAAACGGGTCTACTCTAGG
 GGCTGCAGGTATTATCGAATTGATTAATTGTTTAGCGGCAATAGAGGAAC
 AGACTGTACCAGCAACTAAAAATGAGATTGGGATAGAAGTTTTTCAGAA
 AATTTTGTCTATCATCAAAGAGAGAATACCAATAAGAAATGCTTTAAA
 TTTTTCGTTTGTCTTTTGGTGGAAATAATAGTGGTATCTTATTGTCTCTT
 TAGATTACCTCTAGAAACATTACCTGCTAGAGAAAATCTTAAATGGCT
 ATCTTATCATCTGTTGCTTCCATTTCTAAGAATGAATCACTTTCTATAAC
 CTATGAAAAAGTTGCTAGTAATTTCAACGACTTTGAAGCATTACGCTTTA
 AAGGGGCTAGACCACCCAAACTGTCAACCCAGCACAATTTAGGAAAATG
 GATGATTTTTCCAAAATGGTTGCCGTAACAACAGCTCAAGCACTAATAGA
 AAGCAATATAATCTAAAAAACAAGATACTTCAAAGTAGGAATTGTAT
 TTACAACACTTTCTGGACCAGTTGAGGTTGTTGAAGGTATTGAAAAGCAA
 ATCACAACAGAAGGATATGCACATGTTTCTGCTTCACGATTCCCGTTTAC
 AGTAATGAATGCAGCAGCTGGTATGCTTTCTATCATTTTTAAAATAACAG
 GTCCCTTATCTGTCAATTCGACAAATAGTGGAGCGCTTGATGGTATACAA
 TATGCCAAGGAAATGATGCGTAACGATAATCTAGACTATGTGATCTTGT
 TTCTGCTAATCAGTGGACAGACATGAGTTTTATGTGGTGGCAACAATTAA
 ACTATGATAGTCAAATGTTTGTGCGTTCTGATTATTGTTCAACACAAGTC
 CTCTCTCGTCAAGCATTGGATAATTCTCCTATAATATTAGGTAGTAAACA
 ATTAATAATATAGCCATAAAACATTACAGATGTGATGACTATTTTGTATG
 CTGCGCTTCAAAATTTATTATCAGACTTAGGACTAACCATAAAAGATATC
 AAAGGTTTCTGTTTGGAAATGAGCGGAAGAAGGCAGTTAGTTCAAGATTATGA
 TTTCTTAGCGAAGCTTGTCTGAGTATTATAATATGCCAAACCTTGCTTCTG
 GTCAGTTTGGATTTTCTATCAATGGTGTGCTGGTGAAGAACTGGACTATACT
 GTTAATGAAAGTATAGAAAAGGGCTATTATTTAGTCTATCTTATTCGAT
 CTTTGGTGGTATCTCTTTTGCTATTATTGAAAAAAGG

SEQ ID NO. 7511

STRAIN JM9130013

ATGTTAGTGGGAATAGGAATTATTTCTTCTTTGGGAAAGAATTATAGCGAG
 CATAAACAGCATCTCTTCGACTTAAAAGAAGGAATTTCTAAACATTTATA
 TAAAAATCAGCACTCTATTTTAGAATCTTATACAGGAAGCATAACTAGTG
 ACCCAGAGGTTCTTGAGCAATACAAAGATGAGACACGTAATTTTAAATTT
 GCTTTTACCGCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTTAATTTAAA
 AGCTTATCATAATATTGCTGTGTGTTTAGGGACCTCAGTTGGGGGAAAGA
 GTGCTGGTCAAAATGCCTTGTATCAATTTGAAGAAGGAGAGCGTCAAGTA
 GATGCTAGTTTATTAGAAAAAGCATCTGTTTACCATATTGCTGATGAATT
 GATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTTCAACCGCCT
 GTTCTGCAAGTAATAATGCCGTAATATTAGGAACACAATTACTTCAAGAT
 GCGGATTGTGATTAGCTATTTGTGGTGGCTGTGATGAGTTAAGTGATAT
 TTCTTTAGCAGGCTTCACATCACTAGGAGCTATTAATACAGAAATGGCAT
 GTCAGCCCTATTCTTCTGGAAAAGGAATCAATTTGGGTGAGGGCGCTGGT
 TTTGTTGTTCTTGTCAAAGATCAGTCCTTAGCTAAATATGGAAAAATAT
 CGGTGGTCTTATTACTTCAGATGGTTATCATATAACAGCACCTAAGCCAA
 CAGGTGAAGGGGCGGCACAGATTGCAAAGCAGCTAGTGACTCAAGCAGGT
 ATTGACTACAGTGAGATTGACTATATTAACGGTCACGGTACAGGTACTCA
 AGCTAATGATAAAATGGAAAAAATATGTATGGTAAGTTTTTCCCGACAA
 CGACATTGATCAGCAGTACCAAGGGGCAAACGGGTCTACTCTAGGGGCT
 GCAGGTATTATCGAATTGATTAATTGTTTAGCGGCAATAGAGGAACAGAC
 TGTACCAGCAACTAAAAATGAGATTGGGATAGAAGGTTTTCCAGAAAAAT
 TTGTCTATCATCAAAGAGAGAATACCCAATAAGAAATGCTTTAAATTTT
 TCGTTTGTCTTTGGTGGAAATAATAGTGGTGTCTTATTGTCTCTTTAGA
 TTCACCTCTAGAAACATTACCTGCTAGAGAAAATCTTAAATGGCTATCT
 TATCATCTGTTGCTTCCATTTCTAAGAATGAATCACTTTCTATAACCTAT
 GAAAAAGTTGCTAGTAATTTCAACGACTTTGAAGCATTACGCTTTAAAGG
 GGCTAGACCACCCAAACTGTCAACCCAGCACAATTTAGGAAAATGGATG
 ATTTTCCAAAATGGTTGCCGTAACAACAGCTCAAGCACTAATAGAAAGC
 AATATTAATCTAAAAAACAAGATACTTCAAAGTAGGAATTGTATTTAC
 AACACTTTCTGGACCAGTTGAGGTTGTTGAAGGTATTGAAAAGCAAATCA
 CAACAGAAGGATATGCACATGTTTCTGCTTCACGATTCCCGTTTACAGTA
 ATGAATGCAGCAGCTGGTATGCTTTCTATCATTTTTTAAATAACAGGTCC
 TTTATCTGTCAATTCGACAAATAGTGGAGCGCTTGATGGTATACAATATG

Table 75: Comparative Sequences relating to SAG0671

CCAAGGAAATGATGCGTAACGATAATCTAGACTATGTGATTCTTGTCTTCT
 GCTAATCAGTGGACAGACATGAGTTTTATGTGGTGGCAACAATTAACCTA
 TGATAGTCAAATGTTTGTGCGTTCTGATTATTGTTTCAGCACAAAGTCCTCT
 CTCGTCAAGCATGGATAATTTCTCCTATAATATTAGGTAGTAAACAATTA
 AAATATAGCCATAAAACATTACAGATGTGATGACTATTTTGTGCTGCTGC
 GCTTCAAATTTATTATCAGACTTAGGACTAACCATAAAAGATATCAAAG
 GTTTCGTTTGGAAATGAGCGGAAGAAGGCAGTTAGTTTCAGATTATGATTTT
 TTAGCGAACTTGTCTGAGTATTATAATATGCCAAACCTTGTCTCTGGTCA
 GTTTGGATTTTCATCTAATGGTGTGCTGGTGAAGAAGTGGACTATACTGTTA
 ATGAAAGTATAGAAAAGGGCTATTATTTAGTCCTATCTTATTCTGATCTTC
 GGTGGTATCTCTTTGCTATTATTGAAAAAAGG

PRETTY of: /biotmp/msa118688.2{*} April 9, 2003 02:55 ..

	1				50
msa118688.2{361_18RS21}	-----	ATGTTAGTGG	AATAGGAATT	ATTTCTTCTT	TGGGAAAGAA
msa118688.2{361_A909}	-----	ATGTTAGTGG	AATAGGAATT	ATTTCTTCTT	TGGGAAAGAA
msa118688.2{361_COH1}	-----	ATGTTAGTGG	AATAGGAATT	ATTTCTTCTT	TGGGAAAGAA
msa118688.2{361_H36B}	-----	ATGTTAGTGG	AATAGGAATT	ATTTCTTCTT	TGGGAAAGAA
msa118688.2{361_JM9130013}	-----	ATGTTAGTGG	AATAGGAATT	ATTTCTTCTT	TGGGAAAGAA
msa118688.2{361_M732}	-----	ATGTTAGTGG	AATAGGAATT	ATTTCTTCTT	TGGGAAAGAA
msa118688.2{GBS361_2603}	atgagcgtat	ATGTTAGTGG	AATAGGAATT	ATTTCTTCTT	TGGGAAAGAA
msa118688.2{361_090}	-----	ATGTTAGTGG	AATAGGAATT	ATTTCTTCTT	TGGGAAAGAA
msa118688.2{361_1169NT}	-----	ATGTTAGTGG	AATAGGAATT	ATTTCTTCTT	TGGGAAAGAA
msa118688.2{361_CJB110}	-----	ATGTTAGTGG	AATAGGAATT	ATTTCTTCTT	TGGGAAAGAA
msa118688.2{361_M781}	-----	ATGTTAGTGG	AATAGGAATT	ATTTCTTCTT	TGGGAAAGAA
Consensus	*****	*****	*****	*****	*****
	51				100
msa118688.2{361_18RS21}	TTATAGCGAG	CATAAACAGC	ATCTCTTCGA	CTTAAAAGAA	GGAATTTCTA
msa118688.2{361_A909}	TTATAGCGAG	CATAAACAGC	ATCTCTTCGA	CTTAAAAGAA	GGAATTTCTA
msa118688.2{361_COH1}	TTATAGCGAG	CATAAACAGC	ATCTCTTCGA	CTTAAAAGAA	GGAATTTCTA
msa118688.2{361_H36B}	TTATAGCGAG	CATAAACAGC	ATCTCTTCGA	CTTAAAAGAA	GGAATTTCTA
msa118688.2{361_JM9130013}	TTATAGCGAG	CATAAACAGC	ATCTCTTCGA	CTTAAAAGAA	GGAATTTCTA
msa118688.2{361_M732}	TTATAGCGAG	CATAAACAGC	ATCTCTTCGA	CTTAAAAGAA	GGAATTTCTA
msa118688.2{GBS361_2603}	TTATAGCGAG	CATAAACAGC	ATCTCTTCGA	CTTAAAAGAA	GGAATTTCTA
msa118688.2{361_090}	TTATAGCGAG	CATAAACAGC	ATCTCTTCGA	CTTAAAAGAA	GGAATTTCTA
msa118688.2{361_1169NT}	TTATAGCGAG	CATAAACAGC	ATCTCTTCGA	CTTAAAAGAA	GGAATTTCTA
msa118688.2{361_CJB110}	TTATAGCGAG	CATAAACAGC	ATCTCTTCGA	CTTAAAAGAA	GGAATTTCTA
msa118688.2{361_M781}	TTATAGCGAG	CATAAACAGC	ATCTCTTCGA	CTTAAAAGAA	GGAATTTCTA
Consensus	*****	*****	*****	*****	*****
	101				150
msa118688.2{361_18RS21}	AACATTTATA	TAAAAATCAC	GACTCTATTT	TAGAATCTTA	TACAGGAAGC
msa118688.2{361_A909}	AACATTTATA	TAAAAATCAC	GACTCTATTT	TAGAATCTTA	TACAGGAAGC
msa118688.2{361_COH1}	AACATTTATA	TAAAAATCAC	GACTCTATTT	TAGAATCTTA	TACAGGAAGC
msa118688.2{361_H36B}	AACATTTATA	TAAAAATCAC	GACTCTATTT	TAGAATCTTA	TACAGGAAGC
msa118688.2{361_JM9130013}	AACATTTATA	TAAAAATCAC	GACTCTATTT	TAGAATCTTA	TACAGGAAGC
msa118688.2{361_M732}	AACATTTATA	TAAAAATCAC	GACTCTATTT	TAGAATCTTA	TACAGGAAGC
msa118688.2{GBS361_2603}	AACATTTATA	TAAAAATCAC	GACTCTATTT	TAGAATCTTA	TACAGGAAGC
msa118688.2{361_090}	AACATTTATA	TAAAAATCAC	GACTCTATTT	TAGAATCTTA	TACAGGAAGC
msa118688.2{361_1169NT}	AACATTTATA	TAAAAATCAC	GACTCTATTT	TAGAATCTTA	TACAGGAAGC
msa118688.2{361_CJB110}	AACATTTATA	TAAAAATCAC	GACTCTATTT	TAGAATCTTA	TACAGGAAGC
msa118688.2{361_M781}	AACATTTATA	TAAAAATCAC	GACTCTATTT	TAGAATCTTA	TACAGGAAGC
Consensus	*****	*****	*****	*****	*****
	151				200
msa118688.2{361_18RS21}	ATAACTAGTG	ACCCAGAGGT	TCCTGAGCAA	TACAAAGATG	AGACACGTAA
msa118688.2{361_A909}	ATAACTAGTG	ACCCAGAGGT	TCCTGAGCAA	TACAAAGATG	AGACACGTAA
msa118688.2{361_COH1}	ATAACTAGTG	ACCCAGAGGT	TCCTGAGCAA	TACAAAGATG	AGACACGTAA
msa118688.2{361_H36B}	ATAACTAGTG	ACCCAGAGGT	TCCTGAGCAA	TACAAAGATG	AGACACGTAA
msa118688.2{361_JM9130013}	ATAACTAGTG	ACCCAGAGGT	TCCTGAGCAA	TACAAAGATG	AGACACGTAA
msa118688.2{361_M732}	ATAACTAGTG	ACCCAGAGGT	TCCTGAGCAA	TACAAAGATG	AGACACGTAA
msa118688.2{GBS361_2603}	ATAACTAGTG	ACCCAGAGGT	TCCTGAGCAA	TACAAAGATG	AGACACGTAA
msa118688.2{361_090}	ATAACTAGTG	ACCCAGAGGT	TCCTGAGCAA	TACAAAGATG	AGACACGTAA
msa118688.2{361_1169NT}	ATAACTAGTG	ACCCAGAGGT	TCCTGAGCAA	TACAAAGATG	AGACACGTAA
msa118688.2{361_CJB110}	ATAACTAGTG	ACCCAGAGGT	TCCTGAGCAA	TACAAAGATG	AGACACGTAA
msa118688.2{361_M781}	ATAACTAGTG	ACCCAGAGGT	TCCTGAGCAA	TACAAAGATG	AGACACGTAA
Consensus	*****	*****	*****	*****	*****
	201				250
msa118688.2{361_18RS21}	TTTTAAATTT	GCTTTTACCG	CTTTTGAAGA	GGCTCTTGCT	TCTTCAGGTG
msa118688.2{361_A909}	TTTTAAATTT	GCTTTTACCG	CTTTTGAAGA	GGCTCTTGCT	TCTTCAGGTG
msa118688.2{361_COH1}	TTTTAAATTT	GCTTTTACCG	CTTTTGAAGA	GGCTCTTGCT	TCTTCAGGTG
msa118688.2{361_H36B}	TTTTAAATTT	GCTTTTACCG	CTTTTGAAGA	GGCTCTTGCT	TCTTCAGGTG
msa118688.2{361_JM9130013}	TTTTAAATTT	GCTTTTACCG	CTTTTGAAGA	GGCTCTTGCT	TCTTCAGGTG
msa118688.2{361_M732}	TTTTAAATTT	GCTTTTACCG	CTTTTGAAGA	GGCTCTTGCT	TCTTCAGGTG
msa118688.2{GBS361_2603}	TTTTAAATTT	GCTTTTACCG	CTTTTGAAGA	GGCTCTTGCT	TCTTCAGGTG
msa118688.2{361_090}	TTTTAAATTT	GCTTTTACCG	CTTTTGAAGA	GGCTCTTGCT	TCTTCAGGTG
msa118688.2{361_1169NT}	TTTTAAATTT	GCTTTTACCG	CTTTTGAAGA	GGCTCTTGCT	TCTTCAGGTG
msa118688.2{361_CJB110}	TTTTAAATTT	GCTTTTACCG	CTTTTGAAGA	GGCTCTTGCT	TCTTCAGGTG
msa118688.2{361_M781}	TTTTAAATTT	GCTTTTACCG	CTTTTGAAGA	GGCTCTTGCT	TCTTCAGGTG
Consensus	*****	*****	*****	*****	*****

Table 75: Comparative Sequences relating to SAG0671

	251				300
msa118688.2{361_18RS21}	TTAATTTTAAA	AGCTTATCAT	AATATTGCTG	TGTGTTTAGG	GACCTCACTT
msa118688.2{361_A909}	TTAATTTTAAA	AGCTTATCAT	AATATTGCTG	TGTGTTTAGG	GACCTCACTT
msa118688.2{361_COH1}	TTAATTTTAAA	AGCTTATCAT	AATATTGCTG	TGTGTTTAGG	GACCTCACTT
msa118688.2{361_H36B}	TTAATTTTAAA	AGCTTATCAT	AATATTGCTG	TGTGTTTAGG	GACCTCACTT
msa118688.2{361_JM9130013}	TTAATTTTAAA	AGCTTATCAT	AATATTGCTG	TGTGTTTAGG	GACCTCACTT
msa118688.2{361_M732}	TTAATTTTAAA	AGCTTATCAT	AATATTGCTG	TGTGTTTAGG	GACCTCACTT
msa118688.2{GBS361_2603}	TTAATTTTAAA	AGCTTATCAT	AATATTGCTG	TGTGTTTAGG	GACCTCACTT
msa118688.2{361_090}	TTAATTTTAAA	AGCTTATCAT	AATATTGCTG	TGTGTTTAGG	GACCTCACTT
msa118688.2{361_1169NT}	TTAATTTTAAA	AGCTTATCAT	AATATTGCTG	TGTGTTTAGG	GACCTCACTT
msa118688.2{361_CJB110}	TTAATTTTAAA	AGCTTATCAT	AATATTGCTG	TGTGTTTAGG	GACCTCACTT
msa118688.2{361_M781}	TTAATTTTAAA	AGCTTATCAT	AATATTGCTG	TGTGTTTAGG	GACCTCACTT
Consensus	*****	*****	*****	*****	*****
	301				350
msa118688.2{361_18RS21}	GGGGGAAAGA	GTGCTGGTCA	AAATGCCTTG	TATCAATTTC	AAGAAGGAGA
msa118688.2{361_A909}	GGGGGAAAGA	GTGCTGGTCA	AAATGCCTTG	TATCAATTTC	AAGAAGGAGA
msa118688.2{361_COH1}	GGGGGAAAGA	GTGCTGGTCA	AAATGCCTTG	TATCAATTTC	AAGAAGGAGA
msa118688.2{361_H36B}	GGGGGAAAGA	GTGCTGGTCA	AAATGCCTTG	TATCAATTTC	AAGAAGGAGA
msa118688.2{361_JM9130013}	GGGGGAAAGA	GTGCTGGTCA	AAATGCCTTG	TATCAATTTC	AAGAAGGAGA
msa118688.2{361_M732}	GGGGGAAAGA	GTGCTGGTCA	AAATGCCTTG	TATCAATTTC	AAGAAGGAGA
msa118688.2{GBS361_2603}	GGGGGAAAGA	GTGCTGGTCA	AAATGCCTTG	TATCAATTTC	AAGAAGGAGA
msa118688.2{361_090}	GGGGGAAAGA	GTGCTGGTCA	AAATGCCTTG	TATCAATTTC	AAGAAGGAGA
msa118688.2{361_1169NT}	GGGGGAAAGA	GTGCTGGTCA	AAATGCCTTG	TATCAATTTC	AAGAAGGAGA
msa118688.2{361_CJB110}	GGGGGAAAGA	GTGCTGGTCA	AAATGCCTTG	TATCAATTTC	AAGAAGGAGA
msa118688.2{361_M781}	GGGGGAAAGA	GTGCTGGTCA	AAATGCCTTG	TATCAATTTC	AAGAAGGAGA
Consensus	*****	*****	*****	*****	*****
	351				400
msa118688.2{361_18RS21}	GCGTCAAGTA	GATGCTAGTT	TATTAGAAAA	AGCATCTGTT	TACCATATTG
msa118688.2{361_A909}	GCGTCAAGTA	GATGCTAGTT	TATTAGAAAA	AGCATCTGTT	TACCATATTG
msa118688.2{361_COH1}	GCGTCAAGTA	GATGCTAGTT	TATTAGAAAA	AGCATCTGTT	TACCATATTG
msa118688.2{361_H36B}	GCGTCAAGTA	GATGCTAGTT	TATTAGAAAA	AGCATCTGTT	TACCATATTG
msa118688.2{361_JM9130013}	GCGTCAAGTA	GATGCTAGTT	TATTAGAAAA	AGCATCTGTT	TACCATATTG
msa118688.2{361_M732}	GCGTCAAGTA	GATGCTAGTT	TATTAGAAAA	AGCATCTGTT	TACCATATTG
msa118688.2{GBS361_2603}	GCGTCAAGTA	GATGCTAGTT	TATTAGAAAA	AGCATCTGTT	TACCATATTG
msa118688.2{361_090}	GCGTCAAGTA	GATGCTAGTT	TATTAGAAAA	AGCATCTGTT	TACCATATTG
msa118688.2{361_1169NT}	GCGTCAAGTA	GATGCTAGTT	TATTAGAAAA	AGCATCTGTT	TACCATATTG
msa118688.2{361_CJB110}	GCGTCAAGTA	GATGCTAGTT	TATTAGAAAA	AGCATCTGTT	TACCATATTG
msa118688.2{361_M781}	GCGTCAAGTA	GATGCTAGTT	TATTAGAAAA	AGCATCTGTT	TACCATATTG
Consensus	*****	*****	*****	*****	*****
	401				450
msa118688.2{361_18RS21}	CTGATGAATT	GATGGCTTAT	CATGATATTG	TGGGAGCTTC	GTATGTTATT
msa118688.2{361_A909}	CTGATGAATT	GATGGCTTAT	CATGATATTG	TGGGAGCTTC	GTATGTTATT
msa118688.2{361_COH1}	CTGATGAATT	GATGGCTTAT	CATGATATTG	TGGGAGCTTC	GTATGTTATT
msa118688.2{361_H36B}	CTGATGAATT	GATGGCTTAT	CATGATATTG	TGGGAGCTTC	GTATGTTATT
msa118688.2{361_JM9130013}	CTGATGAATT	GATGGCTTAT	CATGATATTG	TGGGAGCTTC	GTATGTTATT
msa118688.2{361_M732}	CTGATGAATT	GATGGCTTAT	CATGATATTG	TGGGAGCTTC	GTATGTTATT
msa118688.2{GBS361_2603}	CTGATGAATT	GATGGCTTAT	CATGATATTG	TGGGAGCTTC	GTATGTTATT
msa118688.2{361_090}	CTGATGAATT	GATGGCTTAT	CATGATATTG	TGGGAGCTTC	GTATGTTATT
msa118688.2{361_1169NT}	CTGATGAATT	GATGGCTTAT	CATGATATTG	TGGGAGCTTC	GTATGTTATT
msa118688.2{361_CJB110}	CTGATGAATT	GATGGCTTAT	CATGATATTG	TGGGAGCTTC	GTATGTTATT
msa118688.2{361_M781}	CTGATGAATT	GATGGCTTAT	CATGATATTG	TGGGAGCTTC	GTATGTTATT
Consensus	*****	*****	*****	*****	*****
	451				500
msa118688.2{361_18RS21}	TCAACCGCCT	GTTCTGCAAG	TAATAATGCC	GTAATATTAG	GAACACAATT
msa118688.2{361_A909}	TCAACCGCCT	GTTCTGCAAG	TAATAATGCC	GTAATATTAG	GAACACAATT
msa118688.2{361_COH1}	TCAACCGCCT	GTTCTGCAAG	TAATAATGCC	GTAATATTAG	GAACACAATT
msa118688.2{361_H36B}	TCAACCGCCT	GTTCTGCAAG	TAATAATGCC	GTAATATTAG	GAACACAATT
msa118688.2{361_JM9130013}	TCAACCGCCT	GTTCTGCAAG	TAATAATGCC	GTAATATTAG	GAACACAATT
msa118688.2{361_M732}	TCAACCGCCT	GTTCTGCAAG	TAATAATGCC	GTAATATTAG	GAACACAATT
msa118688.2{GBS361_2603}	TCAACCGCCT	GTTCTGCAAG	TAATAATGCC	GTAATATTAG	GAACACAATT
msa118688.2{361_090}	TCAACCGCCT	GTTCTGCAAG	TAATAATGCC	GTAATATTAG	GAACACAATT
msa118688.2{361_1169NT}	TCAACCGCCT	GTTCTGCAAG	TAATAATGCC	GTAATATTAG	GAACACAATT
msa118688.2{361_CJB110}	TCAACCGCCT	GTTCTGCAAG	TAATAATGCC	GTAATATTAG	GAACACAATT
msa118688.2{361_M781}	TCAACCGCCT	GTTCTGCAAG	TAATAATGCC	GTAATATTAG	GAACACAATT
Consensus	*****	*****	*****	*****	*****
	501				550
msa118688.2{361_18RS21}	ACTTCAAGAT	GGCGATTGTG	ATTTAGCTAT	TTGTGGTGGC	TGTGATGAGT
msa118688.2{361_A909}	ACTTCAAGAT	GGCGATTGTG	ATTTAGCTAT	TTGTGGTGGC	TGTGATGAGT
msa118688.2{361_COH1}	ACTTCAAGAT	GGCGATTGTG	ATTTAGCTAT	TTGTGGTGGC	TGTGATGAGT
msa118688.2{361_H36B}	ACTTCAAGAT	GGCGATTGTG	ATTTAGCTAT	TTGTGGTGGC	TGTGATGAGT
msa118688.2{361_JM9130013}	ACTTCAAGAT	GGCGATTGTG	ATTTAGCTAT	TTGTGGTGGC	TGTGATGAGT
msa118688.2{361_M732}	ACTTCAAGAT	GGCGATTGTG	ATTTAGCTAT	TTGTGGTGGC	TGTGATGAGT
msa118688.2{GBS361_2603}	ACTTCAAGAT	GGCGATTGTG	ATTTAGCTAT	TTGTGGTGGC	TGTGATGAGT
msa118688.2{361_090}	ACTTCAAGAT	GGCGATTGTG	ATTTAGCTAT	TTGTGGTGGC	TGTGATGAGT
msa118688.2{361_1169NT}	ACTTCAAGAT	GGCGATTGTG	ATTTAGCTAT	TTGTGGTGGC	TGTGATGAGT
msa118688.2{361_CJB110}	ACTTCAAGAT	GGCGATTGTG	ATTTAGCTAT	TTGTGGTGGC	TGTGATGAGT
msa118688.2{361_M781}	ACTTCAAGAT	GGCGATTGTG	ATTTAGCTAT	TTGTGGTGGC	TGTGATGAGT

Table 75: Comparative Sequences relating to SAG0671

Consensus	*****	*****	*****	*****	*****
	551				600
msa118688.2{361_18RS21}	TAAGTGATAT	TTCTTTAGCA	GGCTTCACAT	CACTAGGAGC	TATTAATACA
msa118688.2{361_A909}	TAAGTGATAT	TTCTTTAGCA	GGCTTCACAT	CACTAGGAGC	TATTAATACA
msa118688.2{361_COH1}	TAAGTGATAT	TTCTTTAGCA	GGCTTCACAT	CACTAGGAGC	TATTAATACA
msa118688.2{361_H36B}	TAAGTGATAT	TTCTTTAGCA	GGCTTCACAT	CACTAGGAGC	TATTAATACA
msa118688.2{361_JM9130013}	TAAGTGATAT	TTCTTTAGCA	GGCTTCACAT	CACTAGGAGC	TATTAATACA
msa118688.2{361_M732}	TAAGTGATAT	TTCTTTAGCA	GGCTTCACAT	CACTAGGAGC	TATTAATACA
msa118688.2{GBS361_2603}	TAAGTGATAT	TTCTTTAGCA	GGCTTCACAT	CACTAGGAGC	TATTAATACA
msa118688.2{361_090}	TAAGTGATAT	TTCTTTAGCA	GGCTTCACAT	CACTAGGAGC	TATTAATACA
msa118688.2{361_1169NT}	TAAGTGATAT	TTCTTTAGCA	GGCTTCACAT	CACTAGGAGC	TATTAATACA
msa118688.2{361_CJB110}	TAAGTGATAT	TTCTTTAGCA	GGCTTCACAT	CACTAGGAGC	TATTAATACA
msa118688.2{361_M781}	TAAGTGATAT	TTCTTTAGCA	GGCTTCACAT	CACTAGGAGC	TATTAATACA
Consensus	*****	*****	*****	*****	*****
	601				650
msa118688.2{361_18RS21}	GAAATGGCAT	GTCAGCCCTA	TTCTTCTGGA	AAAGGAATCA	ATTTGGGTGA
msa118688.2{361_A909}	GAAATGGCAT	GTCAGCCCTA	TTCTTCTGGA	AAAGGAATCA	ATTTGGGTGA
msa118688.2{361_COH1}	GAAATGGCAT	GTCAGCCCTA	TTCTTCTGGA	AAAGGAATCA	ATTTGGGTGA
msa118688.2{361_H36B}	GAAATGGCAT	GTCAGCCCTA	TTCTTCTGGA	AAAGGAATCA	ATTTGGGTGA
msa118688.2{361_JM9130013}	GAAATGGCAT	GTCAGCCCTA	TTCTTCTGGA	AAAGGAATCA	ATTTGGGTGA
msa118688.2{361_M732}	GAAATGGCAT	GTCAGCCCTA	TTCTTCTGGA	AAAGGAATCA	ATTTGGGTGA
msa118688.2{GBS361_2603}	GAAATGGCAT	GTCAGCCCTA	TTCTTCTGGA	AAAGGAATCA	ATTTGGGTGA
msa118688.2{361_090}	GAAATGGCAT	GTCAGCCCTA	TTCTTCTGGA	AAAGGAATCA	ATTTGGGTGA
msa118688.2{361_1169NT}	GAAATGGCAT	GTCAGCCCTA	TTCTTCTGGA	AAAGGAATCA	ATTTGGGTGA
msa118688.2{361_CJB110}	GAAATGGCAT	GTCAGCCCTA	TTCTTCTGGA	AAAGGAATCA	ATTTGGGTGA
msa118688.2{361_M781}	GAAATGGCAT	GTCAGCCCTA	TTCTTCTGGA	AAAGGAATCA	ATTTGGGTGA
Consensus	*****	*****	*****	*****	*****
	651				700
msa118688.2{361_18RS21}	GGGCGCTGGT	TTTGTGTGTC	TTGTCAAAGA	TCAGTCCTTA	GCTAAATATG
msa118688.2{361_A909}	GGGCGCTGGT	TTTGTGTGTC	TTGTCAAAGA	TCAGTCCTTA	GCTAAATATG
msa118688.2{361_COH1}	GGGCGCTGGT	TTTGTGTGTC	TTGTCAAAGA	TCAGTCCTTA	GCTAAATATG
msa118688.2{361_H36B}	GGGCGCTGGT	TTTGTGTGTC	TTGTCAAAGA	TCAGTCCTTA	GCTAAATATG
msa118688.2{361_JM9130013}	GGGCGCTGGT	TTTGTGTGTC	TTGTCAAAGA	TCAGTCCTTA	GCTAAATATG
msa118688.2{361_M732}	GGGCGCTGGT	TTTGTGTGTC	TTGTCAAAGA	TCAGTCCTTA	GCTAAATATG
msa118688.2{GBS361_2603}	GGGCGCTGGT	TTTGTGTGTC	TTGTCAAAGA	TCAGTCCTTA	GCTAAATATG
msa118688.2{361_090}	GGGCGCTGGT	TTTGTGTGTC	TTGTCAAAGA	TCAGTCCTTA	GCTAAATATG
msa118688.2{361_1169NT}	GGGCGCTGGT	TTTGTGTGTC	TTGTCAAAGA	TCAGTCCTTA	GCTAAATATG
msa118688.2{361_CJB110}	GGGCGCTGGT	TTTGTGTGTC	TTGTCAAAGA	TCAGTCCTTA	GCTAAATATG
msa118688.2{361_M781}	GGGCGCTGGT	TTTGTGTGTC	TTGTCAAAGA	TCAGTCCTTA	GCTAAATATG
Consensus	*****	*****	*****	*****	*****
	701				750
msa118688.2{361_18RS21}	GAAAAATTAT	CGGTGGTCTT	ATTACTTCAG	ATGGTTATCA	TATAACAGCA
msa118688.2{361_A909}	GAAAAATTAT	CGGTGGTCTT	ATTACTTCAG	ATGGTTATCA	TATAACAGCA
msa118688.2{361_COH1}	GAAAAATTAT	CGGTGGTCTT	ATTACTTCAG	ATGGTTATCA	TATAACAGCA
msa118688.2{361_H36B}	GAAAAATTAT	CGGTGGTCTT	ATTACTTCAG	ATGGTTATCA	TATAACAGCA
msa118688.2{361_JM9130013}	GAAAAATTAT	CGGTGGTCTT	ATTACTTCAG	ATGGTTATCA	TATAACAGCA
msa118688.2{361_M732}	GAAAAATTAT	CGGTGGTCTT	ATTACTTCAG	ATGGTTATCA	TATAACAGCA
msa118688.2{GBS361_2603}	GAAAAATTAT	CGGTGGTCTT	ATTACTTCAG	ATGGTTATCA	TATAACAGCA
msa118688.2{361_090}	GAAAAATTAT	CGGTGGTCTT	ATTACTTCAG	ATGGTTATCA	TATAACAGCA
msa118688.2{361_1169NT}	GAAAAATTAT	CGGTGGTCTT	ATTACTTCAG	ATGGTTATCA	TATAACAGCA
msa118688.2{361_CJB110}	GAAAAATTAT	CGGTGGTCTT	ATTACTTCAG	ATGGTTATCA	TATAACAGCA
msa118688.2{361_M781}	GAAAAATTAT	CGGTGGTCTT	ATTACTTCAG	ATGGTTATCA	TATAACAGCA
Consensus	*****	*****	*****	*****	*****
	751				800
msa118688.2{361_18RS21}	CCTAAGCCAA	CAGGTGAAGG	GGCGGCACAG	ATTGCAAAGC	AGCTAGTGAC
msa118688.2{361_A909}	CCTAAGCCAA	CAGGTGAAGG	GGCGGCACAG	ATTGCAAAGC	AGCTAGTGAC
msa118688.2{361_COH1}	CCTAAGCCAA	CAGGTGAAGG	GGCGGCACAG	ATTGCAAAGC	AGCTAGTGAC
msa118688.2{361_H36B}	CCTAAGCCAA	CAGGTGAAGG	GGCGGCACAG	ATTGCAAAGC	AGCTAGTGAC
msa118688.2{361_JM9130013}	CCTAAGCCAA	CAGGTGAAGG	GGCGGCACAG	ATTGCAAAGC	AGCTAGTGAC
msa118688.2{361_M732}	CCTAAGCCAA	CAGGTGAAGG	GGCGGCACAG	ATTGCAAAGC	AGCTAGTGAC
msa118688.2{GBS361_2603}	CCTAAGCCAA	CAGGTGAAGG	GGCGGCACAG	ATTGCAAAGC	AGCTAGTGAC
msa118688.2{361_090}	CCTAAGCCAA	CAGGTGAAGG	GGCGGCACAG	ATTGCAAAGC	AGCTAGTGAC
msa118688.2{361_1169NT}	CCTAAGCCAA	CAGGTGAAGG	GGCGGCACAG	ATTGCAAAGC	AGCTAGTGAC
msa118688.2{361_CJB110}	CCTAAGCCAA	CAGGTGAAGG	GGCGGCACAG	ATTGCAAAGC	AGCTAGTGAC
msa118688.2{361_M781}	CCTAAGCCAA	CAGGTGAAGG	GGCGGCACAG	ATTGCAAAGC	AGCTAGTGAC
Consensus	*****	*****	*****	*****	*****
	801				850
msa118688.2{361_18RS21}	TCAAGCAGGT	ATTGACTACA	GTGAGATTGA	CTATATTAAc	GGTCACGGTA
msa118688.2{361_A909}	TCAAGCAGGT	ATTGACTACA	GTGAGATTGA	CTATATTAAc	GGTCACGGTA
msa118688.2{361_COH1}	TCAAGCAGGT	ATTGACTACA	GTGAGATTGA	CTATATTAAc	GGTCACGGTA
msa118688.2{361_H36B}	TCAAGCAGGT	ATTGACTACA	GTGAGATTGA	CTATATTAAc	GGTCACGGTA
msa118688.2{361_JM9130013}	TCAAGCAGGT	ATTGACTACA	GTGAGATTGA	CTATATTAAc	GGTCACGGTA
msa118688.2{361_M732}	TCAAGCAGGT	ATTGACTACA	GTGAGATTGA	CTATATTAAc	GGTCACGGTA
msa118688.2{GBS361_2603}	TCAAGCAGGT	ATTGACTACA	GTGAGATTGA	CTATATTAAc	GGTCACGGTA
msa118688.2{361_090}	TCAAGCAGGT	ATTGACTACA	GTGAGATTGA	CTATATTAAc	GGTCACGGTA
msa118688.2{361_1169NT}	TCAAGCAGGT	ATTGACTACA	GTGAGATTGA	CTATATTAAc	GGTCACGGTA
msa118688.2{361_CJB110}	TCAAGCAGGT	ATTGACTACA	GTGAGATTGA	CTATATTAAc	GGTCACGGTA

Table 75: Comparative Sequences relating to SAG0671

msa118688.2{361_M781}	TCAAGCAGGT	ATTGACTACA	GTGAGATTGA	CTATATTAAT	GGTCACGGTA
Consensus	*****	*****	*****	*****	*****
msa118688.2{361_18RS21}	CAGGTACTCA	AGCTAATGAT	AAAATGGAAA	AAAATATGTA	TGGTAAGTTT
msa118688.2{361_A909}	CAGGTACTCA	AGCTAATGAT	AAAATGGAAA	AAAATATGTA	TGGTAAGTTT
msa118688.2{361_COH1}	CAGGTACTCA	AGCTAATGAT	AAAATGGAAA	AAAATATGTA	TGGTAAGTTT
msa118688.2{361_H36B}	CAGGTACTCA	AGCTAATGAT	AAAATGGAAA	AAAATATGTA	TGGTAAGTTT
msa118688.2{361_JM9130013}	CAGGTACTCA	AGCTAATGAT	AAAATGGAAA	AAAATATGTA	TGGTAAGTTT
msa118688.2{361_M732}	CAGGTACTCA	AGCTAATGAT	AAAATGGAAA	AAAATATGTA	TGGTAAGTTT
msa118688.2{GBS361_2603}	CAGGTACTCA	AGCTAATGAT	AAAATGGAAA	AAAATATGTA	TGGTAAGTTT
msa118688.2{361_090}	CAGGTACTCA	AGCTAATGAT	AAAATGGAAA	AAAATATGTA	TGGTAAGTTT
msa118688.2{361_1169NT}	CAGGTACTCA	AGCTAATGAT	AAAATGGAAA	AAAATATGTA	TGGTAAGTTT
msa118688.2{361_CJB110}	CAGGTACTCA	AGCTAATGAT	AAAATGGAAA	AAAATATGTA	TGGTAAGTTT
msa118688.2{361_M781}	CAGGTACTCA	AGCTAATGAT	AAAATGGAAA	AAAATATGTA	TGGTAAGTTT
Consensus	*****	*****	*****	*****	*****
msa118688.2{361_18RS21}	TTCCCGACAA	CGACATTGAT	CAGCAGTACC	AAGGGGCAAA	CGGGTCATAC
msa118688.2{361_A909}	TTCCCGACAA	CGACATTGAT	CAGCAGTACC	AAGGGGCAAA	CGGGTCATAC
msa118688.2{361_COH1}	TTCCCGACAA	CGACATTGAT	CAGCAGTACC	AAGGGGCAAA	CGGGTCATAC
msa118688.2{361_H36B}	TTCCCGACAA	CGACATTGAT	CAGCAGTACC	AAGGGGCAAA	CGGGTCATAC
msa118688.2{361_JM9130013}	TTCCCGACAA	CGACATTGAT	CAGCAGTACC	AAGGGGCAAA	CGGGTCATAC
msa118688.2{361_M732}	TTCCCGACAA	CGACATTGAT	CAGCAGTACC	AAGGGGCAAA	CGGGTCATAC
msa118688.2{GBS361_2603}	TTCCCGACAA	CGACATTGAT	CAGCAGTACC	AAGGGGCAAA	CGGGTCATAC
msa118688.2{361_090}	TTCCCGACAA	CGACATTGAT	CAGCAGTACC	AAGGGGCAAA	CGGGTCATAC
msa118688.2{361_1169NT}	TTCCCGACAA	CGACATTGAT	CAGCAGTACC	AAGGGGCAAA	CGGGTCATAC
msa118688.2{361_CJB110}	TTCCCGACAA	CGACATTGAT	CAGCAGTACC	AAGGGGCAAA	CGGGTCATAC
msa118688.2{361_M781}	TTCCCGACAA	CGACATTGAT	CAGCAGTACC	AAGGGGCAAA	CGGGTCATAC
Consensus	*****	*****	*****	*****	*****
msa118688.2{361_18RS21}	TCTAGGGGCT	GCAGGTATTA	TCGAATTGAT	TAATTGTTTA	GCGGCAATAG
msa118688.2{361_A909}	TCTAGGGGCT	GCAGGTATTA	TCGAATTGAT	TAATTGTTTA	GCGGCAATAG
msa118688.2{361_COH1}	TCTAGGGGCT	GCAGGTATTA	TCGAATTGAT	TAATTGTTTA	GCGGCAATAG
msa118688.2{361_H36B}	TCTAGGGGCT	GCAGGTATTA	TCGAATTGAT	TAATTGTTTA	GCGGCAATAG
msa118688.2{361_JM9130013}	TCTAGGGGCT	GCAGGTATTA	TCGAATTGAT	TAATTGTTTA	GCGGCAATAG
msa118688.2{361_M732}	TCTAGGGGCT	GCAGGTATTA	TCGAATTGAT	TAATTGTTTA	GCGGCAATAG
msa118688.2{GBS361_2603}	TCTAGGGGCT	GCAGGTATTA	TCGAATTGAT	TAATTGTTTA	GCGGCAATAG
msa118688.2{361_090}	TCTAGGGGCT	GCAGGTATTA	TCGAATTGAT	TAATTGTTTA	GCGGCAATAG
msa118688.2{361_1169NT}	TCTAGGGGCT	GCAGGTATTA	TCGAATTGAT	TAATTGTTTA	GCGGCAATAG
msa118688.2{361_CJB110}	TCTAGGGGCT	GCAGGTATTA	TCGAATTGAT	TAATTGTTTA	GCGGCAATAG
msa118688.2{361_M781}	TCTAGGGGCT	GCAGGTATTA	TCGAATTGAT	TAATTGTTTA	GCGGCAATAG
Consensus	*****	*****	*****	*****	*****
msa118688.2{361_18RS21}	AGGAACAGAC	TGTACCAGCA	ACTAAAAATG	AGATTGGGAT	AGAAGGTTTT
msa118688.2{361_A909}	AGGAACAGAC	TGTACCAGCA	ACTAAAAATG	AGATTGGGAT	AGAAGGTTTT
msa118688.2{361_COH1}	AGGAACAGAC	TGTACCAGCA	ACTAAAAATG	AGATTGGGAT	AGAAGGTTTT
msa118688.2{361_H36B}	AGGAACAGAC	TGTACCAGCA	ACTAAAAATG	AGATTGGGAT	AGAAGGTTTT
msa118688.2{361_JM9130013}	AGGAACAGAC	TGTACCAGCA	ACTAAAAATG	AGATTGGGAT	AGAAGGTTTT
msa118688.2{361_M732}	AGGAACAGAC	TGTACCAGCA	ACTAAAAATG	AGATTGGGAT	AGAAGGTTTT
msa118688.2{GBS361_2603}	AGGAACAGAC	TGTACCAGCA	ACTAAAAATG	AGATTGGGAT	AGAAGGTTTT
msa118688.2{361_090}	AGGAACAGAC	TGTACCAGCA	ACTAAAAATG	AGATTGGGAT	AGAAGGTTTT
msa118688.2{361_1169NT}	AGGAACAGAC	TGTACCAGCA	ACTAAAAATG	AGATTGGGAT	AGAAGGTTTT
msa118688.2{361_CJB110}	AGGAACAGAC	TGTACCAGCA	ACTAAAAATG	AGATTGGGAT	AGAAGGTTTT
msa118688.2{361_M781}	AGGAACAGAC	TGTACCAGCA	ACTAAAAATG	AGATTGGGAT	AGAAGGTTTT
Consensus	*****	*****	*****	*****	*****
msa118688.2{361_18RS21}	CCAGAAAATT	TTGTCTATCA	TCAAAAGAGA	GAATACCCAA	TAAGAAATGC
msa118688.2{361_A909}	CCAGAAAATT	TTGTCTATCA	TCAAAAGAGA	GAATACCCAA	TAAGAAATGC
msa118688.2{361_COH1}	CCAGAAAATT	TTGTCTATCA	TCAAAAGAGA	GAATACCCAA	TAAGAAATGC
msa118688.2{361_H36B}	CCAGAAAATT	TTGTCTATCA	TCAAAAGAGA	GAATACCCAA	TAAGAAATGC
msa118688.2{361_JM9130013}	CCAGAAAATT	TTGTCTATCA	TCAAAAGAGA	GAATACCCAA	TAAGAAATGC
msa118688.2{361_M732}	CCAGAAAATT	TTGTCTATCA	TCAAAAGAGA	GAATACCCAA	TAAGAAATGC
msa118688.2{GBS361_2603}	CCAGAAAATT	TTGTCTATCA	TCAAAAGAGA	GAATACCCAA	TAAGAAATGC
msa118688.2{361_090}	CCAGAAAATT	TTGTCTATCA	TCAAAAGAGA	GAATACCCAA	TAAGAAATGC
msa118688.2{361_1169NT}	CCAGAAAATT	TTGTCTATCA	TCAAAAGAGA	GAATACCCAA	TAAGAAATGC
msa118688.2{361_CJB110}	CCAGAAAATT	TTGTCTATCA	TCAAAAGAGA	GAATACCCAA	TAAGAAATGC
msa118688.2{361_M781}	CCAGAAAATT	TTGTCTATCA	TCAAAAGAGA	GAATACCCAA	TAAGAAATGC
Consensus	*****	*****	*****	*****	*****
msa118688.2{361_18RS21}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAG	TAATAGTGGT	gTCTTATTGT
msa118688.2{361_A909}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAG	TAATAGTGGT	gTCTTATTGT
msa118688.2{361_COH1}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAG	TAATAGTGGT	gTCTTATTGT
msa118688.2{361_H36B}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAG	TAATAGTGGT	gTCTTATTGT
msa118688.2{361_JM9130013}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAG	TAATAGTGGT	gTCTTATTGT
msa118688.2{361_M732}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAG	TAATAGTGGT	gTCTTATTGT
msa118688.2{GBS361_2603}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAG	TAATAGTGGT	gTCTTATTGT
msa118688.2{361_090}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAG	TAATAGTGGT	gTCTTATTGT
msa118688.2{361_1169NT}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAG	TAATAGTGGT	gTCTTATTGT

Table 75: Comparative Sequences relating to SAG0671

msa118688.2{361_CJB110}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAA	TAATAGTGGT	aTCTTATTGT
msa118688.2{361_M781}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAA	TAATAGTGGT	aTCTTATTGT
Consensus	*****	*****	*****	*****	*****
msa118688.2{361_18RS21}	CATCTTTAGA	TTCACCTCTA	GAAACATTAC	CTGCTAGAGA	AAATCTTAAA
msa118688.2{361_A909}	CATCTTTAGA	TTCACCTCTA	GAAACATTAC	CTGCTAGAGA	AAATCTTAAA
msa118688.2{361_COH1}	CATCTTTAGA	TTCACCTCTA	GAAACATTAC	CTGCTAGAGA	AAATCTTAAA
msa118688.2{361_H36B}	CATCTTTAGA	TTCACCTCTA	GAAACATTAC	CTGCTAGAGA	AAATCTTAAA
msa118688.2{361_JM9130013}	CATCTTTAGA	TTCACCTCTA	GAAACATTAC	CTGCTAGAGA	AAATCTTAAA
msa118688.2{361_M732}	CATCTTTAGA	TTCACCTCTA	GAAACATTAC	CTGCTAGAGA	AAATCTTAAA
msa118688.2{GBS361_2603}	CATCTTTAGA	TTCACCTCTA	GAAACATTAC	CTGCTAGAGA	AAATCTTAAA
msa118688.2{361_090}	CATCTTTAGA	TTCACCTCTA	GAAACATTAC	CTGCTAGAGA	AAATCTTAAA
msa118688.2{361_1169NT}	CATCTTTAGA	TTCACCTCTA	GAAACATTAC	CTGCTAGAGA	AAATCTTAAA
msa118688.2{361_CJB110}	CATCTTTAGA	TTCACCTCTA	GAAACATTAC	CTGCTAGAGA	AAATCTTAAA
msa118688.2{361_M781}	CATCTTTAGA	TTCACCTCTA	GAAACATTAC	CTGCTAGAGA	AAATCTTAAA
Consensus	*****	*****	*****	*****	*****
msa118688.2{361_18RS21}	ATGGCTATCT	TATCATCTGT	TGCTTCCATT	TCTAAGAATG	AATCACTTTC
msa118688.2{361_A909}	ATGGCTATCT	TATCATCTGT	TGCTTCCATT	TCTAAGAATG	AATCACTTTC
msa118688.2{361_COH1}	ATGGCTATCT	TATCATCTGT	TGCTTCCATT	TCTAAGAATG	AATCACTTTC
msa118688.2{361_H36B}	ATGGCTATCT	TATCATCTGT	TGCTTCCATT	TCTAAGAATG	AATCACTTTC
msa118688.2{361_JM9130013}	ATGGCTATCT	TATCATCTGT	TGCTTCCATT	TCTAAGAATG	AATCACTTTC
msa118688.2{361_M732}	ATGGCTATCT	TATCATCTGT	TGCTTCCATT	TCTAAGAATG	AATCACTTTC
msa118688.2{GBS361_2603}	ATGGCTATCT	TATCATCTGT	TGCTTCCATT	TCTAAGAATG	AATCACTTTC
msa118688.2{361_090}	ATGGCTATCT	TATCATCTGT	TGCTTCCATT	TCTAAGAATG	AATCACTTTC
msa118688.2{361_1169NT}	ATGGCTATCT	TATCATCTGT	TGCTTCCATT	TCTAAGAATG	AATCACTTTC
msa118688.2{361_CJB110}	ATGGCTATCT	TATCATCTGT	TGCTTCCATT	TCTAAGAATG	AATCACTTTC
msa118688.2{361_M781}	ATGGCTATCT	TATCATCTGT	TGCTTCCATT	TCTAAGAATG	AATCACTTTC
Consensus	*****	*****	*****	*****	*****
msa118688.2{361_18RS21}	TATAACCTAT	GAAAAAGTTG	CTAGTAATTT	CAACGACTTT	GAAGCATTAC
msa118688.2{361_A909}	TATAACCTAT	GAAAAAGTTG	CTAGTAATTT	CAACGACTTT	GAAGCATTAC
msa118688.2{361_COH1}	TATAACCTAT	GAAAAAGTTG	CTAGTAATTT	CAACGACTTT	GAAGCATTAC
msa118688.2{361_H36B}	TATAACCTAT	GAAAAAGTTG	CTAGTAATTT	CAACGACTTT	GAAGCATTAC
msa118688.2{361_JM9130013}	TATAACCTAT	GAAAAAGTTG	CTAGTAATTT	CAACGACTTT	GAAGCATTAC
msa118688.2{361_M732}	TATAACCTAT	GAAAAAGTTG	CTAGTAATTT	CAACGACTTT	GAAGCATTAC
msa118688.2{GBS361_2603}	TATAACCTAT	GAAAAAGTTG	CTAGTAATTT	CAACGACTTT	GAAGCATTAC
msa118688.2{361_090}	TATAACCTAT	GAAAAAGTTG	CTAGTAATTT	CAACGACTTT	GAAGCATTAC
msa118688.2{361_1169NT}	TATAACCTAT	GAAAAAGTTG	CTAGTAATTT	CAACGACTTT	GAAGCATTAC
msa118688.2{361_CJB110}	TATAACCTAT	GAAAAAGTTG	CTAGTAATTT	CAACGACTTT	GAAGCATTAC
msa118688.2{361_M781}	TATAACCTAT	GAAAAAGTTG	CTAGTAATTT	CAACGACTTT	GAAGCATTAC
Consensus	*****	*****	*****	*****	*****
msa118688.2{361_18RS21}	GCTTTAAAGG	GGCTAGACCA	CCCAAACTG	TCAACCCAGC	ACAATTTAGG
msa118688.2{361_A909}	GCTTTAAAGG	GGCTAGACCA	CCCAAACTG	TCAACCCAGC	ACAATTTAGG
msa118688.2{361_COH1}	GCTTTAAAGG	GGCTAGACCA	CCCAAACTG	TCAACCCAGC	ACAATTTAGG
msa118688.2{361_H36B}	GCTTTAAAGG	GGCTAGACCA	CCCAAACTG	TCAACCCAGC	ACAATTTAGG
msa118688.2{361_JM9130013}	GCTTTAAAGG	GGCTAGACCA	CCCAAACTG	TCAACCCAGC	ACAATTTAGG
msa118688.2{361_M732}	GCTTTAAAGG	GGCTAGACCA	CCCAAACTG	TCAACCCAGC	ACAATTTAGG
msa118688.2{GBS361_2603}	GCTTTAAAGG	GGCTAGACCA	CCCAAACTG	TCAACCCAGC	ACAATTTAGG
msa118688.2{361_090}	GCTTTAAAGG	GGCTAGACCA	CCCAAACTG	TCAACCCAGC	ACAATTTAGG
msa118688.2{361_1169NT}	GCTTTAAAGG	GGCTAGACCA	CCCAAACTG	TCAACCCAGC	ACAATTTAGG
msa118688.2{361_CJB110}	GCTTTAAAGG	GGCTAGACCA	CCCAAACTG	TCAACCCAGC	ACAATTTAGG
msa118688.2{361_M781}	GCTTTAAAGG	GGCTAGACCA	CCCAAACTG	TCAACCCAGC	ACAATTTAGG
Consensus	*****	*****	*****	*****	*****
msa118688.2{361_18RS21}	AAAATGGATG	ATTTTTCCTA	AATGGTTGCC	GTAACAACAG	CTCAAGCACT
msa118688.2{361_A909}	AAAATGGATG	ATTTTTCCTA	AATGGTTGCC	GTAACAACAG	CTCAAGCACT
msa118688.2{361_COH1}	AAAATGGATG	ATTTTTCCTA	AATGGTTGCC	GTAACAACAG	CTCAAGCACT
msa118688.2{361_H36B}	AAAATGGATG	ATTTTTCCTA	AATGGTTGCC	GTAACAACAG	CTCAAGCACT
msa118688.2{361_JM9130013}	AAAATGGATG	ATTTTTCCTA	AATGGTTGCC	GTAACAACAG	CTCAAGCACT
msa118688.2{361_M732}	AAAATGGATG	ATTTTTCCTA	AATGGTTGCC	GTAACAACAG	CTCAAGCACT
msa118688.2{GBS361_2603}	AAAATGGATG	ATTTTTCCTA	AATGGTTGCC	GTAACAACAG	CTCAAGCACT
msa118688.2{361_090}	AAAATGGATG	ATTTTTCCTA	AATGGTTGCC	GTAACAACAG	CTCAAGCACT
msa118688.2{361_1169NT}	AAAATGGATG	ATTTTTCCTA	AATGGTTGCC	GTAACAACAG	CTCAAGCACT
msa118688.2{361_CJB110}	AAAATGGATG	ATTTTTCCTA	AATGGTTGCC	GTAACAACAG	CTCAAGCACT
msa118688.2{361_M781}	AAAATGGATG	ATTTTTCCTA	AATGGTTGCC	GTAACAACAG	CTCAAGCACT
Consensus	*****	*****	*****	*****	*****
msa118688.2{361_18RS21}	AATAGAAAGC	AATATTAATC	TAAAAAACA	AGATACTTCA	AAAGTAGGAA
msa118688.2{361_A909}	AATAGAAAGC	AATATTAATC	TAAAAAACA	AGATACTTCA	AAAGTAGGAA
msa118688.2{361_COH1}	AATAGAAAGC	AATATTAATC	TAAAAAACA	AGATACTTCA	AAAGTAGGAA
msa118688.2{361_H36B}	AATAGAAAGC	AATATTAATC	TAAAAAACA	AGATACTTCA	AAAGTAGGAA
msa118688.2{361_JM9130013}	AATAGAAAGC	AATATTAATC	TAAAAAACA	AGATACTTCA	AAAGTAGGAA
msa118688.2{361_M732}	AATAGAAAGC	AATATTAATC	TAAAAAACA	AGATACTTCA	AAAGTAGGAA
msa118688.2{GBS361_2603}	AATAGAAAGC	AATATTAATC	TAAAAAACA	AGATACTTCA	AAAGTAGGAA
msa118688.2{361_090}	AATAGAAAGC	AATATTAATC	TAAAAAACA	AGATACTTCA	AAAGTAGGAA

Table 75: Comparative Sequences relating to SAG0671

msa118688.2{361_1169NT}	AATAGAAAGC	AATATTAATC	TAAAAAAACA	AGATACTTCA	AAAGTAGGAA
msa118688.2{361_CJB110}	AATAGAAAGC	AATATTAATC	TAAAAAAACA	AGATACTTCA	AAAGTAGGAA
msa118688.2{361_M781}	AATAGAAAGC	AATATTAATC	TAAAAAAACA	AGATACTTCA	AAAGTAGGAA
Consensus	*****	*****	*****	*****	*****
msa118688.2{361_18RS21}	1451	TTGTATTTAC	AACACTTTCT	GGACCAGTTG	AGGTTGTTGA
msa118688.2{361_A909}	1500	TTGTATTTAC	AACACTTTCT	GGACCAGTTG	AGGTTGTTGA
msa118688.2{361_COH1}	1451	TTGTATTTAC	AACACTTTCT	GGACCAGTTG	AGGTTGTTGA
msa118688.2{361_H36B}	1500	TTGTATTTAC	AACACTTTCT	GGACCAGTTG	AGGTTGTTGA
msa118688.2{361_JM9130013}	1451	TTGTATTTAC	AACACTTTCT	GGACCAGTTG	AGGTTGTTGA
msa118688.2{361_M732}	1500	TTGTATTTAC	AACACTTTCT	GGACCAGTTG	AGGTTGTTGA
msa118688.2{GBS361_2603}	1451	TTGTATTTAC	AACACTTTCT	GGACCAGTTG	AGGTTGTTGA
msa118688.2{361_090}	1500	TTGTATTTAC	AACACTTTCT	GGACCAGTTG	AGGTTGTTGA
msa118688.2{361_1169NT}	1451	TTGTATTTAC	AACACTTTCT	GGACCAGTTG	AGGTTGTTGA
msa118688.2{361_CJB110}	1500	TTGTATTTAC	AACACTTTCT	GGACCAGTTG	AGGTTGTTGA
msa118688.2{361_M781}	1451	TTGTATTTAC	AACACTTTCT	GGACCAGTTG	AGGTTGTTGA
Consensus	*****	*****	*****	*****	*****
msa118688.2{361_18RS21}	1501	AAGCAAATCA	CAACAGAAGG	ATATGCACAT	GTTTCTGCTT
msa118688.2{361_A909}	1550	AAGCAAATCA	CAACAGAAGG	ATATGCACAT	GTTTCTGCTT
msa118688.2{361_COH1}	1501	AAGCAAATCA	CAACAGAAGG	ATATGCACAT	GTTTCTGCTT
msa118688.2{361_H36B}	1550	AAGCAAATCA	CAACAGAAGG	ATATGCACAT	GTTTCTGCTT
msa118688.2{361_JM9130013}	1501	AAGCAAATCA	CAACAGAAGG	ATATGCACAT	GTTTCTGCTT
msa118688.2{361_M732}	1550	AAGCAAATCA	CAACAGAAGG	ATATGCACAT	GTTTCTGCTT
msa118688.2{GBS361_2603}	1501	AAGCAAATCA	CAACAGAAGG	ATATGCACAT	GTTTCTGCTT
msa118688.2{361_090}	1550	AAGCAAATCA	CAACAGAAGG	ATATGCACAT	GTTTCTGCTT
msa118688.2{361_1169NT}	1501	AAGCAAATCA	CAACAGAAGG	ATATGCACAT	GTTTCTGCTT
msa118688.2{361_CJB110}	1550	AAGCAAATCA	CAACAGAAGG	ATATGCACAT	GTTTCTGCTT
msa118688.2{361_M781}	1501	AAGCAAATCA	CAACAGAAGG	ATATGCACAT	GTTTCTGCTT
Consensus	*****	*****	*****	*****	*****
msa118688.2{361_18RS21}	1551	GTTTACAGTA	ATGAATGCAG	CAGCTGGTAT	GCTTTCTATC
msa118688.2{361_A909}	1600	GTTTACAGTA	ATGAATGCAG	CAGCTGGTAT	GCTTTCTATC
msa118688.2{361_COH1}	1551	GTTTACAGTA	ATGAATGCAG	CAGCTGGTAT	GCTTTCTATC
msa118688.2{361_H36B}	1600	GTTTACAGTA	ATGAATGCAG	CAGCTGGTAT	GCTTTCTATC
msa118688.2{361_JM9130013}	1551	GTTTACAGTA	ATGAATGCAG	CAGCTGGTAT	GCTTTCTATC
msa118688.2{361_M732}	1600	GTTTACAGTA	ATGAATGCAG	CAGCTGGTAT	GCTTTCTATC
msa118688.2{GBS361_2603}	1551	GTTTACAGTA	ATGAATGCAG	CAGCTGGTAT	GCTTTCTATC
msa118688.2{361_090}	1600	GTTTACAGTA	ATGAATGCAG	CAGCTGGTAT	GCTTTCTATC
msa118688.2{361_1169NT}	1551	GTTTACAGTA	ATGAATGCAG	CAGCTGGTAT	GCTTTCTATC
msa118688.2{361_CJB110}	1600	GTTTACAGTA	ATGAATGCAG	CAGCTGGTAT	GCTTTCTATC
msa118688.2{361_M781}	1551	GTTTACAGTA	ATGAATGCAG	CAGCTGGTAT	GCTTTCTATC
Consensus	*****	*****	*****	*****	*****
msa118688.2{361_18RS21}	1601	TAACAGGTCC	TTTATCTGTC	ATTTTCGACAA	ATAGTGGAGC
msa118688.2{361_A909}	1650	TAACAGGTCC	TTTATCTGTC	ATTTTCGACAA	ATAGTGGAGC
msa118688.2{361_COH1}	1601	TAACAGGTCC	TTTATCTGTC	ATTTTCGACAA	ATAGTGGAGC
msa118688.2{361_H36B}	1650	TAACAGGTCC	TTTATCTGTC	ATTTTCGACAA	ATAGTGGAGC
msa118688.2{361_JM9130013}	1601	TAACAGGTCC	TTTATCTGTC	ATTTTCGACAA	ATAGTGGAGC
msa118688.2{361_M732}	1650	TAACAGGTCC	TTTATCTGTC	ATTTTCGACAA	ATAGTGGAGC
msa118688.2{GBS361_2603}	1601	TAACAGGTCC	TTTATCTGTC	ATTTTCGACAA	ATAGTGGAGC
msa118688.2{361_090}	1650	TAACAGGTCC	TTTATCTGTC	ATTTTCGACAA	ATAGTGGAGC
msa118688.2{361_1169NT}	1601	TAACAGGTCC	TTTATCTGTC	ATTTTCGACAA	ATAGTGGAGC
msa118688.2{361_CJB110}	1650	TAACAGGTCC	TTTATCTGTC	ATTTTCGACAA	ATAGTGGAGC
msa118688.2{361_M781}	1601	TAACAGGTCC	TTTATCTGTC	ATTTTCGACAA	ATAGTGGAGC
Consensus	*****	*****	*****	*****	*****
msa118688.2{361_18RS21}	1651	ATACAATATG	CCAAGGAAAT	GATGCGTAAC	GATAATCTAG
msa118688.2{361_A909}	1700	ATACAATATG	CCAAGGAAAT	GATGCGTAAC	GATAATCTAG
msa118688.2{361_COH1}	1651	ATACAATATG	CCAAGGAAAT	GATGCGTAAC	GATAATCTAG
msa118688.2{361_H36B}	1700	ATACAATATG	CCAAGGAAAT	GATGCGTAAC	GATAATCTAG
msa118688.2{361_JM9130013}	1651	ATACAATATG	CCAAGGAAAT	GATGCGTAAC	GATAATCTAG
msa118688.2{361_M732}	1700	ATACAATATG	CCAAGGAAAT	GATGCGTAAC	GATAATCTAG
msa118688.2{GBS361_2603}	1651	ATACAATATG	CCAAGGAAAT	GATGCGTAAC	GATAATCTAG
msa118688.2{361_090}	1700	ATACAATATG	CCAAGGAAAT	GATGCGTAAC	GATAATCTAG
msa118688.2{361_1169NT}	1651	ATACAATATG	CCAAGGAAAT	GATGCGTAAC	GATAATCTAG
msa118688.2{361_CJB110}	1700	ATACAATATG	CCAAGGAAAT	GATGCGTAAC	GATAATCTAG
msa118688.2{361_M781}	1651	ATACAATATG	CCAAGGAAAT	GATGCGTAAC	GATAATCTAG
Consensus	*****	*****	*****	*****	*****
msa118688.2{361_18RS21}	1701	TCTTGTCTTCT	GCTAATCAGT	GGACAGACAT	GAGTTTTATG
msa118688.2{361_A909}	1750	TCTTGTCTTCT	GCTAATCAGT	GGACAGACAT	GAGTTTTATG
msa118688.2{361_COH1}	1701	TCTTGTCTTCT	GCTAATCAGT	GGACAGACAT	GAGTTTTATG
msa118688.2{361_H36B}	1750	TCTTGTCTTCT	GCTAATCAGT	GGACAGACAT	GAGTTTTATG
msa118688.2{361_JM9130013}	1701	TCTTGTCTTCT	GCTAATCAGT	GGACAGACAT	GAGTTTTATG
msa118688.2{361_M732}	1750	TCTTGTCTTCT	GCTAATCAGT	GGACAGACAT	GAGTTTTATG
msa118688.2{GBS361_2603}	1701	TCTTGTCTTCT	GCTAATCAGT	GGACAGACAT	GAGTTTTATG

Table 75: Comparative Sequences relating to SAG0671

msa118688.2{361_090}	TCTTGTCTCT	GCTAATCAGT	GGACAGACAT	GAGTTTTATG	TGGTGGCAAC
msa118688.2{361_1169NT}	TCTTGTCTCT	GCTAATCAGT	GGACAGACAT	GAGTTTTATG	TGGTGGCAAC
msa118688.2{361_CJB110}	TCTTGTCTCT	GCTAATCAGT	GGACAGACAT	GAGTTTTATG	TGGTGGCAAC
msa118688.2{361_M781}	TCTTGTCTCT	GCTAATCAGT	GGACAGACAT	GAGTTTTATG	TGGTGGCAAC
Consensus	*****	*****	*****	*****	*****
1751					
msa118688.2{361_18RS21}	AATTAAACTA	TGATAGTCAA	ATGTTTGTCT	GTTCTGATTA	TTGTTTCAGCA
msa118688.2{361_A909}	AATTAAACTA	TGATAGTCAA	ATGTTTGTCT	GTTCTGATTA	TTGTTTCAGCA
msa118688.2{361_COH1}	AATTAAACTA	TGATAGTCAA	ATGTTTGTCT	GTTCTGATTA	TTGTTTCAGCA
msa118688.2{361_H36B}	AATTAAACTA	TGATAGTCAA	ATGTTTGTCT	GTTCTGATTA	TTGTTTCAGCA
msa118688.2{361_JM9130013}	AATTAAACTA	TGATAGTCAA	ATGTTTGTCT	GTTCTGATTA	TTGTTTCAGCA
msa118688.2{361_M732}	AATTAAACTA	TGATAGTCAA	ATGTTTGTCT	GTTCTGATTA	TTGTTTCAGCA
msa118688.2{GBS361_2603}	AATTAAACTA	TGATAGTCAA	ATGTTTGTCT	GTTCTGATTA	TTGTTTCAGCA
msa118688.2{361_090}	AATTAAACTA	TGATAGTCAA	ATGTTTGTCT	GTTCTGATTA	TTGTTTCAGCA
msa118688.2{361_1169NT}	AATTAAACTA	TGATAGTCAA	ATGTTTGTCT	GTTCTGATTA	TTGTTTCAGCA
msa118688.2{361_CJB110}	AATTAAACTA	TGATAGTCAA	ATGTTTGTCT	GTTCTGATTA	TTGTTTCAGCA
msa118688.2{361_M781}	AATTAAACTA	TGATAGTCAA	ATGTTTGTCT	GTTCTGATTA	TTGTTTCAGCA
Consensus	*****	*****	*****	*****	*****
1801					
msa118688.2{361_18RS21}	CAAGTCCTCT	CTCGTCAAGC	ATTGGATAAT	TCTCCTATAA	TATTAGGTAG
msa118688.2{361_A909}	CAAGTCCTCT	CTCGTCAAGC	ATTGGATAAT	TCTCCTATAA	TATTAGGTAG
msa118688.2{361_COH1}	CAAGTCCTCT	CTCGTCAAGC	ATTGGATAAT	TCTCCTATAA	TATTAGGTAG
msa118688.2{361_H36B}	CAAGTCCTCT	CTCGTCAAGC	ATTGGATAAT	TCTCCTATAA	TATTAGGTAG
msa118688.2{361_JM9130013}	CAAGTCCTCT	CTCGTCAAGC	ATTGGATAAT	TCTCCTATAA	TATTAGGTAG
msa118688.2{361_M732}	CAAGTCCTCT	CTCGTCAAGC	ATTGGATAAT	TCTCCTATAA	TATTAGGTAG
msa118688.2{GBS361_2603}	CAAGTCCTCT	CTCGTCAAGC	ATTGGATAAT	TCTCCTATAA	TATTAGGTAG
msa118688.2{361_090}	CAAGTCCTCT	CTCGTCAAGC	ATTGGATAAT	TCTCCTATAA	TATTAGGTAG
msa118688.2{361_1169NT}	CAAGTCCTCT	CTCGTCAAGC	ATTGGATAAT	TCTCCTATAA	TATTAGGTAG
msa118688.2{361_CJB110}	CAAGTCCTCT	CTCGTCAAGC	ATTGGATAAT	TCTCCTATAA	TATTAGGTAG
msa118688.2{361_M781}	CAAGTCCTCT	CTCGTCAAGC	ATTGGATAAT	TCTCCTATAA	TATTAGGTAG
Consensus	*****	*****	*****	*****	*****
1851					
msa118688.2{361_18RS21}	TAAACAATTA	AAATATAGCC	ATAAAAACATT	CACAGATGTG	ATGACTATTT
msa118688.2{361_A909}	TAAACAATTA	AAATATAGCC	ATAAAAACATT	CACAGATGTG	ATGACTATTT
msa118688.2{361_COH1}	TAAACAATTA	AAATATAGCC	ATAAAAACATT	CACAGATGTG	ATGACTATTT
msa118688.2{361_H36B}	TAAACAATTA	AAATATAGCC	ATAAAAACATT	CACAGATGTG	ATGACTATTT
msa118688.2{361_JM9130013}	TAAACAATTA	AAATATAGCC	ATAAAAACATT	CACAGATGTG	ATGACTATTT
msa118688.2{361_M732}	TAAACAATTA	AAATATAGCC	ATAAAAACATT	CACAGATGTG	ATGACTATTT
msa118688.2{GBS361_2603}	TAAACAATTA	AAATATAGCC	ATAAAAACATT	CACAGATGTG	ATGACTATTT
msa118688.2{361_090}	TAAACAATTA	AAATATAGCC	ATAAAAACATT	CACAGATGTG	ATGACTATTT
msa118688.2{361_1169NT}	TAAACAATTA	AAATATAGCC	ATAAAAACATT	CACAGATGTG	ATGACTATTT
msa118688.2{361_CJB110}	TAAACAATTA	AAATATAGCC	ATAAAAACATT	CACAGATGTG	ATGACTATTT
msa118688.2{361_M781}	TAAACAATTA	AAATATAGCC	ATAAAAACATT	CACAGATGTG	ATGACTATTT
Consensus	*****	*****	*****	*****	*****
1901					
msa118688.2{361_18RS21}	TTGATGCTGC	GCTTCAAAAT	TTATTATCAG	ACTTAGGACT	AACCATAAAA
msa118688.2{361_A909}	TTGATGCTGC	GCTTCAAAAT	TTATTATCAG	ACTTAGGACT	AACCATAAAA
msa118688.2{361_COH1}	TTGATGCTGC	GCTTCAAAAT	TTATTATCAG	ACTTAGGACT	AACCATAAAA
msa118688.2{361_H36B}	TTGATGCTGC	GCTTCAAAAT	TTATTATCAG	ACTTAGGACT	AACCATAAAA
msa118688.2{361_JM9130013}	TTGATGCTGC	GCTTCAAAAT	TTATTATCAG	ACTTAGGACT	AACCATAAAA
msa118688.2{361_M732}	TTGATGCTGC	GCTTCAAAAT	TTATTATCAG	ACTTAGGACT	AACCATAAAA
msa118688.2{GBS361_2603}	TTGATGCTGC	GCTTCAAAAT	TTATTATCAG	ACTTAGGACT	AACCATAAAA
msa118688.2{361_090}	TTGATGCTGC	GCTTCAAAAT	TTATTATCAG	ACTTAGGACT	AACCATAAAA
msa118688.2{361_1169NT}	TTGATGCTGC	GCTTCAAAAT	TTATTATCAG	ACTTAGGACT	AACCATAAAA
msa118688.2{361_CJB110}	TTGATGCTGC	GCTTCAAAAT	TTATTATCAG	ACTTAGGACT	AACCATAAAA
msa118688.2{361_M781}	TTGATGCTGC	GCTTCAAAAT	TTATTATCAG	ACTTAGGACT	AACCATAAAA
Consensus	*****	*****	*****	*****	*****
1951					
msa118688.2{361_18RS21}	GATATCAAAG	GTTTCGTTTG	GAATGAGCGG	AAGAAGGCAG	TTAGTTCAGA
msa118688.2{361_A909}	GATATCAAAG	GTTTCGTTTG	GAATGAGCGG	AAGAAGGCAG	TTAGTTCAGA
msa118688.2{361_COH1}	GATATCAAAG	GTTTCGTTTG	GAATGAGCGG	AAGAAGGCAG	TTAGTTCAGA
msa118688.2{361_H36B}	GATATCAAAG	GTTTCGTTTG	GAATGAGCGG	AAGAAGGCAG	TTAGTTCAGA
msa118688.2{361_JM9130013}	GATATCAAAG	GTTTCGTTTG	GAATGAGCGG	AAGAAGGCAG	TTAGTTCAGA
msa118688.2{361_M732}	GATATCAAAG	GTTTCGTTTG	GAATGAGCGG	AAGAAGGCAG	TTAGTTCAGA
msa118688.2{GBS361_2603}	GATATCAAAG	GTTTCGTTTG	GAATGAGCGG	AAGAAGGCAG	TTAGTTCAGA
msa118688.2{361_090}	GATATCAAAG	GTTTCGTTTG	GAATGAGCGG	AAGAAGGCAG	TTAGTTCAGA
msa118688.2{361_1169NT}	GATATCAAAG	GTTTCGTTTG	GAATGAGCGG	AAGAAGGCAG	TTAGTTCAGA
msa118688.2{361_CJB110}	GATATCAAAG	GTTTCGTTTG	GAATGAGCGG	AAGAAGGCAG	TTAGTTCAGA
msa118688.2{361_M781}	GATATCAAAG	GTTTCGTTTG	GAATGAGCGG	AAGAAGGCAG	TTAGTTCAGA
Consensus	*****	*****	*****	*****	*****
2001					
msa118688.2{361_18RS21}	TTATGATTTT	TTAGCGAACT	TGTCTGAGTA	TTATAATATG	CCAAACCTTG
msa118688.2{361_A909}	TTATGATTTT	TTAGCGAACT	TGTCTGAGTA	TTATAATATG	CCAAACCTTG
msa118688.2{361_COH1}	TTATGATTTT	TTAGCGAACT	TGTCTGAGTA	TTATAATATG	CCAAACCTTG
msa118688.2{361_H36B}	TTATGATTTT	TTAGCGAACT	TGTCTGAGTA	TTATAATATG	CCAAACCTTG
msa118688.2{361_JM9130013}	TTATGATTTT	TTAGCGAACT	TGTCTGAGTA	TTATAATATG	CCAAACCTTG
msa118688.2{361_M732}	TTATGATTTT	TTAGCGAACT	TGTCTGAGTA	TTATAATATG	CCAAACCTTG
2050					

Table 75: Comparative Sequences relating to SAG0671

msa118688.2{GBS361_2603}	TTATGATTTC	TTAGCGAACT	TGTCTGAGTA	TTATAATATG	CCAAACCTTG
msa118688.2{361_090}	TTATGATTTC	TTAGCGAACT	TGTCTGAGTA	TTATAATATG	CCAAACCTTG
msa118688.2{361_1169NT}	TTATGATTTC	TTAGCGAACT	TGTCTGAGTA	TTATAATATG	CCAAACCTTG
msa118688.2{361_CJB110}	TTATGATTTC	TTAGCGAACT	TGTCTGAGTA	TTATAATATG	CCAAACCTTG
msa118688.2{361_M781}	TTATGATTTC	TTAGCGAACT	TGTCTGAGTA	TTATAATATG	CCAAACCTTG
Consensus	*****	*****	*****	*****	*****
2051					
msa118688.2{361_18RS21}	CTTCTGGTCA	GTTTGGATTT	TCATCTAATG	GTGCTGGTGA	AGAACTGGAC
msa118688.2{361_A909}	CTTCTGGTCA	GTTTGGATTT	TCATCTAATG	GTGCTGGTGA	AGAACTGGAC
msa118688.2{361_COH1}	CTTCTGGTCA	GTTTGGATTT	TCATCTAATG	GTGCTGGTGA	AGAACTGGAC
msa118688.2{361_H36B}	CTTCTGGTCA	GTTTGGATTT	TCATCTAATG	GTGCTGGTGA	AGAACTGGAC
msa118688.2{361_JM9130013}	CTTCTGGTCA	GTTTGGATTT	TCATCTAATG	GTGCTGGTGA	AGAACTGGAC
msa118688.2{361_M732}	CTTCTGGTCA	GTTTGGATTT	TCATCTAATG	GTGCTGGTGA	AGAACTGGAC
msa118688.2{GBS361_2603}	CTTCTGGTCA	GTTTGGATTT	TCATCTAATG	GTGCTGGTGA	AGAACTGGAC
msa118688.2{361_090}	CTTCTGGTCA	GTTTGGATTT	TCATCTAATG	GTGCTGGTGA	AGAACTGGAC
msa118688.2{361_1169NT}	CTTCTGGTCA	GTTTGGATTT	TCATCTAATG	GTGCTGGTGA	AGAACTGGAC
msa118688.2{361_CJB110}	CTTCTGGTCA	GTTTGGATTT	TCATCTAATG	GTGCTGGTGA	AGAACTGGAC
msa118688.2{361_M781}	CTTCTGGTCA	GTTTGGATTT	TCATCTAATG	GTGCTGGTGA	AGAACTGGAC
Consensus	*****	*****	*****	*****	*****
2101					
msa118688.2{361_18RS21}	TATACTGTTA	ATGAAAGTAT	AGAAAAGGGC	TATTATTTAG	TCCTATCTTA
msa118688.2{361_A909}	TATACTGTTA	ATGAAAGTAT	AGAAAAGGGC	TATTATTTAG	TCCTATCTTA
msa118688.2{361_COH1}	TATACTGTTA	ATGAAAGTAT	AGAAAAGGGC	TATTATTTAG	TCCTATCTTA
msa118688.2{361_H36B}	TATACTGTTA	ATGAAAGTAT	AGAAAAGGGC	TATTATTTAG	TCCTATCTTA
msa118688.2{361_JM9130013}	TATACTGTTA	ATGAAAGTAT	AGAAAAGGGC	TATTATTTAG	TCCTATCTTA
msa118688.2{361_M732}	TATACTGTTA	ATGAAAGTAT	AGAAAAGGGC	TATTATTTAG	TCCTATCTTA
msa118688.2{GBS361_2603}	TATACTGTTA	ATGAAAGTAT	AGAAAAGGGC	TATTATTTAG	TCCTATCTTA
msa118688.2{361_090}	TATACTGTTA	ATGAAAGTAT	AGAAAAGGGC	TATTATTTAG	TCCTATCTTA
msa118688.2{361_1169NT}	TATACTGTTA	ATGAAAGTAT	AGAAAAGGGC	TATTATTTAG	TCCTATCTTA
msa118688.2{361_CJB110}	TATACTGTTA	ATGAAAGTAT	AGAAAAGGGC	TATTATTTAG	TCCTATCTTA
msa118688.2{361_M781}	TATACTGTTA	ATGAAAGTAT	AGAAAAGGGC	TATTATTTAG	TCCTATCTTA
Consensus	*****	*****	*****	*****	*****
2151					
msa118688.2{361_18RS21}	TTCGATCTTc	GGTGGTATCT	CTTTTGCTAT	TATTGAAAAA	AGG
msa118688.2{361_A909}	TTCGATCTTc	GGTGGTATCT	CTTTTGCTAT	TATTGAAAAA	AGG
msa118688.2{361_COH1}	TTCGATCTTc	GGTGGTATCT	CTTTTGCTAT	TATTGAAAAA	AGG
msa118688.2{361_H36B}	TTCGATCTTc	GGTGGTATCT	CTTTTGCTAT	TATTGAAAAA	AGG
msa118688.2{361_JM9130013}	TTCGATCTTc	GGTGGTATCT	CTTTTGCTAT	TATTGAAAAA	AGG
msa118688.2{361_M732}	TTCGATCTTc	GGTGGTATCT	CTTTTGCTAT	TATTGAAAAA	AGG
msa118688.2{GBS361_2603}	TTCGATCTTc	GGTGGTATCT	CTTTTGCTAT	TATTGAAAAA	AGG
msa118688.2{361_090}	TTCGATCTTc	GGTGGTATCT	CTTTTGCTAT	TATTGAAAAA	AGG
msa118688.2{361_1169NT}	TTCGATCTTc	GGTGGTATCT	CTTTTGCTAT	TATTGAAAAA	AGG
msa118688.2{361_CJB110}	TTCGATCTTc	GGTGGTATCT	CTTTTGCTAT	TATTGAAAAA	AGG
msa118688.2{361_M781}	TTCGATCTTc	GGTGGTATCT	CTTTTGCTAT	TATTGAAAAA	AGG
Consensus	*****	*****	*****	*****	***

SEQ ID NO. 7512

STRAIN 2603 frame: 1

MSVYVSGIGI ISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILES YTGSI TS DPEVPEQ
 YKDETRNFKFAFTAFEEALASSGVNLKAYHNI AVCLGTS LGGKSAGQNALYQFE EGERQV
 DASLLEKASVYHIADELMAYHDI VGASYVI STACSASNNAVILGTQLLQDGDCLAI CGG
 CDELS DISLAGFTSLGA INTEMACQPYSSGKGINLGEGAGFVVLVKDQSLAKY GKI IGGL
 ITSDGYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKF
 FPTTTLISSTKGQTGHTLGAAGI IELINCLAAIEEQTVPATKNEIGIEGFPENFVYHQKR
 EYPI RNALNFSFAFGNNSGVLLSSLDSPLETLPARENLKMAILSSVASISKNESLSITY
 EKVASNFNDFEALRFK GARPPKTVNPAQFRKMDDFSKMVAVT TAQALIESNINLKKQDTS
 KVGIVFTTSLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSII FKITGPLSV
 ISTNSGALDGIQYAKEMMRNDNLDYVILV SANQWTDMSFMWWQQLNYDSQMFVGS DYCSA
 QVLSRQALDNSPI ILGSKQLKYSHKTFTDVTI FDAALQNL LSDLGLTI KD IKGFVWNER
 KKAVSSDYDFLANLSEY YNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYLVLSYSIF
 GGISFAIEKR

SEQ ID NO. 7513

STRAIN 090 frame: 3

VSGIGI ISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILES YTGSI TS DPEVPEQYKDE
 TRNFKFAFTAFEEALASSGVNLKAYHNI AVCLGTS LGGKSAGQNALYQFE EGERQVDASL
 LEKASVYHIADELMAYHDI VGASYVI STACSASNNAVILGTQLLQDGDCLAI CGG CDEL
 SDISLAGFTSLGA INTEMACQPYSSGKGINLGEGAGFVVLVKDQSLAKY GKI IGGLITSD
 GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKF FPTT
 TLISSTKGQTGHTLGAAGI IELINCLAAIEEQTVPATKNEIGIEGFPENFVYHQKREYPI
 RNALNFSFAFGNNSGILLSSLDSPLETLPARENLKMAILSSVASISKNESLSITY EKVA
 SNFNDFEALRFK GARPPKTVNPAQFRKMDDFSKMVAVT TAQALIESNINLKKQDTSKVG I
 VFTTSLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSII FKITGPLSVISTN
 SGALDGIQYAKEMMRNDNLDYVILV SANQWTDMSFMWWQQLNYDSQMFVGS DYCSAQVLS
 RQALDNSPI ILGSKQLKYSHKTFTDVTI FDAALQNL LSDLGLTI KD IKGFVWNERKKAV
 SSDYDFLANLSEY YNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYLVLSYSIFGGIS
 FAIEKR

SEQ ID NO. 7514

STRAIN A909 frame: 3

Table 75: Comparative Sequences relating to SAG0671

VSGIGI ISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILES YTGSI TSDPEVPEQYKDE
 TRNFKFAFTAFEEALASSGVNLKAYHNI AVCLGTS LGGKSAGQNALYQFEEGERQVDASL
 LEKASVYHIADELMAYHDI VGASYVISTACSASNNAVILGTQLLQDGDCLAI CGGCDEL
 SDISLAGFTSLGAINTEMACQPYSSGKGINLGEAGFVVLVKDQSLAKYGI IGGLITSD
 GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
 TLISSTKGQTGHTLGAAGI IELINCLAAIEEQTVPATKNEIGIEGFPENFVYHQREYPI
 RNALNFSFAFGNNSGVLLSSLDSPLETL PARENLKMAILSSVASISKNESLSITYEKVA
 SNFNDFEALRFKGPAPKTVNPAQFRKMDDFSKMVAVTTAQALIESNINLKKQDTSKVGI
 VFTTTLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSII FKITGPLSVISTN
 SGALDGIQYAKEMMRNDNDYVILVSANQWTDMSFMWWQQLNYDSQMFVGS DYCSAQVLS
 RQALDNSPI ILGSKQLKYSHKTFDVTI FDAALQNL LSDLGLTI KD IKGFWNERKKAV
 SSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYLVL SYSIFGGIS
 FAIEKR

SEQ ID NO. 7515

STRAIN H36B frame: 3

VSGIGI ISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILES YTGSI TSDPEVPEQYKDE
 TRNFKFAFTAFEEALASSGVNLKAYHNI AVCLGTS LGGKSAGQNALYQFEEGERQVDASL
 LEKASVYHIADELMAYHDI VGASYVISTACSASNNAVILGTQLLQDGDCLAI CGGCDEL
 SDISLAGFTSLGAINTEMACQPYSSGKGINLGEAGFVVLVKDQSLAKYGI IGGLITSD
 GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
 TLISSTKGQTGHTLGAAGI IELINCLAAIEEQTVPATKNEIGIEGFPENFVYHQREYPI
 RNALNFSFAFGNNSGVLLSSLDSPLETL PARENLKMAILSSVASISKNESLSITYEKVA
 SNFNDFEALRFKGPAPKTVNPAQFRKMDDFSKMVAVTTAQALIESNINLKKQDTSKVGI
 VFTTTLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSII FKITGPLSVISTN
 SGALDGIQYAKEMMRNDNDYVILVSANQWTDMSFMWWQQLNYDSQMFVGS DYCSAQVLS
 RQALDNSPI ILGSKQLKYSHKTFDVTI FDAALQNL LSDLGLTI KD IKGFWNERKKAV
 SSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYLVL SYSIFGGIS
 FAIEKR

SEQ ID NO. 7516

STRAIN 18RS21 frame: 3

VSGIGI ISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILES YTGSI TSDPEVPEQYKDE
 TRNFKFAFTAFEEALASSGVNLKAYHNI AVCLGTS LGGKSAGQNALYQFEEGERQVDASL
 LEKASVYHIADELMAYHDI VGASYVISTACSASNNAVILGTQLLQDGDCLAI CGGCDEL
 SDISLAGFTSLGAINTEMACQPYSSGKGINLGEAGFVVLVKDQSLAKYGI IGGLITSD
 GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
 TLISSTKGQTGHTLGAAGI IELINCLAAIEEQTVPATKNEIGIEGFPENFVYHQREYPI
 RNALNFSFAFGNNSGVLLSSLDSPLETL PARENLKMAILSSVASISKNESLSITYEKVA
 SNFNDFEALRFKGPAPKTVNPAQFRKMDDFSKMVAVTTAQALIESNINLKKQDTSKVGI
 VFTTTLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSII FKITGPLSVISTN
 SGALDGIQYAKEMMRNDNDYVILVSANQWTDMSFMWWQQLNYDSQMFVGS DYCSAQVLS
 RQALDNSPI ILGSKQLKYSHKTFDVTI FDAALQNL LSDLGLTI KD IKGFWNERKKAV
 SSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYLVL SYSIFGGIS
 FAIEKR

SEQ ID NO. 7517

STRAIN M732 frame: 3

VSGIGI ISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILES YTGSI TSDPEVPEQYKDE
 TRNFKFAFTAFEEALASSGVNLKAYHNI AVCLGTS LGGKSAGQNALYQFEEGERQVDASL
 LEKASVYHIADELMAYHDI VGASYVISTACSASNNAVILGTQLLQDGDCLAI CGGCDEL
 SDISLAGFTSLGAINTEMACQPYSSGKGINLGEAGFVVLVKDQSLAKYGI IGGLITSD
 GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
 TLISSTKGQTGHTLGAAGI IELINCLAAIEEQTVPATKNEIGIEGFPENFVYHQREYPI
 RNALNFSFAFGNNSGVLLSSLDSPLETL PARENLKMAILSSVASISKNESLSITYEKVA
 SNFNDFEALRFKGPAPKTVNPAQFRKMDDFSKMVAVTTAQALIESNINLKKQDTSKVGI
 VFTTTLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSII FKITGPLSVISTN
 SGALDGIQYAKEMMRNDNDYVILVSANQWTDMSFMWWQQLNYDSQMFVGS DYCSAQVLS
 RQALDNSPI ILGSKQLKYSHKTFDVTI FDAALQNL LSDLGLTI KD IKGFWNERKKAV
 SSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYLVL SYSIFGGIS
 FAIEKR

SEQ ID NO. 7518

STRAIN COH1 frame: 3

VSGIGI ISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILES YTGSI TSDPEVPEQYKDE
 TRNFKFAFTAFEEALASSGVNLKAYHNI AVCLGTS LGGKSAGQNALYQFEEGERQVDASL
 LEKASVYHIADELMAYHDI VGASYVISTACSASNNAVILGTQLLQDGDCLAI CGGCDEL
 SDISLAGFTSLGAINTEMACQPYSSGKGINLGEAGFVVLVKDQSLAKYGI IGGLITSD
 GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
 TLISSTKGQTGHTLGAAGI IELINCLAAIEEQTVPATKNEIGIEGFPENFVYHQREYPI
 RNALNFSFAFGNNSGVLLSSLDSPLETL PARENLKMAILSSVASISKNESLSITYEKVA
 SNFNDFEALRFKGPAPKTVNPAQFRKMDDFSKMVAVTTAQALIESNINLKKQDTSKVGI
 VFTTTLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSII FKITGPLSVISTN
 SGALDGIQYAKEMMRNDNDYVILVSANQWTDMSFMWWQQLNYDSQMFVGS DYCSAQVLS
 RQALDNSPI ILGSKQLKYSHKTFDVTI FDAALQNL LSDLGLTI KD IKGFWNERKKAV
 SSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYLVL SYSIFGGIS
 FAIEKR

SEQ ID NO. 7519

STRAIN M781 frame: 3

VSGIGI ISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILES YTGSI TSDPEVPEQYKDE
 TRNFKFAFTAFEEALASSGVNLKAYHNI AVCLGTS LGGKSAGQNALYQFEEGERQVDASL

Table 75: Comparative Sequences relating to SAG0671

LEKASVYHIADELMAYHDI VGASYVISTACSASNNAVILGTQLLQDGDCLAI CGGCDEL
SDISLAGFTSLGAINTEMACQPYSSGKGINLGEAGFVVLVKDQSLAKYGKI IGGITSD
GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
TLISSTKGQTGHTLGAAGI IELINCLAAIEEQTVPATKNEIGIEGFPENFVYHQREYPI
RNALNFSFAFGGNNSGILLSSLDSPLETL PARENLKMAILSSVASISKNESLSITYEKVA
SNFNDFEALRFK GARPPKTVNPAQFRKMDDFSKMVAVTTAQAALIESNINLKKQDTSKVGI
VFTTSLGPPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSII FKITGPLSVISTN
SGALDGIQYAKEMMRNDNLDYVILV SANQWTDMSFMWWQQLNYDSQMFVGS DYCSAQVLS
RQALDNSPI ILGSKQLKYSHKTFTDVTI FDAALQNL LSDLGLTIKDIKGFVWNERKKAV
SSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYLVL SYSIFGGIS
FAIEKR

SEQ ID NO. 7520

STRAIN CJB110 frame: 3

VSGIGI ISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILES YTGSI TS DPEVPEQYKDE
TRNFKFAFTAFEEALASSGVNLKAYHNI AVCLGTS LGGKSAGQNALYQFEGERQVDASL
LEKASVYHIADELMAYHDI VGASYVISTACSASNNAVILGTQLLQDGDCLAI CGGCDEL
SDISLAGFTSLGAINTEMACQPYSSGKGINLGEAGFVVLVKDQSLAKYGKI IGGITSD
GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
TLISSTKGQTGHTLGAAGI IELINCLAAIEEQTVPATKNEIGIEGFPENFVYHQREYPI
RNALNFSFAFGGNNSGILLSSLDSPLETL PARENLKMAILSSVASISKNESLSITYEKVA
SNFNDFEALRFK GARPPKTVNPAQFRKMDDFSKMVAVTTAQAALIESNINLKKQDTSKVGI
VFTTSLGPPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSII FKITGPLSVISTN
SGALDGIQYAKEMMRNDNLDYVILV SANQWTDMSFMWWQQLNYDSQMFVGS DYCSAQVLS
RQALDNSPI ILGSKQLKYSHKTFTDVTI FDAALQNL LSDLGLTIKDIKGFVWNERKKAV
SSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYLVL SYSIFGGIS
FAIEKR

SEQ ID NO. 7521

STRAIN 1169NT frame: 3

VSGIGI ISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILES YTGSI TS DPEVPEQYKDE
TRNFKFAFTAFEEALASSGVNLKAYHNI AVCLGTS LGGKSAGQNALYQFEGERQVDASL
LEKASVYHIADELMAYHDI VGASYVISTACSASNNAVILGTQLLQDGDCLAI CGGCDEL
SDISLAGFTSLGAINTEMACQPYSSGKGINLGEAGFVVLVKDQSLAKYGKI IGGITSD
GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
TLISSTKGQTGHTLGAAGI IELINCLAAIEEQTVPATKNEIGIEGFPENFVYHQREYPI
RNALNFSFAFGGNNSGILLSSLDSPLETL PARENLKMAILSSVASISKNESLSITYEKVA
SNFNDFEALRFK GARPPKTVNPAQFRKMDDFSKMVAVTTAQAALIESNINLKKQDTSKVGI
VFTTSLGPPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSII FKITGPLSVISTN
SGALDGIQYAKEMMRNDNLDYVILV SANQWTDMSFMWWQQLNYDSQMFVGS DYCSAQVLS
RQALDNSPI ILGSKQLKYSHKTFTDVTI FDAALQNL LSDLGLTIKDIKGFVWNERKKAV
SSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYLVL SYSIFGGIS
FAIEKR

SEQ ID NO. 7522

STRAIN JM9130013 frame: 3

VSGIGI ISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILES YTGSI TS DPEVPEQYKDE
TRNFKFAFTAFEEALASSGVNLKAYHNI AVCLGTS LGGKSAGQNALYQFEGERQVDASL
LEKASVYHIADELMAYHDI VGASYVISTACSASNNAVILGTQLLQDGDCLAI CGGCDEL
SDISLAGFTSLGAINTEMACQPYSSGKGINLGEAGFVVLVKDQSLAKYGKI IGGITSD
GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
TLISSTKGQTGHTLGAAGI IELINCLAAIEEQTVPATKNEIGIEGFPENFVYHQREYPI
RNALNFSFAFGGNNSGVLLSSLDSPLETL PARENLKMAILSSVASISKNESLSITYEKVA
SNFNDFEALRFK GARPPKTVNPAQFRKMDDFSKMVAVTTAQAALIESNINLKKQDTSKVGI
VFTTSLGPPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSII FKITGPLSVISTN
SGALDGIQYAKEMMRNDNLDYVILV SANQWTDMSFMWWQQLNYDSQMFVGS DYCSAQVLS
RQALDNSPI ILGSKQLKYSHKTFTDVTI FDAALQNL LSDLGLTIKDIKGFVWNERKKAV
SSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYLVL SYSIFGGIS
FAIEKR

PRETTY of: /biotmp/msa118713.2{*} April 9, 2003 02:54 ..

	1		50
msa118713.2{361_090}	----VSGIGI	ISSLGKNYSE HKQHLFDLKE	GISKHLYKNH DSILES YTGSI
msa118713.2{361_1169NT}	----VSGIGI	ISSLGKNYSE HKQHLFDLKE	GISKHLYKNH DSILES YTGSI
msa118713.2{361_CJB110}	----VSGIGI	ISSLGKNYSE HKQHLFDLKE	GISKHLYKNH DSILES YTGSI
msa118713.2{361_M781}	----VSGIGI	ISSLGKNYSE HKQHLFDLKE	GISKHLYKNH DSILES YTGSI
msa118713.2{361_18RS21}	----VSGIGI	ISSLGKNYSE HKQHLFDLKE	GISKHLYKNH DSILES YTGSI
msa118713.2{361_A909}	----VSGIGI	ISSLGKNYSE HKQHLFDLKE	GISKHLYKNH DSILES YTGSI
msa118713.2{361_COH1}	----VSGIGI	ISSLGKNYSE HKQHLFDLKE	GISKHLYKNH DSILES YTGSI
msa118713.2{361_H36B}	----VSGIGI	ISSLGKNYSE HKQHLFDLKE	GISKHLYKNH DSILES YTGSI
msa118713.2{361_JM9130013}	----VSGIGI	ISSLGKNYSE HKQHLFDLKE	GISKHLYKNH DSILES YTGSI
msa118713.2{361_M732}	----VSGIGI	ISSLGKNYSE HKQHLFDLKE	GISKHLYKNH DSILES YTGSI
msa118713.2{GBS361_2603}	msvyVSGIGI	ISSLGKNYSE HKQHLFDLKE	GISKHLYKNH DSILES YTGSI
Consensus	*****	*****	*****
	51		100
msa118713.2{361_090}	ITSDPEVPEQ	YKDETRNFKF AFTAFEEALA	SSGVNLKAYH NIAVCLGTSL
msa118713.2{361_1169NT}	ITSDPEVPEQ	YKDETRNFKF AFTAFEEALA	SSGVNLKAYH NIAVCLGTSL
msa118713.2{361_CJB110}	ITSDPEVPEQ	YKDETRNFKF AFTAFEEALA	SSGVNLKAYH NIAVCLGTSL
msa118713.2{361_M781}	ITSDPEVPEQ	YKDETRNFKF AFTAFEEALA	SSGVNLKAYH NIAVCLGTSL
msa118713.2{361_18RS21}	ITSDPEVPEQ	YKDETRNFKF AFTAFEEALA	SSGVNLKAYH NIAVCLGTSL

Table 75: Comparative Sequences relating to SAG0671

msa118713.2{361_A909}	ITSDPEVPEQ	YKDETRNFKF	AFTAFEEALA	SSGVNLKAYH	NIAVCLGTSL
msa118713.2{361_COH1}	ITSDPEVPEQ	YKDETRNFKF	AFTAFEEALA	SSGVNLKAYH	NIAVCLGTSL
msa118713.2{361_H36B}	ITSDPEVPEQ	YKDETRNFKF	AFTAFEEALA	SSGVNLKAYH	NIAVCLGTSL
msa118713.2{361_JM9130013}	ITSDPEVPEQ	YKDETRNFKF	AFTAFEEALA	SSGVNLKAYH	NIAVCLGTSL
msa118713.2{361_M732}	ITSDPEVPEQ	YKDETRNFKF	AFTAFEEALA	SSGVNLKAYH	NIAVCLGTSL
msa118713.2{GBS361_2603}	ITSDPEVPEQ	YKDETRNFKF	AFTAFEEALA	SSGVNLKAYH	NIAVCLGTSL
Consensus	*****	*****	*****	*****	*****
101					
msa118713.2{361_090}	GGKSAGQNAL	YQFEEGERQV	DASLLEKASV	YHIADELMAY	HDIVGASYVI
msa118713.2{361_1169NT}	GGKSAGQNAL	YQFEEGERQV	DASLLEKASV	YHIADELMAY	HDIVGASYVI
msa118713.2{361_CJB110}	GGKSAGQNAL	YQFEEGERQV	DASLLEKASV	YHIADELMAY	HDIVGASYVI
msa118713.2{361_M781}	GGKSAGQNAL	YQFEEGERQV	DASLLEKASV	YHIADELMAY	HDIVGASYVI
msa118713.2{361_18RS21}	GGKSAGQNAL	YQFEEGERQV	DASLLEKASV	YHIADELMAY	HDIVGASYVI
msa118713.2{361_A909}	GGKSAGQNAL	YQFEEGERQV	DASLLEKASV	YHIADELMAY	HDIVGASYVI
msa118713.2{361_COH1}	GGKSAGQNAL	YQFEEGERQV	DASLLEKASV	YHIADELMAY	HDIVGASYVI
msa118713.2{361_H36B}	GGKSAGQNAL	YQFEEGERQV	DASLLEKASV	YHIADELMAY	HDIVGASYVI
msa118713.2{361_JM9130013}	GGKSAGQNAL	YQFEEGERQV	DASLLEKASV	YHIADELMAY	HDIVGASYVI
msa118713.2{361_M732}	GGKSAGQNAL	YQFEEGERQV	DASLLEKASV	YHIADELMAY	HDIVGASYVI
msa118713.2{GBS361_2603}	GGKSAGQNAL	YQFEEGERQV	DASLLEKASV	YHIADELMAY	HDIVGASYVI
Consensus	*****	*****	*****	*****	*****
151					
msa118713.2{361_090}	STACSASNNA	VILGTQLLQD	GDCDLAICGG	CDELSDISLA	GFTSLGAIN
msa118713.2{361_1169NT}	STACSASNNA	VILGTQLLQD	GDCDLAICGG	CDELSDISLA	GFTSLGAIN
msa118713.2{361_CJB110}	STACSASNNA	VILGTQLLQD	GDCDLAICGG	CDELSDISLA	GFTSLGAIN
msa118713.2{361_M781}	STACSASNNA	VILGTQLLQD	GDCDLAICGG	CDELSDISLA	GFTSLGAIN
msa118713.2{361_18RS21}	STACSASNNA	VILGTQLLQD	GDCDLAICGG	CDELSDISLA	GFTSLGAIN
msa118713.2{361_A909}	STACSASNNA	VILGTQLLQD	GDCDLAICGG	CDELSDISLA	GFTSLGAIN
msa118713.2{361_COH1}	STACSASNNA	VILGTQLLQD	GDCDLAICGG	CDELSDISLA	GFTSLGAIN
msa118713.2{361_H36B}	STACSASNNA	VILGTQLLQD	GDCDLAICGG	CDELSDISLA	GFTSLGAIN
msa118713.2{361_JM9130013}	STACSASNNA	VILGTQLLQD	GDCDLAICGG	CDELSDISLA	GFTSLGAIN
msa118713.2{361_M732}	STACSASNNA	VILGTQLLQD	GDCDLAICGG	CDELSDISLA	GFTSLGAIN
msa118713.2{GBS361_2603}	STACSASNNA	VILGTQLLQD	GDCDLAICGG	CDELSDISLA	GFTSLGAIN
Consensus	*****	*****	*****	*****	*****
201					
msa118713.2{361_090}	EMACQPYSSG	KGINLGEAG	FVVLVKDQSL	AKYGKIIGGL	ITSDGYHITA
msa118713.2{361_1169NT}	EMACQPYSSG	KGINLGEAG	FVVLVKDQSL	AKYGKIIGGL	ITSDGYHITA
msa118713.2{361_CJB110}	EMACQPYSSG	KGINLGEAG	FVVLVKDQSL	AKYGKIIGGL	ITSDGYHITA
msa118713.2{361_M781}	EMACQPYSSG	KGINLGEAG	FVVLVKDQSL	AKYGKIIGGL	ITSDGYHITA
msa118713.2{361_18RS21}	EMACQPYSSG	KGINLGEAG	FVVLVKDQSL	AKYGKIIGGL	ITSDGYHITA
msa118713.2{361_A909}	EMACQPYSSG	KGINLGEAG	FVVLVKDQSL	AKYGKIIGGL	ITSDGYHITA
msa118713.2{361_COH1}	EMACQPYSSG	KGINLGEAG	FVVLVKDQSL	AKYGKIIGGL	ITSDGYHITA
msa118713.2{361_H36B}	EMACQPYSSG	KGINLGEAG	FVVLVKDQSL	AKYGKIIGGL	ITSDGYHITA
msa118713.2{361_JM9130013}	EMACQPYSSG	KGINLGEAG	FVVLVKDQSL	AKYGKIIGGL	ITSDGYHITA
msa118713.2{361_M732}	EMACQPYSSG	KGINLGEAG	FVVLVKDQSL	AKYGKIIGGL	ITSDGYHITA
msa118713.2{GBS361_2603}	EMACQPYSSG	KGINLGEAG	FVVLVKDQSL	AKYGKIIGGL	ITSDGYHITA
Consensus	*****	*****	*****	*****	*****
251					
msa118713.2{361_090}	PKPTGEGAAQ	IAKQLVTQAG	IDYSEIDYIN	GHGTGTQAND	KMEKNMYGKF
msa118713.2{361_1169NT}	PKPTGEGAAQ	IAKQLVTQAG	IDYSEIDYIN	GHGTGTQAND	KMEKNMYGKF
msa118713.2{361_CJB110}	PKPTGEGAAQ	IAKQLVTQAG	IDYSEIDYIN	GHGTGTQAND	KMEKNMYGKF
msa118713.2{361_M781}	PKPTGEGAAQ	IAKQLVTQAG	IDYSEIDYIN	GHGTGTQAND	KMEKNMYGKF
msa118713.2{361_18RS21}	PKPTGEGAAQ	IAKQLVTQAG	IDYSEIDYIN	GHGTGTQAND	KMEKNMYGKF
msa118713.2{361_A909}	PKPTGEGAAQ	IAKQLVTQAG	IDYSEIDYIN	GHGTGTQAND	KMEKNMYGKF
msa118713.2{361_COH1}	PKPTGEGAAQ	IAKQLVTQAG	IDYSEIDYIN	GHGTGTQAND	KMEKNMYGKF
msa118713.2{361_H36B}	PKPTGEGAAQ	IAKQLVTQAG	IDYSEIDYIN	GHGTGTQAND	KMEKNMYGKF
msa118713.2{361_JM9130013}	PKPTGEGAAQ	IAKQLVTQAG	IDYSEIDYIN	GHGTGTQAND	KMEKNMYGKF
msa118713.2{361_M732}	PKPTGEGAAQ	IAKQLVTQAG	IDYSEIDYIN	GHGTGTQAND	KMEKNMYGKF
msa118713.2{GBS361_2603}	PKPTGEGAAQ	IAKQLVTQAG	IDYSEIDYIN	GHGTGTQAND	KMEKNMYGKF
Consensus	*****	*****	*****	*****	*****
301					
msa118713.2{361_090}	FPTTTTLLISST	KGQTGHTLGA	AGIIELINCL	AAIEEQTVPA	TKNEIGIEGF
msa118713.2{361_1169NT}	FPTTTTLLISST	KGQTGHTLGA	AGIIELINCL	AAIEEQTVPA	TKNEIGIEGF
msa118713.2{361_CJB110}	FPTTTTLLISST	KGQTGHTLGA	AGIIELINCL	AAIEEQTVPA	TKNEIGIEGF
msa118713.2{361_M781}	FPTTTTLLISST	KGQTGHTLGA	AGIIELINCL	AAIEEQTVPA	TKNEIGIEGF
msa118713.2{361_18RS21}	FPTTTTLLISST	KGQTGHTLGA	AGIIELINCL	AAIEEQTVPA	TKNEIGIEGF
msa118713.2{361_A909}	FPTTTTLLISST	KGQTGHTLGA	AGIIELINCL	AAIEEQTVPA	TKNEIGIEGF
msa118713.2{361_COH1}	FPTTTTLLISST	KGQTGHTLGA	AGIIELINCL	AAIEEQTVPA	TKNEIGIEGF
msa118713.2{361_H36B}	FPTTTTLLISST	KGQTGHTLGA	AGIIELINCL	AAIEEQTVPA	TKNEIGIEGF
msa118713.2{361_JM9130013}	FPTTTTLLISST	KGQTGHTLGA	AGIIELINCL	AAIEEQTVPA	TKNEIGIEGF
msa118713.2{361_M732}	FPTTTTLLISST	KGQTGHTLGA	AGIIELINCL	AAIEEQTVPA	TKNEIGIEGF
msa118713.2{GBS361_2603}	FPTTTTLLISST	KGQTGHTLGA	AGIIELINCL	AAIEEQTVPA	TKNEIGIEGF
Consensus	*****	*****	*****	*****	*****
351					
msa118713.2{361_090}	PENFVYHQKR	EYPIRNALNF	SFAFGGNNSG	ILLSSLDSP	ETLPARENLK
msa118713.2{361_1169NT}	PENFVYHQKR	EYPIRNALNF	SFAFGGNNSG	ILLSSLDSP	ETLPARENLK
msa118713.2{361_CJB110}	PENFVYHQKR	EYPIRNALNF	SFAFGGNNSG	ILLSSLDSP	ETLPARENLK
msa118713.2{361_M781}	PENFVYHQKR	EYPIRNALNF	SFAFGGNNSG	ILLSSLDSP	ETLPARENLK

Table 75: Comparative Sequences relating to SAG0671

msa118713.2{361_18RS21}	PENFVYHQKR	EYPIRNALNF	SFAFGGNNSG	VLLSSLDSPL	ETLPARENLK
msa118713.2{361_A909}	PENFVYHQKR	EYPIRNALNF	SFAFGGNNSG	VLLSSLDSPL	ETLPARENLK
msa118713.2{361_COH1}	PENFVYHQKR	EYPIRNALNF	SFAFGGNNSG	VLLSSLDSPL	ETLPARENLK
msa118713.2{361_H36B}	PENFVYHQKR	EYPIRNALNF	SFAFGGNNSG	VLLSSLDSPL	ETLPARENLK
msa118713.2{361_JM9130013}	PENFVYHQKR	EYPIRNALNF	SFAFGGNNSG	VLLSSLDSPL	ETLPARENLK
msa118713.2{361_M732}	PENFVYHQKR	EYPIRNALNF	SFAFGGNNSG	VLLSSLDSPL	ETLPARENLK
msa118713.2{GBS361_2603}	PENFVYHQKR	EYPIRNALNF	SFAFGGNNSG	VLLSSLDSPL	ETLPARENLK
Consensus	*****	*****	*****	-*****	*****
401					
msa118713.2{361_090}	MAILSSVASI	SKNESLSITY	EKVASNFNDF	EALRFKGARP	PKTVNPAQFR
msa118713.2{361_1169NT}	MAILSSVASI	SKNESLSITY	EKVASNFNDF	EALRFKGARP	PKTVNPAQFR
msa118713.2{361_CJB110}	MAILSSVASI	SKNESLSITY	EKVASNFNDF	EALRFKGARP	PKTVNPAQFR
msa118713.2{361_M781}	MAILSSVASI	SKNESLSITY	EKVASNFNDF	EALRFKGARP	PKTVNPAQFR
msa118713.2{361_18RS21}	MAILSSVASI	SKNESLSITY	EKVASNFNDF	EALRFKGARP	PKTVNPAQFR
msa118713.2{361_A909}	MAILSSVASI	SKNESLSITY	EKVASNFNDF	EALRFKGARP	PKTVNPAQFR
msa118713.2{361_COH1}	MAILSSVASI	SKNESLSITY	EKVASNFNDF	EALRFKGARP	PKTVNPAQFR
msa118713.2{361_H36B}	MAILSSVASI	SKNESLSITY	EKVASNFNDF	EALRFKGARP	PKTVNPAQFR
msa118713.2{361_JM9130013}	MAILSSVASI	SKNESLSITY	EKVASNFNDF	EALRFKGARP	PKTVNPAQFR
msa118713.2{361_M732}	MAILSSVASI	SKNESLSITY	EKVASNFNDF	EALRFKGARP	PKTVNPAQFR
msa118713.2{GBS361_2603}	MAILSSVASI	SKNESLSITY	EKVASNFNDF	EALRFKGARP	PKTVNPAQFR
Consensus	*****	*****	*****	*****	*****
451					
msa118713.2{361_090}	KMDDFSKMVA	VTTAALIES	NINLKKQDTS	KVGIVFTTLS	GPVEVVEGIE
msa118713.2{361_1169NT}	KMDDFSKMVA	VTTAALIES	NINLKKQDTS	KVGIVFTTLS	GPVEVVEGIE
msa118713.2{361_CJB110}	KMDDFSKMVA	VTTAALIES	NINLKKQDTS	KVGIVFTTLS	GPVEVVEGIE
msa118713.2{361_M781}	KMDDFSKMVA	VTTAALIES	NINLKKQDTS	KVGIVFTTLS	GPVEVVEGIE
msa118713.2{361_18RS21}	KMDDFSKMVA	VTTAALIES	NINLKKQDTS	KVGIVFTTLS	GPVEVVEGIE
msa118713.2{361_A909}	KMDDFSKMVA	VTTAALIES	NINLKKQDTS	KVGIVFTTLS	GPVEVVEGIE
msa118713.2{361_COH1}	KMDDFSKMVA	VTTAALIES	NINLKKQDTS	KVGIVFTTLS	GPVEVVEGIE
msa118713.2{361_H36B}	KMDDFSKMVA	VTTAALIES	NINLKKQDTS	KVGIVFTTLS	GPVEVVEGIE
msa118713.2{361_JM9130013}	KMDDFSKMVA	VTTAALIES	NINLKKQDTS	KVGIVFTTLS	GPVEVVEGIE
msa118713.2{361_M732}	KMDDFSKMVA	VTTAALIES	NINLKKQDTS	KVGIVFTTLS	GPVEVVEGIE
msa118713.2{GBS361_2603}	KMDDFSKMVA	VTTAALIES	NINLKKQDTS	KVGIVFTTLS	GPVEVVEGIE
Consensus	*****	*****	*****	*****	*****
501					
msa118713.2{361_090}	KQITTEGYAH	VSASRFPFTV	MNAAAGMLSI	IFKITGPLSV	ISTNSGALDG
msa118713.2{361_1169NT}	KQITTEGYAH	VSASRFPFTV	MNAAAGMLSI	IFKITGPLSV	ISTNSGALDG
msa118713.2{361_CJB110}	KQITTEGYAH	VSASRFPFTV	MNAAAGMLSI	IFKITGPLSV	ISTNSGALDG
msa118713.2{361_M781}	KQITTEGYAH	VSASRFPFTV	MNAAAGMLSI	IFKITGPLSV	ISTNSGALDG
msa118713.2{361_18RS21}	KQITTEGYAH	VSASRFPFTV	MNAAAGMLSI	IFKITGPLSV	ISTNSGALDG
msa118713.2{361_A909}	KQITTEGYAH	VSASRFPFTV	MNAAAGMLSI	IFKITGPLSV	ISTNSGALDG
msa118713.2{361_COH1}	KQITTEGYAH	VSASRFPFTV	MNAAAGMLSI	IFKITGPLSV	ISTNSGALDG
msa118713.2{361_H36B}	KQITTEGYAH	VSASRFPFTV	MNAAAGMLSI	IFKITGPLSV	ISTNSGALDG
msa118713.2{361_JM9130013}	KQITTEGYAH	VSASRFPFTV	MNAAAGMLSI	IFKITGPLSV	ISTNSGALDG
msa118713.2{361_M732}	KQITTEGYAH	VSASRFPFTV	MNAAAGMLSI	IFKITGPLSV	ISTNSGALDG
msa118713.2{GBS361_2603}	KQITTEGYAH	VSASRFPFTV	MNAAAGMLSI	IFKITGPLSV	ISTNSGALDG
Consensus	*****	*****	*****	*****	*****
551					
msa118713.2{361_090}	IQYAKEMMRN	DNLDYVILVS	ANQWTDMSFM	WWQQLNYDSQ	MFVGS DYCSA
msa118713.2{361_1169NT}	IQYAKEMMRN	DNLDYVILVS	ANQWTDMSFM	WWQQLNYDSQ	MFVGS DYCSA
msa118713.2{361_CJB110}	IQYAKEMMRN	DNLDYVILVS	ANQWTDMSFM	WWQQLNYDSQ	MFVGS DYCSA
msa118713.2{361_M781}	IQYAKEMMRN	DNLDYVILVS	ANQWTDMSFM	WWQQLNYDSQ	MFVGS DYCSA
msa118713.2{361_18RS21}	IQYAKEMMRN	DNLDYVILVS	ANQWTDMSFM	WWQQLNYDSQ	MFVGS DYCSA
msa118713.2{361_A909}	IQYAKEMMRN	DNLDYVILVS	ANQWTDMSFM	WWQQLNYDSQ	MFVGS DYCSA
msa118713.2{361_COH1}	IQYAKEMMRN	DNLDYVILVS	ANQWTDMSFM	WWQQLNYDSQ	MFVGS DYCSA
msa118713.2{361_H36B}	IQYAKEMMRN	DNLDYVILVS	ANQWTDMSFM	WWQQLNYDSQ	MFVGS DYCSA
msa118713.2{361_JM9130013}	IQYAKEMMRN	DNLDYVILVS	ANQWTDMSFM	WWQQLNYDSQ	MFVGS DYCSA
msa118713.2{361_M732}	IQYAKEMMRN	DNLDYVILVS	ANQWTDMSFM	WWQQLNYDSQ	MFVGS DYCSA
msa118713.2{GBS361_2603}	IQYAKEMMRN	DNLDYVILVS	ANQWTDMSFM	WWQQLNYDSQ	MFVGS DYCSA
Consensus	*****	*****	*****	*****	*****
601					
msa118713.2{361_090}	QVLSRQALDN	SPIILGSKQL	KYSHKTFTDV	MTIFDAALQN	LLSDLGLTIK
msa118713.2{361_1169NT}	QVLSRQALDN	SPIILGSKQL	KYSHKTFTDV	MTIFDAALQN	LLSDLGLTIK
msa118713.2{361_CJB110}	QVLSRQALDN	SPIILGSKQL	KYSHKTFTDV	MTIFDAALQN	LLSDLGLTIK
msa118713.2{361_M781}	QVLSRQALDN	SPIILGSKQL	KYSHKTFTDV	MTIFDAALQN	LLSDLGLTIK
msa118713.2{361_18RS21}	QVLSRQALDN	SPIILGSKQL	KYSHKTFTDV	MTIFDAALQN	LLSDLGLTIK
msa118713.2{361_A909}	QVLSRQALDN	SPIILGSKQL	KYSHKTFTDV	MTIFDAALQN	LLSDLGLTIK
msa118713.2{361_COH1}	QVLSRQALDN	SPIILGSKQL	KYSHKTFTDV	MTIFDAALQN	LLSDLGLTIK
msa118713.2{361_H36B}	QVLSRQALDN	SPIILGSKQL	KYSHKTFTDV	MTIFDAALQN	LLSDLGLTIK
msa118713.2{361_JM9130013}	QVLSRQALDN	SPIILGSKQL	KYSHKTFTDV	MTIFDAALQN	LLSDLGLTIK
msa118713.2{361_M732}	QVLSRQALDN	SPIILGSKQL	KYSHKTFTDV	MTIFDAALQN	LLSDLGLTIK
msa118713.2{GBS361_2603}	QVLSRQALDN	SPIILGSKQL	KYSHKTFTDV	MTIFDAALQN	LLSDLGLTIK
Consensus	*****	*****	*****	*****	*****
651					
msa118713.2{361_090}	DIKGFVWNER	KKAVSSDYDF	LANLSEYYNM	PNLASGQFGF	SSNGAGEELD
msa118713.2{361_1169NT}	DIKGFVWNER	KKAVSSDYDF	LANLSEYYNM	PNLASGQFGF	SSNGAGEELD
msa118713.2{361_CJB110}	DIKGFVWNER	KKAVSSDYDF	LANLSEYYNM	PNLASGQFGF	SSNGAGEELD
700					

Table 75: Comparative Sequences relating to SAG0671

msa118713.2{361_M781}	DIKGFVWNER	KKAVSSDYDF	LANLSEYYNM	PNLASGQFGF	SSNGAGEELD
msa118713.2{361_18RS21}	DIKGFVWNER	KKAVSSDYDF	LANLSEYYNM	PNLASGQFGF	SSNGAGEELD
msa118713.2{361_A909}	DIKGFVWNER	KKAVSSDYDF	LANLSEYYNM	PNLASGQFGF	SSNGAGEELD
msa118713.2{361_COH1}	DIKGFVWNER	KKAVSSDYDF	LANLSEYYNM	PNLASGQFGF	SSNGAGEELD
msa118713.2{361_H36B}	DIKGFVWNER	KKAVSSDYDF	LANLSEYYNM	PNLASGQFGF	SSNGAGEELD
msa118713.2{361_JM9130013}	DIKGFVWNER	KKAVSSDYDF	LANLSEYYNM	PNLASGQFGF	SSNGAGEELD
msa118713.2{361_M732}	DIKGFVWNER	KKAVSSDYDF	LANLSEYYNM	PNLASGQFGF	SSNGAGEELD
msa118713.2{GBS361_2603}	DIKGFVWNER	KKAVSSDYDF	LANLSEYYNM	PNLASGQFGF	SSNGAGEELD
Consensus	*****	*****	*****	*****	*****
msa118713.2{361_090}	YTVNESIEKG	YYLVLSYSIF	GGISFAIEK	R	731
msa118713.2{361_1169NT}	YTVNESIEKG	YYLVLSYSIF	GGISFAIEK	R	
msa118713.2{361_CJB110}	YTVNESIEKG	YYLVLSYSIF	GGISFAIEK	R	
msa118713.2{361_M781}	YTVNESIEKG	YYLVLSYSIF	GGISFAIEK	R	
msa118713.2{361_18RS21}	YTVNESIEKG	YYLVLSYSIF	GGISFAIEK	R	
msa118713.2{361_A909}	YTVNESIEKG	YYLVLSYSIF	GGISFAIEK	R	
msa118713.2{361_COH1}	YTVNESIEKG	YYLVLSYSIF	GGISFAIEK	R	
msa118713.2{361_H36B}	YTVNESIEKG	YYLVLSYSIF	GGISFAIEK	R	
msa118713.2{361_JM9130013}	YTVNESIEKG	YYLVLSYSIF	GGISFAIEK	R	
msa118713.2{361_M732}	YTVNESIEKG	YYLVLSYSIF	GGISFAIEK	R	
msa118713.2{GBS361_2603}	YTVNESIEKG	YYLVLSYSIF	GGISFAIEK	R	
Consensus	*****	*****	*****	*	

Table 76: Comparative Sequences relating to SAG0260

SEQ ID NO. 7601

STRAIN 2603

ATGAAAAAAGTCATCGATTTAAAAAACTACAAAAAGCATATGCCTCAGAAACCGTTTTA
 AATAATATTAATTTGGAGGTGTTTTAAAGGCGAAATAATTGGATTAATAGGACCCTCTGGA
 GCAGGGAAATCTACCTTGATTAAAACTATGCTTGGCATGGAAAAAGCAGATAAGGGAACA
 GCTCTTGTCTTGATACTCAAATGCCAGATCGTAATATTTTAAATCAAATTGGCTATATG
 GCTCAATCTGATGCCCTTATACGAGTCTTTAACTGGCTTAGAAAATTTATTATTCTTTGGA
 AAAATGAAAGGTATTCAAAAACTGAATTTAAACAGCAGATAACTCATATTTCTAAAGTA
 GTAGATCTAGAAAACCAACTTGATAAATTTGTCTCAGGTTACTCAGGAGGTATGAAAAGA
 CGGCTTTCTCTAGCCATCGCCCTACTTGGAAACCCACAGTTTTAATCCTAGATGAACCT
 ACCGTTGGAATTGATCCATCCTTGAGGAGAAAAATCTGGCAAGAGCTAATTAATATTAAG
 GATGAAGGACATTCTATCTTTATTACAACCCACGTTATGGATGAAGCAGAATTAACAAGT
 AAGGTTGCCTACTATTACGTGGAAACATTATTGCCTTTGATACTCCATTACATTTAAAA
 AAACAATTTAATGTGAGTACTATTGAGGAAGTTTTCTTAAAAGCTGAAGGAGAA

SEQ ID NO. 7602

STRAIN 090

ATTTAAAAAACTACAAAAAGCATATGCCTCAGAAACTGTTTTAAATAAT
 ATTAATTTGGAGGTGTTTTAAAGGCGAAATAATTGGATTAATAGGACCCTC
 TGGAGCAGGGAAATCTACCTTGATTAAAACTATGCTTGGCATGGAAAAAG
 CAGATAAGGGAACAGCTCTTGTCTTGATACTCAAATGCCAGATCGTAAT
 ATTTTAAATCAAATTGGCTATATGGCTCAATCTGATGCCCTTATACGAATC
 TTTAACTGCCCTTAGAAaATTTATTATTCTTTGGAAAAATGAAAGGTATTCT
 AAAAACTGAATTTAAACAGCAGATAACTCATATTTCTAAAGTAGTAGAT
 CTAGAAAACCAACTTGATAAATTTGTCTCAGGTTACTCAGGAGGTATGAA
 AAGACGGCTTTCTCTAGCCATCGCCCTACTTGGAAACCCACAGTTTTAA
 TCCTAGATGAACCTACCGTTGGAATTGATCCATCCTTGAGGAGAAAAATC
 TGGCAAGAGCTAATTAATATTAaGGATGAAGGACGTTCTATCTTTATTAC
 AACCCACGTTATGGATGAAGCAGAATTAACAAGTAAGGTTGCACTACTAT
 TACGTGGAAACATTATTGCCTTTGATACTCCATTACATTTAAAAAAACAA
 TTTAATGTGAGTACTATTGAGGAAGTTTTCTTAAAAGCTGAAGGAGAA

SEQ ID NO. 7603

STRAIN A909

AAAAAAGTCATCGATTTAAAAAACTACAAAAAGCATATGCCTCA
 GAAACCGTTTTAAATAATATTAATTTGGAGGTGTTTTAAAGGCGAAATAAT
 TGGATTAATAGGACCCTCTGGAGCAGGGAAATCTACCTTGATTAAAACTA
 TGCTTGGCATGGAAAAAGCAGATAAGGGAACAGCTCTTGTCTTGATACT
 CAAATGCCAGATCATAATATTTTAAATCAAATTGGCTATATGGCTCAATC
 TGATGCCCTTATACGAGTCTTTAACTGGCTTAGAAAATTTATTATTCTTTG
 GAAAAATGAAAGGTATTCAAAAACTGAATTTAAACAGCAGATAACTCAT
 ATTTCTAAAGTAGTAGATCTAGAAAACCAACTTGATAAATTTGTCTCAGG
 TTACTCAGGAGGTATGAAAAGACGGCTTTCTCTAGCCATCGCCCTACTTG
 GAAACCCACAGTTTTAATCCTAGATGAACCTACCGTTGGAATTGATCCA
 TCCTTGAGGAGAAAAATCTGGCAAGAGCTAATTAATATTAAGGATGAAGG
 ACGTTCTATCTTTATTACAACCCACGTTATGGATGAAGCAGAATTAACAA
 GTAAGGTTGCACTACTATTACGTGGAAACATTATTGCCTTTGATACTCCA
 TTACATTTAAAAAAACAAATTTAATGTGAGTACTATTGAGGAAGTTTTCTT
 AAAAGCTGAAGGAGAA

SEQ ID NO. 7604

STRAIN H36B

AAAAAAGTCATTGATTTAAAAAACTACAAAAAGCATATGCC
 TCAGAAACCGTTTTAAATAATATTAATTTGGAGGTGTTTTAAAGGCGAAAT
 AATTGGATTAATAGGACCCTCTGGAGCAGGGAAATCTACCTTGATTAAAA
 CTATGCTTGGCATGGAAAAAGCAGATAAGGGAaCAGCTCTTGTCTTGAT
 ACTCAAATGCCAGATCGTAATATTTTAAATCAAATTGGCTATATGGCTCA
 ATCTGATGCCCTTATACGAGTCTTTAACTGGCTTAGAAAATTTATTATTCT
 TTGGAAAAATGAAAGGTATTCAAAAACTGAATTTAAACAGCAGATAACT
 CATATTTCTAAAGTAGTAGATCTAGAAAACCAACTTGATAAATTTGTCTC
 AGGTTACTCAGGAGGTATGAAAAGACGGCTTTCTCTAGCCATCGCCCTAC
 TTGGAAACCCACAGTTTTAATCCTAGATGAACCTACCGTTGGAATTGAT
 CCATCCTTGAGGAGAAAAATCTGGCAAGAGCTAATTAATATTAAGGATGA
 AGGACGTTCTATCTTTATTACAACCCACGTTATGGATGAAGCAGAATTA
 CAAGTAAGGTTGCACTACTATTACGTGGAAACATTATTGCCTTTGATACT
 CCATTACATTTAAAAAAACAAATTTAATGTGAGTACTATTGAGGAAGTTTT
 CTTAAAAGCTGAAGGAGAA

SEQ ID NO. 7605

STRAIN 18RS21

GATTTAAAAAACTACAAAAAGCATATGCCTCAGAAACCGTTTTAAATAA
 TATTAATTTGGAGGTGTTTTAAAGGCGAAATAATTGGATTAATAGGACCCT
 TGGAGCAGGGAAATCTACCTTGATTAAAACTATGCTTGGCATGGAAAAA
 GCAGATAAGGGAACAGCTCTTGTCTTGATACTCAAATGCCAGATCGTAA
 TATTTTAAATCAAATTGGCTATATGGCTCAATCTGATGCCCTTATACGAGT
 CTTTAACTGGCTTAGAAAATTTATTATTCTTTGGAAAAATGAAAGGTATT
 CAAAAAAGTGAATTTAAACAGCAGATAACTCATATTTCTAAAGTAGTAGA
 TCTAGAAAACCAACTTGATAAATTTGTCTCAGGTTACTCAGGAGGTATGA
 AAAGACGGCTTTCTCTAGCCATCGCCCTACTTGGAAACCCACAGTTTTA
 ATCCTAGATGAACCTACCGTTGGAATTGATCCATCCTTGAGGAGAAAAAT
 CTGGCAAGAGCTAATTAATATTAaGGATGAAGGACATTCTATCTTTATTA
 CAACCCACGTTATGGATGAAGCAGAATTAACAAGTAAGGTTGCACTACTA

Table 76: Comparative Sequences relating to SAG0260

TTACGTGGAAACATTATTGCCTTTGATACTCCATTACATTTAAAAAAACA
ATTTAATGTGAGTACTATTGAGGAAGTTTTCTTAAAAAGCTGAAGGAGAA

SEQ ID NO. 7606**STRAIN M732**

AAAAAAGTCATCGATTTAAAAAACTACAAAAAGCATACGCCTCA
GAAACTGTTTTAAATAATATTAATTTGGAGGTGTTTAAAGGAGAAATAAT
TGGATTAATAGGACCCTCTGGAGCAGGGAAATCTACCTTGATTAAAACTA
TGCTTGGCATGGAAAAAGCAGATAAGGGAACAGCTCTTGTTCTTGATACT
CAAATGCCAGATCGTAATATTTTAAATCAAATTGGCTATATGGCTCAATC
TGATGCCTTACACGAGTCTTTAACTGGCTTAGAAAAATTTATTATTCTTTG
GAAAAATGAAAGGTATTCAAAAACTGAATTAAAAACAGCAGATAACTCAT
ATTTCTAAAGTAGTAGATCTAGAAAACCAACTTGATAAATTTGTCTCAGG
TTACTCAGGAGGTATGAAAAGACGGCTTTCTCTAGCCATCGCCCTACTTG
GAAACCCACAGTTTTAATCCTAGATGAACCTACCGTTGGAATTGATCCA
TCCTTGAGGAGAAAAATCTGGCAAGAGCTAATTAATATTAAGGATGAAGG
ACGTTCTATCTTTATTACAACCCACGTTATGGATGAAGCAGAATTAACAA
GTAAGGTTGCACTACTATTACGTGGAAACATTATTGCCTTTGATACTCCA
TTACATTTAAAAAAACAATTTAATGTGAGTACTATTGAGGAAGTTTTCTT
AAAAGCTGAAGGAGAA

SEQ ID NO. 7607**STRAIN COH1**

AAAAAAGTCATCGATTTAAAAAACTACAAAAAGCATACGCCTCAGAA
ACTGTTTTAAATAATATTAATTTGGAGGTGTTTAAAGGAGAAATAATTGG
ATTAATAGGACCCTCTGGAGCAGGGAAATCTACCTTGATTAAAACTATGC
TTGGCATGGAAAAAGCAGATAAGGGAACAGCTCTTGTTCTTGATACTCAA
ATGCCAGATCGTAATATTTTAAATCAAATTGGCTATATGGCTCAATCTGA
TGCTTTACACGAGTCTTTAACTGGCTTAGAAAAATTTATTATTCTTTGGAA
AAATGAAAGGTATTCAAAAACTGAATTAAAAACAGCAGATAACTCATATT
TCTAAAGTAGTAGATCTAGAAAACCAACTTGATAAATTTGTCTCAGGTTA
CTCAGGAGGTATGAAAAGACGGCTTTCTCTAGCCATCGCCCTACTTGGA
ACCCACAGTTTTAATCCTAGATGAACCTACCGTTGGAATTGATCCATCC
TTGAGGAGAAAAATCTGGCAAGAGCTAATTAATATTAAGGATGAAGGACG
TTCTATCTTTATTACAACCCACGTTATGGATGAAGCAGAATTAACAAAGTA
AGGTTGCACTACTATTACGTGGAAACATTATTGCCTTTGATACTCCATTA
CATTTAAAAAAACAATTTAATGTGAGTACTATTGAGGAAG

SEQ ID NO. 7608**STRAIN M781**

AAAAAAGTCATCGATTTAAAAAACTACAAAAAGCATAC
GCCTCAGAAACTGTTTTAAATAATATTAATTTGGAGGTGTTTAAAGGAGA
AATAATTGGATTAAATAGGACCCTCTGGAGCAGGGAAATCTACCTTGATTAA
AACTATGCTTGGCATGGAAAAAGCAGATAAGGGAACAGCTCTTGTTCTT
GATACTCAAATGCCAGATCGTAATATTTTAAATCAAATTGGCTATATGGC
TCAATCTGATGCCTTACACGAGTCTTTAACTGGCTTAGAAAAATTTATTAT
TCTTTGGAAAAATGAAAGGTATTCAAAAACTGAATTAAAAACAGCAGATA
ACTCATATTTCTAAAGTAGTAGATCTAGAAAACCAACTTGATAAATTTGT
CTCAGGTTACTCAGGAGGTATGAAAAGACGGCTTTCTCTAGCCATCGCCC
TACTTGGAAACCCACAGTTTTAATCCTAGATGAACCTACCGTTGGAATT
GATCCATCCTTGAGGAGAAAAATCTGGCAAGAGCTAATTAATATTAAGGA
TGAAGGACGTTCTATCTTTATTACAACCCACGTTATGGATGAAGCAGAAT
TAACAAGTAAGGTTGCACTACTATTACGTGGAAACATTATTGCCTTTGAT
ACTCCATTACATTTAAAAAAACAATTTAATGTGAGTACTATTGAGGAAGT
TTTTCTTAAAAAGCTGAAGGAGAA

SEQ ID NO. 7609**STRAIN CJB110**

AAAAAAGTCATCGATTTAAAAAACTACAAAAAGCATATG
CCTCAGAAACTGTTTTAAATAATATTAATTTGGAGGTGTTTAAAGGCGAA
ATAATTGGATTAAATAGGACCCTCTGGAGCAGGGAAATCTACCTTGATTAA
AACTATGCTTGGCATGGAAAAAGCAGATAAGGGAACAGCTCTTGTTCTTG
ATACTCAAATGCCAGATCGTAATATTTTAAATCAAATTGGCTATATGGCT
CAATCTGATGCCTTATACGAATCTTTAACTGCCTTAGAAAAATTTATTATT
CTTTGGAAAAATGAAAGGTATTCAAAAACTGAATTAAAAACAGCAGATAA
CTCATATTTCTAAAGTAGTAGATCTAGAAAACCAACTTGATAAATTTGTC
TCAGGTTACTCAGGAGGTATGAAAAGACGGCTTTCTCTAGCCATCGCCCT
ACTTGGAAACCCACAGTTTTAATCCTAGATGAACCTACCGTTGGAATTG
ATCCATCCTTGAGGAGAAAAATCTGGCAAGAGCTAATTAATATTAAGGAT
GAAGGACGTTCTATCTTTATTACAACCCACGTTATGGATGAAGCAGAATT
AACAAGTAAGGTTGCACTACTATTACGTGGAAACATTATTGCCTTTGATA
CTCCATTACATTTAAAAAAACAATTTAATGTGAGTACTATTGAGGAAGTT
TTCTTAAAAAGCTGAAGGAGAA

SEQ ID NO. 7610**STRAIN 1169NT**

AAAAAAGTCATCGATTTAAAAAACTACAAAAAGCATAC
GCCTCAGAAACTGTTTTAAATAATATTAATTTGGAGGTGTTTAAAGGCGA
AATAATTGGATTAAATAGGACCCTCTGGAGCAGGGAAATCTACCTTGATTAA
AACTATGCTTGGCATGGAAAAAGCAGATAAGGGAACAGCTCTTGTTCTT
GATACTCAAATGCCAGATCGTAATATTTTAAATCAAATTGGCTATATGGC
TCAATCTGATGCCTTATACGAATCTTTAACTGCCTTAGAAAAATTTATTAT

Table 76: Comparative Sequences relating to SAG0260

TCTTTGGAAAAATGAAAGGTATTCAAAAACTGAATTAAAAACAGCAGATA
 ACTCATATTTCTAAAGTAGTAGATCTAGAAAACCAACTTGATAAATTTGT
 CTCAGGTTACTCAGGAGGTATGAAAAGACGGCTTTCTCTAGCCATCGCCC
 TACTTGGAAACCCACAGTTTAAATCCTAGATGAACCTACCGTTGGAATT
 GATCCATCCTTGAGGAGAAAAATCTGGCAAGAGCTAATTAATATTAAGGA
 TGAAGGACGTTCTATCTTTATTACAACCCACGTTATGGATGAAGCAGAAT
 TAACAAGTAAGGTTGCACTACTATTACGTGGAAACATTATTGCCTTTGAT
 ACTCCATTACATTTAAAAAACAATTTAATGTGAGTACTATTGAGGAAGT
 TTTCTTAAAAGCTGAAGGAGAA

SEQ ID NO. 7611

STRAIN JM9130013

AAAAAAGTCATCGATTTAAAAAACTACAAAAAGCATATGCC
 TCAGAAACCGTTTTAAATAATATTAATTTGGAGGTGTTTAAAGGCGAAAT
 AATTGGATTAAATAGGACCCTCTGGAGCAGGGAAATCTACCTTGATTAAAA
 CTATGCTTGGCATGGAAGAACAGATAAGGGAACAGCTCTTGTTCTTGAT
 ACTCAAATGCCAGATCGTAATATTTTAAATCAAATTGGCTATATGGCTCA
 ATCTGATGCCCTTATACGAGTCTTTAACTGGCTTAGAAAAATTTATTATTCT
 TTGGAAAAATGAAAGGTATTCAAAAACTGAATTAAAAACAGCAGATAACT
 CATATTTCTAAAGTAGTAGATCTAGAAAACCAACTTGATAAATTTGTCTC
 AGGTTACTCAGGAGGTATGAAAAGACGGCTTTCTCTAGCCATCGCCCTAC
 TTGGAAACCCACAGTTTAAATCCTAGATGAACCTACCGTTGGAATTGAT
 CCATCCCTTGAGGAGAAAAATCTGGCAAGAGCTAATTAATATTAAGGATGA
 AGGACGTTCTATCTTTATTACAACCCACGTTATGGATGAAGCAGAATTAA
 CAAGTAAGGTTGCACTACTATTACGTGGAAACATTATTGCCTTTGATACT
 CCATTACATTTAAAAAACAATTTAATGTGAGTACTATTGAGGAAGTTTT
 CTTAAAAGCTGAAGGAGAA

PRETTY of: /biotmp/msa134270.2{*} April 10, 2003 02:14 ..

	1		50
msa134270.2{391_COH1}	---aaaaaag tcatcgATTT	AAAAAACTA CAAAAAGCAT	AcGCCTCAGA
msa134270.2{391_M732}	---aaaaaag tcatcgATTT	AAAAAACTA CAAAAAGCAT	AcGCCTCAGA
msa134270.2{391_M781}	---aaaaaag tcatcgATTT	AAAAAACTA CAAAAAGCAT	AcGCCTCAGA
msa134270.2{391_090}	-----ATTT	AAAAAACTA CAAAAAGCAT	AtGCCTCAGA
msa134270.2{391_CJB110}	---aaaaaag tcatcgATTT	AAAAAACTA CAAAAAGCAT	AtGCCTCAGA
msa134270.2{391_1169NT}	---aaaaaag tcatcgATTT	AAAAAACTA CAAAAAGCAT	AcGCCTCAGA
msa134270.2{391_18RS21}	-----gATTT	AAAAAACTA CAAAAAGCAT	AtGCCTCAGA
msa134270.2{391_2603}	atgaaaaaag tcatcgATTT	AAAAAACTA CAAAAAGCAT	AtGCCTCAGA
msa134270.2{391_A909}	---aaaaaag tcatcgATTT	AAAAAACTA CAAAAAGCAT	AtGCCTCAGA
msa134270.2{391_JM9130013}	---aaaaaag tcatcgATTT	AAAAAACTA CAAAAAGCAT	AtGCCTCAGA
msa134270.2{391_H36B}	---aaaaaag tcattgATTT	AAAAAACTA CAAAAAGCAT	AtGCCTCAGA
Consensus	***-----*****	*****	*-*****

	51		100
msa134270.2{391_COH1}	AACtGTTTTA AATAATATTA ATTTGGAGGT	GTTTAAAGGa GAAATAATTG	
msa134270.2{391_M732}	AACtGTTTTA AATAATATTA ATTTGGAGGT	GTTTAAAGGa GAAATAATTG	
msa134270.2{391_M781}	AACtGTTTTA AATAATATTA ATTTGGAGGT	GTTTAAAGGa GAAATAATTG	
msa134270.2{391_090}	AACtGTTTTA AATAATATTA ATTTGGAGGT	GTTTAAAGGc GAAATAATTG	
msa134270.2{391_CJB110}	AACtGTTTTA AATAATATTA ATTTGGAGGT	GTTTAAAGGc GAAATAATTG	
msa134270.2{391_1169NT}	AACtGTTTTA AATAATATTA ATTTGGAGGT	GTTTAAAGGc GAAATAATTG	
msa134270.2{391_18RS21}	AACcGTTTTA AATAATATTA ATTTGGAGGT	GTTTAAAGGc GAAATAATTG	
msa134270.2{391_2603}	AACcGTTTTA AATAATATTA ATTTGGAGGT	GTTTAAAGGc GAAATAATTG	
msa134270.2{391_A909}	AACcGTTTTA AATAATATTA ATTTGGAGGT	GTTTAAAGGc GAAATAATTG	
msa134270.2{391_JM9130013}	AACcGTTTTA AATAATATTA ATTTGGAGGT	GTTTAAAGGc GAAATAATTG	
msa134270.2{391_H36B}	AACcGTTTTA AATAATATTA ATTTGGAGGT	GTTTAAAGGc GAAATAATTG	
Consensus	***-*****	*****	*****

	101		150
msa134270.2{391_COH1}	GATTAATAGG ACCCTCTGGA GCAGGGAAAT	CTACCTTGAT TAAAACTATG	
msa134270.2{391_M732}	GATTAATAGG ACCCTCTGGA GCAGGGAAAT	CTACCTTGAT TAAAACTATG	
msa134270.2{391_M781}	GATTAATAGG ACCCTCTGGA GCAGGGAAAT	CTACCTTGAT TAAAACTATG	
msa134270.2{391_090}	GATTAATAGG ACCCTCTGGA GCAGGGAAAT	CTACCTTGAT TAAAACTATG	
msa134270.2{391_CJB110}	GATTAATAGG ACCCTCTGGA GCAGGGAAAT	CTACCTTGAT TAAAACTATG	
msa134270.2{391_1169NT}	GATTAATAGG ACCCTCTGGA GCAGGGAAAT	CTACCTTGAT TAAAACTATG	
msa134270.2{391_18RS21}	GATTAATAGG ACCCTCTGGA GCAGGGAAAT	CTACCTTGAT TAAAACTATG	
msa134270.2{391_2603}	GATTAATAGG ACCCTCTGGA GCAGGGAAAT	CTACCTTGAT TAAAACTATG	
msa134270.2{391_A909}	GATTAATAGG ACCCTCTGGA GCAGGGAAAT	CTACCTTGAT TAAAACTATG	
msa134270.2{391_JM9130013}	GATTAATAGG ACCCTCTGGA GCAGGGAAAT	CTACCTTGAT TAAAACTATG	
msa134270.2{391_H36B}	GATTAATAGG ACCCTCTGGA GCAGGGAAAT	CTACCTTGAT TAAAACTATG	
Consensus	*****	*****	*****

	151		200
msa134270.2{391_COH1}	CTTGGCATGG AAAAAGCAGA TAAGGGAACA	GCTCTTGTTT TTGATACTCA	
msa134270.2{391_M732}	CTTGGCATGG AAAAAGCAGA TAAGGGAACA	GCTCTTGTTT TTGATACTCA	
msa134270.2{391_M781}	CTTGGCATGG AAAAAGCAGA TAAGGGAACA	GCTCTTGTTT TTGATACTCA	
msa134270.2{391_090}	CTTGGCATGG AAAAAGCAGA TAAGGGAACA	GCTCTTGTTT TTGATACTCA	
msa134270.2{391_CJB110}	CTTGGCATGG AAAAAGCAGA TAAGGGAACA	GCTCTTGTTT TTGATACTCA	
msa134270.2{391_1169NT}	CTTGGCATGG AAAAAGCAGA TAAGGGAACA	GCTCTTGTTT TTGATACTCA	
msa134270.2{391_18RS21}	CTTGGCATGG AAAAAGCAGA TAAGGGAACA	GCTCTTGTTT TTGATACTCA	
msa134270.2{391_2603}	CTTGGCATGG AAAAAGCAGA TAAGGGAACA	GCTCTTGTTT TTGATACTCA	
msa134270.2{391_A909}	CTTGGCATGG AAAAAGCAGA TAAGGGAACA	GCTCTTGTTT TTGATACTCA	

Table 76: Comparative Sequences relating to SAG0260

msa134270.2{391_JM9130013}	CTTGGCATGG	AAAAAGCAGA	TAAGGGAACA	GCTCTTGTTT	TTGATACTCA
msa134270.2{391_H36B}	CTTGGCATGG	AAAAAGCAGA	TAAGGGAACA	GCTCTTGTTT	TTGATACTCA
Consensus	*****	*****	*****	*****	*****
	201				250
msa134270.2{391_COH1}	AATGCCAGAT	CgTAATATTT	TAAATCAAAT	TGGCTATATG	GCTCAATCTG
msa134270.2{391_M732}	AATGCCAGAT	CgTAATATTT	TAAATCAAAT	TGGCTATATG	GCTCAATCTG
msa134270.2{391_M781}	AATGCCAGAT	CgTAATATTT	TAAATCAAAT	TGGCTATATG	GCTCAATCTG
msa134270.2{391_090}	AATGCCAGAT	CgTAATATTT	TAAATCAAAT	TGGCTATATG	GCTCAATCTG
msa134270.2{391_CJB110}	AATGCCAGAT	CgTAATATTT	TAAATCAAAT	TGGCTATATG	GCTCAATCTG
msa134270.2{391_1169NT}	AATGCCAGAT	CgTAATATTT	TAAATCAAAT	TGGCTATATG	GCTCAATCTG
msa134270.2{391_18RS21}	AATGCCAGAT	CgTAATATTT	TAAATCAAAT	TGGCTATATG	GCTCAATCTG
msa134270.2{391_2603}	AATGCCAGAT	CgTAATATTT	TAAATCAAAT	TGGCTATATG	GCTCAATCTG
msa134270.2{391_A909}	AATGCCAGAT	CaTAATATTT	TAAATCAAAT	TGGCTATATG	GCTCAATCTG
msa134270.2{391_JM9130013}	AATGCCAGAT	CgTAATATTT	TAAATCAAAT	TGGCTATATG	GCTCAATCTG
msa134270.2{391_H36B}	AATGCCAGAT	CgTAATATTT	TAAATCAAAT	TGGCTATATG	GCTCAATCTG
Consensus	*****	*-*****	*****	*****	*****
	251				300
msa134270.2{391_COH1}	ATGCCCTTAcA	CGAgTCTTTA	ACTGgCTTAG	AAAATTTATT	ATTCTTTGGA
msa134270.2{391_M732}	ATGCCCTTAcA	CGAgTCTTTA	ACTGgCTTAG	AAAATTTATT	ATTCTTTGGA
msa134270.2{391_M781}	ATGCCCTTAcA	CGAgTCTTTA	ACTGgCTTAG	AAAATTTATT	ATTCTTTGGA
msa134270.2{391_090}	ATGCCCTTAcA	CGAaTCTTTA	ACTGcCTTAG	AAAATTTATT	ATTCTTTGGA
msa134270.2{391_CJB110}	ATGCCCTTAcA	CGAaTCTTTA	ACTGcCTTAG	AAAATTTATT	ATTCTTTGGA
msa134270.2{391_1169NT}	ATGCCCTTAcA	CGAaTCTTTA	ACTGcCTTAG	AAAATTTATT	ATTCTTTGGA
msa134270.2{391_18RS21}	ATGCCCTTAcA	CGAgTCTTTA	ACTGgCTTAG	AAAATTTATT	ATTCTTTGGA
msa134270.2{391_2603}	ATGCCCTTAcA	CGAgTCTTTA	ACTGgCTTAG	AAAATTTATT	ATTCTTTGGA
msa134270.2{391_A909}	ATGCCCTTAcA	CGAgTCTTTA	ACTGgCTTAG	AAAATTTATT	ATTCTTTGGA
msa134270.2{391_JM9130013}	ATGCCCTTAcA	CGAgTCTTTA	ACTGgCTTAG	AAAATTTATT	ATTCTTTGGA
msa134270.2{391_H36B}	ATGCCCTTAcA	CGAgTCTTTA	ACTGgCTTAG	AAAATTTATT	ATTCTTTGGA
Consensus	*****-*	***-*****	****-*****	*****	*****
	301				350
msa134270.2{391_COH1}	AAAATGAAAG	GTATTCAAAA	AACTGAATTA	AAACAGCAGA	TAACTCATAT
msa134270.2{391_M732}	AAAATGAAAG	GTATTCAAAA	AACTGAATTA	AAACAGCAGA	TAACTCATAT
msa134270.2{391_M781}	AAAATGAAAG	GTATTCAAAA	AACTGAATTA	AAACAGCAGA	TAACTCATAT
msa134270.2{391_090}	AAAATGAAAG	GTATTCAAAA	AACTGAATTA	AAACAGCAGA	TAACTCATAT
msa134270.2{391_CJB110}	AAAATGAAAG	GTATTCAAAA	AACTGAATTA	AAACAGCAGA	TAACTCATAT
msa134270.2{391_1169NT}	AAAATGAAAG	GTATTCAAAA	AACTGAATTA	AAACAGCAGA	TAACTCATAT
msa134270.2{391_18RS21}	AAAATGAAAG	GTATTCAAAA	AACTGAATTA	AAACAGCAGA	TAACTCATAT
msa134270.2{391_2603}	AAAATGAAAG	GTATTCAAAA	AACTGAATTA	AAACAGCAGA	TAACTCATAT
msa134270.2{391_A909}	AAAATGAAAG	GTATTCAAAA	AACTGAATTA	AAACAGCAGA	TAACTCATAT
msa134270.2{391_JM9130013}	AAAATGAAAG	GTATTCAAAA	AACTGAATTA	AAACAGCAGA	TAACTCATAT
msa134270.2{391_H36B}	AAAATGAAAG	GTATTCAAAA	AACTGAATTA	AAACAGCAGA	TAACTCATAT
Consensus	*****	*****	*****	*****	*****
	351				400
msa134270.2{391_COH1}	TTCTAAAGTA	GTAGATCTAG	AAAACCAACT	TGATAAATTT	GTCTCAGGTT
msa134270.2{391_M732}	TTCTAAAGTA	GTAGATCTAG	AAAACCAACT	TGATAAATTT	GTCTCAGGTT
msa134270.2{391_M781}	TTCTAAAGTA	GTAGATCTAG	AAAACCAACT	TGATAAATTT	GTCTCAGGTT
msa134270.2{391_090}	TTCTAAAGTA	GTAGATCTAG	AAAACCAACT	TGATAAATTT	GTCTCAGGTT
msa134270.2{391_CJB110}	TTCTAAAGTA	GTAGATCTAG	AAAACCAACT	TGATAAATTT	GTCTCAGGTT
msa134270.2{391_1169NT}	TTCTAAAGTA	GTAGATCTAG	AAAACCAACT	TGATAAATTT	GTCTCAGGTT
msa134270.2{391_18RS21}	TTCTAAAGTA	GTAGATCTAG	AAAACCAACT	TGATAAATTT	GTCTCAGGTT
msa134270.2{391_2603}	TTCTAAAGTA	GTAGATCTAG	AAAACCAACT	TGATAAATTT	GTCTCAGGTT
msa134270.2{391_A909}	TTCTAAAGTA	GTAGATCTAG	AAAACCAACT	TGATAAATTT	GTCTCAGGTT
msa134270.2{391_JM9130013}	TTCTAAAGTA	GTAGATCTAG	AAAACCAACT	TGATAAATTT	GTCTCAGGTT
msa134270.2{391_H36B}	TTCTAAAGTA	GTAGATCTAG	AAAACCAACT	TGATAAATTT	GTCTCAGGTT
Consensus	*****	*****	*****	*****	*****
	401				450
msa134270.2{391_COH1}	ACTCAGGAGG	TATGAAAAGA	CGGCTTTCTC	TAGCCATCGC	CCTACTTGGA
msa134270.2{391_M732}	ACTCAGGAGG	TATGAAAAGA	CGGCTTTCTC	TAGCCATCGC	CCTACTTGGA
msa134270.2{391_M781}	ACTCAGGAGG	TATGAAAAGA	CGGCTTTCTC	TAGCCATCGC	CCTACTTGGA
msa134270.2{391_090}	ACTCAGGAGG	TATGAAAAGA	CGGCTTTCTC	TAGCCATCGC	CCTACTTGGA
msa134270.2{391_CJB110}	ACTCAGGAGG	TATGAAAAGA	CGGCTTTCTC	TAGCCATCGC	CCTACTTGGA
msa134270.2{391_1169NT}	ACTCAGGAGG	TATGAAAAGA	CGGCTTTCTC	TAGCCATCGC	CCTACTTGGA
msa134270.2{391_18RS21}	ACTCAGGAGG	TATGAAAAGA	CGGCTTTCTC	TAGCCATCGC	CCTACTTGGA
msa134270.2{391_2603}	ACTCAGGAGG	TATGAAAAGA	CGGCTTTCTC	TAGCCATCGC	CCTACTTGGA
msa134270.2{391_A909}	ACTCAGGAGG	TATGAAAAGA	CGGCTTTCTC	TAGCCATCGC	CCTACTTGGA
msa134270.2{391_JM9130013}	ACTCAGGAGG	TATGAAAAGA	CGGCTTTCTC	TAGCCATCGC	CCTACTTGGA
msa134270.2{391_H36B}	ACTCAGGAGG	TATGAAAAGA	CGGCTTTCTC	TAGCCATCGC	CCTACTTGGA
Consensus	*****	*****	*****	*****	*****
	451				500
msa134270.2{391_COH1}	AACCCACAG	TTTTAATCCT	AGATGAACCT	ACCGTTGGAA	TTGATCCATC
msa134270.2{391_M732}	AACCCACAG	TTTTAATCCT	AGATGAACCT	ACCGTTGGAA	TTGATCCATC
msa134270.2{391_M781}	AACCCACAG	TTTTAATCCT	AGATGAACCT	ACCGTTGGAA	TTGATCCATC
msa134270.2{391_090}	AACCCACAG	TTTTAATCCT	AGATGAACCT	ACCGTTGGAA	TTGATCCATC
msa134270.2{391_CJB110}	AACCCACAG	TTTTAATCCT	AGATGAACCT	ACCGTTGGAA	TTGATCCATC
msa134270.2{391_1169NT}	AACCCACAG	TTTTAATCCT	AGATGAACCT	ACCGTTGGAA	TTGATCCATC
msa134270.2{391_18RS21}	AACCCACAG	TTTTAATCCT	AGATGAACCT	ACCGTTGGAA	TTGATCCATC
msa134270.2{391_2603}	AACCCACAG	TTTTAATCCT	AGATGAACCT	ACCGTTGGAA	TTGATCCATC

Table 76: Comparative Sequences relating to SAG0260

msa134270.2{391_A909}	AACCCACAG	TTTTAATCCT	AGATGAACCT	ACCGTTGGAA	TTGATCCATC
msa134270.2{391_JM9130013}	AACCCACAG	TTTTAATCCT	AGATGAACCT	ACCGTTGGAA	TTGATCCATC
msa134270.2{391_H36B}	AACCCACAG	TTTTAATCCT	AGATGAACCT	ACCGTTGGAA	TTGATCCATC
Consensus	*****	*****	*****	*****	*****
msa134270.2{391_COH1}	CTTGAGGAGA	AAAATCTGGC	AAGAGCTAAT	TAATATTAAG	GATGAAGGAC
msa134270.2{391_M732}	CTTGAGGAGA	AAAATCTGGC	AAGAGCTAAT	TAATATTAAG	GATGAAGGAC
msa134270.2{391_M781}	CTTGAGGAGA	AAAATCTGGC	AAGAGCTAAT	TAATATTAAG	GATGAAGGAC
msa134270.2{391_090}	CTTGAGGAGA	AAAATCTGGC	AAGAGCTAAT	TAATATTAAG	GATGAAGGAC
msa134270.2{391_CJB110}	CTTGAGGAGA	AAAATCTGGC	AAGAGCTAAT	TAATATTAAG	GATGAAGGAC
msa134270.2{391_1169NT}	CTTGAGGAGA	AAAATCTGGC	AAGAGCTAAT	TAATATTAAG	GATGAAGGAC
msa134270.2{391_18RS21}	CTTGAGGAGA	AAAATCTGGC	AAGAGCTAAT	TAATATTAAG	GATGAAGGAC
msa134270.2{391_2603}	CTTGAGGAGA	AAAATCTGGC	AAGAGCTAAT	TAATATTAAG	GATGAAGGAC
msa134270.2{391_A909}	CTTGAGGAGA	AAAATCTGGC	AAGAGCTAAT	TAATATTAAG	GATGAAGGAC
msa134270.2{391_JM9130013}	CTTGAGGAGA	AAAATCTGGC	AAGAGCTAAT	TAATATTAAG	GATGAAGGAC
msa134270.2{391_H36B}	CTTGAGGAGA	AAAATCTGGC	AAGAGCTAAT	TAATATTAAG	GATGAAGGAC
Consensus	*****	*****	*****	*****	*****
msa134270.2{391_COH1}	gTTCTATCTT	TATTACAACC	CACGTTATGG	ATGAAGCAGA	ATTAACAAGT
msa134270.2{391_M732}	gTTCTATCTT	TATTACAACC	CACGTTATGG	ATGAAGCAGA	ATTAACAAGT
msa134270.2{391_M781}	gTTCTATCTT	TATTACAACC	CACGTTATGG	ATGAAGCAGA	ATTAACAAGT
msa134270.2{391_090}	gTTCTATCTT	TATTACAACC	CACGTTATGG	ATGAAGCAGA	ATTAACAAGT
msa134270.2{391_CJB110}	gTTCTATCTT	TATTACAACC	CACGTTATGG	ATGAAGCAGA	ATTAACAAGT
msa134270.2{391_1169NT}	gTTCTATCTT	TATTACAACC	CACGTTATGG	ATGAAGCAGA	ATTAACAAGT
msa134270.2{391_18RS21}	aTTCTATCTT	TATTACAACC	CACGTTATGG	ATGAAGCAGA	ATTAACAAGT
msa134270.2{391_2603}	aTTCTATCTT	TATTACAACC	CACGTTATGG	ATGAAGCAGA	ATTAACAAGT
msa134270.2{391_A909}	gTTCTATCTT	TATTACAACC	CACGTTATGG	ATGAAGCAGA	ATTAACAAGT
msa134270.2{391_JM9130013}	gTTCTATCTT	TATTACAACC	CACGTTATGG	ATGAAGCAGA	ATTAACAAGT
msa134270.2{391_H36B}	gTTCTATCTT	TATTACAACC	CACGTTATGG	ATGAAGCAGA	ATTAACAAGT
Consensus	-*****	*****	*****	*****	*****
msa134270.2{391_COH1}	AAGGTTGCAC	TACTATTACG	TGGAAACATT	ATTGCCTTTG	ATACTCCATT
msa134270.2{391_M732}	AAGGTTGCAC	TACTATTACG	TGGAAACATT	ATTGCCTTTG	ATACTCCATT
msa134270.2{391_M781}	AAGGTTGCAC	TACTATTACG	TGGAAACATT	ATTGCCTTTG	ATACTCCATT
msa134270.2{391_090}	AAGGTTGCAC	TACTATTACG	TGGAAACATT	ATTGCCTTTG	ATACTCCATT
msa134270.2{391_CJB110}	AAGGTTGCAC	TACTATTACG	TGGAAACATT	ATTGCCTTTG	ATACTCCATT
msa134270.2{391_1169NT}	AAGGTTGCAC	TACTATTACG	TGGAAACATT	ATTGCCTTTG	ATACTCCATT
msa134270.2{391_18RS21}	AAGGTTGCAC	TACTATTACG	TGGAAACATT	ATTGCCTTTG	ATACTCCATT
msa134270.2{391_2603}	AAGGTTGCAC	TACTATTACG	TGGAAACATT	ATTGCCTTTG	ATACTCCATT
msa134270.2{391_A909}	AAGGTTGCAC	TACTATTACG	TGGAAACATT	ATTGCCTTTG	ATACTCCATT
msa134270.2{391_JM9130013}	AAGGTTGCAC	TACTATTACG	TGGAAACATT	ATTGCCTTTG	ATACTCCATT
msa134270.2{391_H36B}	AAGGTTGCAC	TACTATTACG	TGGAAACATT	ATTGCCTTTG	ATACTCCATT
Consensus	*****	*****	*****	*****	*****
msa134270.2{391_COH1}	ACATTTAAAA	AAACAATTTA	ATGTGAGTAC	TATTGAGGAA	G-----
msa134270.2{391_M732}	ACATTTAAAA	AAACAATTTA	ATGTGAGTAC	TATTGAGGAA	GTTTCTTAA
msa134270.2{391_M781}	ACATTTAAAA	AAACAATTTA	ATGTGAGTAC	TATTGAGGAA	GTTTCTTAA
msa134270.2{391_090}	ACATTTAAAA	AAACAATTTA	ATGTGAGTAC	TATTGAGGAA	GTTTCTTAA
msa134270.2{391_CJB110}	ACATTTAAAA	AAACAATTTA	ATGTGAGTAC	TATTGAGGAA	GTTTCTTAA
msa134270.2{391_1169NT}	ACATTTAAAA	AAACAATTTA	ATGTGAGTAC	TATTGAGGAA	GTTTCTTAA
msa134270.2{391_18RS21}	ACATTTAAAA	AAACAATTTA	ATGTGAGTAC	TATTGAGGAA	GTTTCTTAA
msa134270.2{391_2603}	ACATTTAAAA	AAACAATTTA	ATGTGAGTAC	TATTGAGGAA	GTTTCTTAA
msa134270.2{391_A909}	ACATTTAAAA	AAACAATTTA	ATGTGAGTAC	TATTGAGGAA	GTTTCTTAA
msa134270.2{391_JM9130013}	ACATTTAAAA	AAACAATTTA	ATGTGAGTAC	TATTGAGGAA	GTTTCTTAA
msa134270.2{391_H36B}	ACATTTAAAA	AAACAATTTA	ATGTGAGTAC	TATTGAGGAA	GTTTCTTAA
Consensus	*****	*****	*****	*****	*****
msa134270.2{391_COH1}	-----	-----	-----	-----	-----
msa134270.2{391_M732}	AAGCTGAAGG	AGAA	-----	-----	-----
msa134270.2{391_M781}	AAGCTGAAGG	AGAA	-----	-----	-----
msa134270.2{391_090}	AAGCTGAAGG	AGAA	-----	-----	-----
msa134270.2{391_CJB110}	AAGCTGAAGG	AGAA	-----	-----	-----
msa134270.2{391_1169NT}	AAGCTGAAGG	AGAA	-----	-----	-----
msa134270.2{391_18RS21}	AAGCTGAAGG	AGAA	-----	-----	-----
msa134270.2{391_2603}	AAGCTGAAGG	AGAA	-----	-----	-----
msa134270.2{391_A909}	AAGCTGAAGG	AGAA	-----	-----	-----
msa134270.2{391_JM9130013}	AAGCTGAAGG	AGAA	-----	-----	-----
msa134270.2{391_H36B}	AAGCTGAAGG	AGAA	-----	-----	-----
Consensus	*****	****	-----	-----	-----

SEQ ID NO. 7612

STRAIN 2603 frame: 1

KKVIDLKKLQKAYASETVLNNINLEVFKEIIGLIGPSGAGKSTLIKTMLEKADKGTA
 LVLDTQMPDRNINLQIGYMAQSDALYESLTGLENLLFFGKMKGIQKTELKQOITHISKVV
 DLENQLDKFVSGYSGMKRRSLAIALGNPTVLILDEPTVGDPSLRKRWQELINIKD
 EGHSIFITTHVMEAELETSKVALLLRGNI IAFDTPHLHLKKQFNV

SEQ ID NO. 7613

Table 76: Comparative Sequences relating to SAG0260

STRAIN 090 frame: 3
 LKKLQKAYASETVLNNINLEVFKEIIGLIGPSGAGKSTLIKTMLGMEKADKGTA
 QMPDRNINLQIGYMAQSDALYESLTALLENLLFFGKMKGIQKTELKQQITHISKVVDLENQ
 LDKFVSGYSGGMRRLSLAIALLGNTPTVLILDEPTVGIDPSLRRKIWQELINIKDEGRSI
 FITTHVMDEAELTSKVALLLRGNI IAFDTPHLHLKKQFNV

SEQ ID NO. 7614
 STRAIN A909 frame: 1
 KKVIDLKKLQKAYASETVLNNINLEVFKEIIGLIGPSGAGKSTLIKTMLGMEKADKGTA
 LVLDTQMPDRNINLQIGYMAQSDALYESLTALLENLLFFGKMKGIQKTELKQQITHISKVV
 DLENQLDKFVSGYSGGMRRLSLAIALLGNTPTVLILDEPTVGIDPSLRRKIWQELINIKD
 EGRSIFITTHVMDEAELTSKVALLLRGNI IAFDTPHLHLKKQFNV

SEQ ID NO. 7615
 STRAIN H36B frame: 1
 KKVIDLKKLQKAYASETVLNNINLEVFKEIIGLIGPSGAGKSTLIKTMLGMEKADKGTA
 LVLDTQMPDRNINLQIGYMAQSDALYESLTALLENLLFFGKMKGIQKTELKQQITHISKVV
 DLENQLDKFVSGYSGGMRRLSLAIALLGNTPTVLILDEPTVGIDPSLRRKIWQELINIKD
 EGRSIFITTHVMDEAELTSKVALLLRGNI IAFDTPHLHLKKQFNV

SEQ ID NO. 7616
 STRAIN 18RS21 frame: 1
 DLKKLQKAYASETVLNNINLEVFKEIIGLIGPSGAGKSTLIKTMLGMEKADKGTA
 TQMPDRNINLQIGYMAQSDALYESLTALLENLLFFGKMKGIQKTELKQQITHISKVVDLEN
 QLDKFVSGYSGGMRRLSLAIALLGNTPTVLILDEPTVGIDPSLRRKIWQELINIKDEGHS
 IFITTHVMDEAELTSKVALLLRGNI IAFDTPHLHLKKQFNV

SEQ ID NO. 7617
 STRAIN M732 frame: 1
 KKVIDLKKLQKAYASETVLNNINLEVFKEIIGLIGPSGAGKSTLIKTMLGMEKADKGTA
 LVLDTQMPDRNINLQIGYMAQSDALHESLTALLENLLFFGKMKGIQKTELKQQITHISKVV
 DLENQLDKFVSGYSGGMRRLSLAIALLGNTPTVLILDEPTVGIDPSLRRKIWQELINIKD
 EGRSIFITTHVMDEAELTSKVALLLRGNI IAFDTPHLHLKKQFNV

SEQ ID NO. 7618
 STRAIN COH1 frame: 1
 KKVIDLKKLQKAYASETVLNNINLEVFKEIIGLIGPSGAGKSTLIKTMLGMEKADKGTA
 LVLDTQMPDRNINLQIGYMAQSDALHESLTALLENLLFFGKMKGIQKTELKQQITHISKVV
 DLENQLDKFVSGYSGGMRRLSLAIALLGNTPTVLILDEPTVGIDPSLRRKIWQELINIKD
 EGRSIFITTHVMDEAELTSKVALLLRGNI IAFDTPHLHLKKQFNV

SEQ ID NO. 7619
 STRAIN M781 frame: 1
 KKVIDLKKLQKAYASETVLNNINLEVFKEIIGLIGPSGAGKSTLIKTMLGMEKADKGTA
 LVLDTQMPDRNINLQIGYMAQSDALHESLTALLENLLFFGKMKGIQKTELKQQITHISKVV
 DLENQLDKFVSGYSGGMRRLSLAIALLGNTPTVLILDEPTVGIDPSLRRKIWQELINIKD
 EGRSIFITTHVMDEAELTSKVALLLRGNI IAFDTPHLHLKKQFNV

SEQ ID NO. 7620
 STRAIN CJB110 frame: 1
 KKVIDLKKLQKAYASETVLNNINLEVFKEIIGLIGPSGAGKSTLIKTMLGMEKADKGTA
 LVLDTQMPDRNINLQIGYMAQSDALYESLTALLENLLFFGKMKGIQKTELKQQITHISKVV
 DLENQLDKFVSGYSGGMRRLSLAIALLGNTPTVLILDEPTVGIDPSLRRKIWQELINIKD
 EGRSIFITTHVMDEAELTSKVALLLRGNI IAFDTPHLHLKKQFNV

SEQ ID NO. 7621
 STRAIN 1169NT frame: 1
 KKVIDLKKLQKAYASETVLNNINLEVFKEIIGLIGPSGAGKSTLIKTMLGMEKADKGTA
 LVLDTQMPDRNINLQIGYMAQSDALYESLTALLENLLFFGKMKGIQKTELKQQITHISKVV
 DLENQLDKFVSGYSGGMRRLSLAIALLGNTPTVLILDEPTVGIDPSLRRKIWQELINIKD
 EGRSIFITTHVMDEAELTSKVALLLRGNI IAFDTPHLHLKKQFNV

SEQ ID NO. 7622
 STRAIN JM9130013 frame: 1
 KKVIDLKKLQKAYASETVLNNINLEVFKEIIGLIGPSGAGKSTLIKTMLGMEKADKGTA
 LVLDTQMPDRNINLQIGYMAQSDALYESLTALLENLLFFGKMKGIQKTELKQQITHISKVV
 DLENQLDKFVSGYSGGMRRLSLAIALLGNTPTVLILDEPTVGIDPSLRRKIWQELINIKD
 EGRSIFITTHVMDEAELTSKVALLLRGNI IAFDTPHLHLKKQFNV

PRETTY of: /biotmp/msa134470.2{*} April 10, 2003 02:16 ..

	1		50
msa134470.2{391_090}	-----LKKLQ	KAYASETVLN NINLEVFKEI	IIGLIGPSGA GKSTLIKTML
msa134470.2{391_1169NT}	KKVIDLKKLQ	KAYASETVLN NINLEVFKEI	IIGLIGPSGA GKSTLIKTML
msa134470.2{391_CJB110}	KKVIDLKKLQ	KAYASETVLN NINLEVFKEI	IIGLIGPSGA GKSTLIKTML
msa134470.2{391_COH1}	KKVIDLKKLQ	KAYASETVLN NINLEVFKEI	IIGLIGPSGA GKSTLIKTML
msa134470.2{391_M732}	KKVIDLKKLQ	KAYASETVLN NINLEVFKEI	IIGLIGPSGA GKSTLIKTML
msa134470.2{391_M781}	KKVIDLKKLQ	KAYASETVLN NINLEVFKEI	IIGLIGPSGA GKSTLIKTML
msa134470.2{391_18RS21}	----DLKKLQ	KAYASETVLN NINLEVFKEI	IIGLIGPSGA GKSTLIKTML
msa134470.2{391_2603}	KKVIDLKKLQ	KAYASETVLN NINLEVFKEI	IIGLIGPSGA GKSTLIKTML
msa134470.2{391_H36B}	KKVIDLKKLQ	KAYASETVLN NINLEVFKEI	IIGLIGPSGA GKSTLIKTML
msa134470.2{391_JM9130013}	KKVIDLKKLQ	KAYASETVLN NINLEVFKEI	IIGLIGPSGA GKSTLIKTML

Table 76: Comparative Sequences relating to SAG0260

msa134470.2{391_A909}	KKVIDLKKLQ	KAYASETVLN	NINLEVFKE	IIGLIGPSGA	GKSTLIKTML
Consensus	*****	*****	*****	*****	*****
	51				100
msa134470.2{391_090}	GMEKADKGTA	LVLDTQMPDr	NILNQIGYMA	QSDALyESLT	aLENLLFFGK
msa134470.2{391_1169NT}	GMEKADKGTA	LVLDTQMPDr	NILNQIGYMA	QSDALyESLT	aLENLLFFGK
msa134470.2{391_CJB110}	GMEKADKGTA	LVLDTQMPDr	NILNQIGYMA	QSDALyESLT	aLENLLFFGK
msa134470.2{391_COH1}	GMEKADKGTA	LVLDTQMPDr	NILNQIGYMA	QSDALhESLT	gLENLLFFGK
msa134470.2{391_M732}	GMEKADKGTA	LVLDTQMPDr	NILNQIGYMA	QSDALhESLT	gLENLLFFGK
msa134470.2{391_M781}	GMEKADKGTA	LVLDTQMPDr	NILNQIGYMA	QSDALhESLT	gLENLLFFGK
msa134470.2{391_18RS21}	GMEKADKGTA	LVLDTQMPDr	NILNQIGYMA	QSDALyESLT	gLENLLFFGK
msa134470.2{391_2603}	GMEKADKGTA	LVLDTQMPDr	NILNQIGYMA	QSDALyESLT	gLENLLFFGK
msa134470.2{391_H36B}	GMEKADKGTA	LVLDTQMPDr	NILNQIGYMA	QSDALyESLT	gLENLLFFGK
msa134470.2{391_JM9130013}	GMEKADKGTA	LVLDTQMPDr	NILNQIGYMA	QSDALyESLT	gLENLLFFGK
msa134470.2{391_A909}	GMEKADKGTA	LVLDTQMPDh	NILNQIGYMA	QSDALyESLT	gLENLLFFGK
Consensus	*****	*****	*****	*****	*****
	101				150
msa134470.2{391_090}	MKGIQKTELK	QQITHISKVV	DLENQLDKFV	SGYSGGMKRR	LSLAIALLGN
msa134470.2{391_1169NT}	MKGIQKTELK	QQITHISKVV	DLENQLDKFV	SGYSGGMKRR	LSLAIALLGN
msa134470.2{391_CJB110}	MKGIQKTELK	QQITHISKVV	DLENQLDKFV	SGYSGGMKRR	LSLAIALLGN
msa134470.2{391_COH1}	MKGIQKTELK	QQITHISKVV	DLENQLDKFV	SGYSGGMKRR	LSLAIALLGN
msa134470.2{391_M732}	MKGIQKTELK	QQITHISKVV	DLENQLDKFV	SGYSGGMKRR	LSLAIALLGN
msa134470.2{391_M781}	MKGIQKTELK	QQITHISKVV	DLENQLDKFV	SGYSGGMKRR	LSLAIALLGN
msa134470.2{391_18RS21}	MKGIQKTELK	QQITHISKVV	DLENQLDKFV	SGYSGGMKRR	LSLAIALLGN
msa134470.2{391_2603}	MKGIQKTELK	QQITHISKVV	DLENQLDKFV	SGYSGGMKRR	LSLAIALLGN
msa134470.2{391_H36B}	MKGIQKTELK	QQITHISKVV	DLENQLDKFV	SGYSGGMKRR	LSLAIALLGN
msa134470.2{391_JM9130013}	MKGIQKTELK	QQITHISKVV	DLENQLDKFV	SGYSGGMKRR	LSLAIALLGN
msa134470.2{391_A909}	MKGIQKTELK	QQITHISKVV	DLENQLDKFV	SGYSGGMKRR	LSLAIALLGN
Consensus	*****	*****	*****	*****	*****
	151				200
msa134470.2{391_090}	PTVLILDEPT	VGIDPSLRRK	IWQELINIKD	EGrSIFITTH	VMDEAELTSK
msa134470.2{391_1169NT}	PTVLILDEPT	VGIDPSLRRK	IWQELINIKD	EGrSIFITTH	VMDEAELTSK
msa134470.2{391_CJB110}	PTVLILDEPT	VGIDPSLRRK	IWQELINIKD	EGrSIFITTH	VMDEAELTSK
msa134470.2{391_COH1}	PTVLILDEPT	VGIDPSLRRK	IWQELINIKD	EGrSIFITTH	VMDEAELTSK
msa134470.2{391_M732}	PTVLILDEPT	VGIDPSLRRK	IWQELINIKD	EGrSIFITTH	VMDEAELTSK
msa134470.2{391_M781}	PTVLILDEPT	VGIDPSLRRK	IWQELINIKD	EGrSIFITTH	VMDEAELTSK
msa134470.2{391_18RS21}	PTVLILDEPT	VGIDPSLRRK	IWQELINIKD	EGhSIFITTH	VMDEAELTSK
msa134470.2{391_2603}	PTVLILDEPT	VGIDPSLRRK	IWQELINIKD	EGhSIFITTH	VMDEAELTSK
msa134470.2{391_H36B}	PTVLILDEPT	VGIDPSLRRK	IWQELINIKD	EGrSIFITTH	VMDEAELTSK
msa134470.2{391_JM9130013}	PTVLILDEPT	VGIDPSLRRK	IWQELINIKD	EGrSIFITTH	VMDEAELTSK
msa134470.2{391_A909}	PTVLILDEPT	VGIDPSLRRK	IWQELINIKD	EGrSIFITTH	VMDEAELTSK
Consensus	*****	*****	*****	**_*****	*****
	201				224
msa134470.2{391_090}	VALLLRGNII	AFDTPLHLKK	QFNV		
msa134470.2{391_1169NT}	VALLLRGNII	AFDTPLHLKK	QFNV		
msa134470.2{391_CJB110}	VALLLRGNII	AFDTPLHLKK	QFNV		
msa134470.2{391_COH1}	VALLLRGNII	AFDTPLHLKK	QFNV		
msa134470.2{391_M732}	VALLLRGNII	AFDTPLHLKK	QFNV		
msa134470.2{391_M781}	VALLLRGNII	AFDTPLHLKK	QFNV		
msa134470.2{391_18RS21}	VALLLRGNII	AFDTPLHLKK	QFNV		
msa134470.2{391_2603}	VALLLRGNII	AFDTPLHLKK	QFNV		
msa134470.2{391_H36B}	VALLLRGNII	AFDTPLHLKK	QFNV		
msa134470.2{391_JM9130013}	VALLLRGNII	AFDTPLHLKK	QFNV		
msa134470.2{391_A909}	VALLLRGNII	AFDTPLHLKK	QFNV		
Consensus	*****	*****	****		

Table 77: Comparative Sequences relating to SAG2059

SEQ ID NO. 7701

STRAIN 2603

TTGCCTATGTTGCTGTTGGTTTAGTTTTAGAGGGTGGCGGAATGAGAGGTCTTTATACT
 GCTGGAGTTTTAGATGCTTTTCTAGATGCAGGAATAAAAAATAGATGGTATCGTATCTGTC
 TCTGCTGGTGCAATTGTTTGGTGTTAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGA
 TACAATAAAAAAGTATTTATCCCACCCTAAATATATGAGTCTAAGGTCATGGTTTCGAACA
 GGAATTTTGTAAATAAAGATTTTACCTATTATGAAGTTCCTATGAAATTGGATGTATTT
 GACGATGAAGCATTTAAAAAATCAAGTATTGATTTTTACGTAGTTGCTACAGAGATGACA
 TCTGGTAAACCTGAATATTTTAAATGATAGTGTTTTTGAACAAATGGAATTTTACGT
 GCTAGTTTACGATTACCACTAGTCTCAAAGATGGTTGATTGGCAGGGGAAAAAGTACTTA
 GATGGTGGTTTATCTGATAGTATTCCCGTTGATTTTGCCCGTGGTTTAGGATTTGACAAG
 TTGATTGTTGTGATGACTAGGCCGCTCAATTATCAGAAAAAGCCTTCAAGTGGACGATTG
 TATAAACTCTGTATAGGAAATATCCTAATTTTGTAAAGACAGCCTCGAATCGGTACCAA
 CAGTATAATAATAGTCTTGAAAAGGTCATGAGCCTTGAAAAACAGGCGATCTATTTGCA
 ATTAGACCGAGTAAGAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAACTTGAT
 AGTATTTATCAGCTTGGTATGAAAGATGCTAAAAGTGTGATGCCTGAGCTGAATAGTTAT
 CTAATGAAA

SEQ ID NO. 7702

STRAIN 090

CCTATGTTGCTGTTGGTTTAGTTTTAG
 AGGGTGGCGGAATGAGAGGTCTTTATACTGCTGGAGTTTTAGATGCTTTT
 CTAGATGCAGGAATAAAAAATAGATGGTATCGTATCTGTCTCTGCTGGTG
 ATTGTTTGGTGTTAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGAT
 ACAATAAAAAAGTATTTATCCCACCCTAAATATATGAGTCTAAGGTCATGG
 TTTTGAACAGGGAATTTTGTAAATAAAGATTTTACCTATTATGAAGTTCC
 TATGAAATTTGGATGTATTTGACGATGAAGCATTTAAAAAATCAAGTATTG
 ATTTTACGTAGTTGCTACAGAGATGACATCTGGTAAACCTGAATATTTT
 AAAATTGATAGTGTTTTTGAACAAATGGAATTTTACGTGCTAGTTTACG
 ATTACCACTAGTCTCAAAGATGGTTGATTGGCAGGGGAAAAAGTACTTAG
 ATGGTGGTTTATCTGATAGTATTCCCGTTGATTTTGCCCGTGGTTTAGGA
 TTTGACAAGTTGATTGTTGTGATGACTAGGCCGCTCAATTATCAGAAAAA
 GCCTTCAAGTGGACGATTGTATAAACTCTGTATAGGAAATATCCTAATT
 TTGTAAAGACAGCCTCGAATCGGTACCAACAGTATAATAATAGTCTTGAA
 AAGGTCATGAGCCTTGAAAAACAGGCGATCTATTTGCAATTAGACCGAG
 TAAGAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAACTTGATA
 GTATTTATCAGCTTGGTATGAAAGATGCTAAAAGTGTGATGCCTGAGCTG
 AATAGTTATCTAATGAAA

SEQ ID NO. 7703

STRAIN A909

CCTATGTTGCTGTTGGTTTAGTTTTAGAG
 GGTGGCGGAATGAGAGGTCTTTATACTGCTGGAGTTTTAGATGCTTTTCT
 AGATGCAGGAATAAAAGTAGATGGTATCATATCTGTCTCTGCTGGTGAT
 TGTTTGGTGTTAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGATAC
 AATAAAAAAGTATTTATCCCACCCTAAATATATGAGTCTAAGGTCATGGCT
 TCGAACAGGGAATTTTGTAAATAAAGATTTTACCTATTATGAAGTTCTTA
 TGAATTTGGATGTATTTGACGATGAAGCATTTAAAAAATCAAGTATTGAT
 TTTTACGCAGTTGCTACAGAGATGACATCTGGTAAACCTGAGTATTTTAA
 AATTGATAGTGTTTTTGAACAAATGGAATTTTACGTGCTAGTTTACGAT
 TACCACTAGTCTCAAAGATGGTTGTTTGGCAGGGGAAAAAGTACTTAGAT
 GGTGGTTTATCTGATAGTATTCCCGTTGATTTTGCCCGTGGTTTAGGATT
 TGACAAGTTGATTGTTGTGATGACTAGGCCGCTCAATTATCAGAAAAAGC
 CTTCAGTGGACGATTGTATAAACTCTGTATAGGAAATATCCTAATTTT
 GTAAAGACAGCCTCGAACCCTGACCAACAGTATAATAATAGCCTTGAAAA
 GGTGATGAGCCTTGAAAAACAGGCGATCTATTTGCAATTAGACCAAGTA
 AGAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAACTTGATAGT
 ATTTATCAGCTTGGTATGAAAGATGCTAAAAGTGGGATGCCTGAGCTGAA
 TAGTTATCTAATGAAA

SEQ ID NO. 7704

STRAIN H36B

CCTATGTTGCTGTTGGTTTAGTTTTAG
 AGGGTGGCGGAATGAGAGGTCTTTATACTGCTGGAGTTTTAGATGCTTTT
 CTAGATGCAGGAATAAAAGTAGATGGTATCATATCTGTCTCTGCTGGTG
 ATTGTTTGGTGTTAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGAT
 ACAATAAAAAAGTATTTATCCCACCCTAAATATATGAGTCTAAGGTCATGG
 CTTCGAACAGGGAATTTTGTAAATAAAGATTTTACCTATTATGAAGTTCC
 TATGAAATTTGGATGTATTTGACGATGAAGCATTTAAAAAATCAAGTATTG
 ATTTTACGCAGTTGCTACAGAGATGACATCTGGTAAACCTGAGTATTTT
 AAAATTGATAGTGTTTTTGAACAAATGGAATTTTACGTGCTAGTTTACG
 ATTACCACTAGTCTCAAAGATGGTTGTTTGGCAGGGGAAAAAGTACTTAG
 ATGGTGGTTTATCTGATAGTATTCCCGTTGATTTTGCCCGTGGTTTAGGA
 TTTGACAAGTTGATTGTTGTGATGACTAGGCCGCTCAATTATCAGAAAAA
 GCCTTCAAGTGGACGATTGTATAAACTCTGTATAGGAAATATCCTAATT
 TTGTAAAGACAGCCTCGAACCCTGACCAACAGTATAATAATAGCCTTGAA
 AAGGTCATGAGCCTTGAAAAACAGGCGATCTATTTGCAATTAGACCAAG
 TAAGAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAACTTGATA
 GTATTTATCAGCTTGGTATGAAAGATGCTAAAAGTGGGATGCCTGAGCTG
 AATAGTTATCTAATGAAA

SEQ ID NO. 7705

Table 77: Comparative Sequences relating to SAG2059

STRAIN 18RS21

CCTATGTTGTCTGTTGGTTTGTAGTTTGTAGAGG
GTGGCGGAATGAGAGGTCTTTATACTGCTGGAGTTTGTAGATGCTTTTCTA
GATGCAGGAATAAAAATAGATGGTATCGTATCTGTCTCTGCTGGTGCATT
GTTTGGTGTAAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGATACA
ATAAAAAGTATTTATCCACCCTAAATATATGAGTCTAAGGTCATGGTTT
CGAACAGGGAATTTTGTAAATAAAGATTTACCTATTATGAAGTTCCTAT
GAAATTGGATGTATTTGACGATGAAGCATTAAAAAATCAAGTATTGATT
TTTACGTAGTTGCTACAGAGATGACATCTGGTAAACCTGAATATTTTAAA
ATTGATAGTGTTTTGAACAAATGGAAATTTTACGTGCTAGTTCAGCATT
ACCAGTAGTCTCAAAGATGGTTGATTGGCAGGGGAAAAAGTACTTAGATG
GTGGTTTATCTGATAGTATTCCCGTTGATTTTGCCCGTGGTTTAGGATTT
GACAAGTTGATTGTTGTGATGACTAGGCCGCTCAATTATCAGAAAAAGCC
TTCAAGTGGACGATTGTATAAACTCTGTATAGGAAATATCCTAATTTTG
TAAAGACAGCCTCGAATCGGTACCAACAGTATAATAATAGTCTTGAAAAG
GTCAATGAGCCTTGAAAAACAGGCGATCTATTTGCAATTAGACCGAGTAA
GAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAACTTGATAGTA
TTTATCAGCTTGGTATGAAAGATGCTAAAAGTGTGATGCCTGAGCTGAAT
AGTTATCTAATGAAA

SEQ ID NO. 7706

STRAIN M732

CCTATGTTGTCTGTTGGTTTGTAGTTTGTAGA
GGGTGGCGGAATGAGAGGTCTTTATACTGCTGGAGTTTGTAGATGCTTTTC
TAGATGCAGGAATAAAAATAGATGGTATCGTATCTGTCTCTGCGGGTGCA
TTGTTTGGTGTAAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGATA
CAATAAAAAGTATTTATCCACCCTGAATATATGAGTCTAAGATCATGGC
TTCGAACAGGGAATTTTGTAAATAAAGATTTACCTATTATGAAGTTCCT
ATGAAATTGGATGTATTTGACGATGAAGCATTAAAAAATCAAGTATTGA
TTTTTACGTAGTTGCTACAGAGATGACATCTGGTAAACCTGAATATTTTA
AAATTGATAGTGTTTTGAACAAATGGAAATTTTACGTGCTAGTTCAGCA
TTACCAGTAGTCTCAAAGATGGTTGATTGGCAGGGGAAAAAGTACTTAGA
TGGTGGTTTATCTGATAGTATTCCCGTTGATTTTGCCCGTGGTTTAGGAT
TTGACAAGTTGATTGTTGTGATGACTAGGCCGCTCAATTATCAGAAAAAG
CCTTCAAGTGGACGATTGTATAAACTCTGTATAGGAAATATCCTAATTT
TGTAAGACAGCCTCGAATCGGTACCAACAGTATAATAATAGTCTTGAAA
AGGTCAATGAGCCTTGAAAAACAGGCGATCTATTTGCAATTAGACCGAGT
AAGAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAACTTGATAG
TATTTATCAGCTTGGTATGAAATATGCTAAAAGTGTGATGCCTGAGCTGA
ATAGTTATCTAATGAAA

SEQ ID NO. 7707

STRAIN COH1

CCTATGTTGTCTGTTGGTTTGTAGTTTGA
GAGGGTGGCGGAATGAGAGGTCTTTATACTGCTGGAGTTTGTAGATGCTTT
TCTAGATGCAGGAATAAAAATAGATGGTATCGTATCTGTCTCTGCGGGTG
CATTGTTTGGTGTAAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGA
TACAATAAAAAGTATTTATCCACCCTGAATATATGAGTCTAAGATCATG
GCTTCGAACAGGGAATTTTGTAAATAAAGATTTACCTATTATGAAGTTC
CTATGAAATTGGATGTATTTGACGATGAAGCATTAAAAAATCAAGTATT
GATTTTTACGTAGTTGCTACAGAGATGACATCTGGTAAACCTGAATATTT
TAAAATTGATAGTGTTTTGAACAAATGGAAATTTTACGTGCTAGTTCAG
CATTACCAGTAGTCTCAAAGATGGTTGATTGGCAGGGGAAAAAGTACTTA
GATGGTGGTTTATCTGATAGTATTCCCGTTGATTTTGCCCGTGGTTTAGG
ATTTGACAAGTTGATTGTTGTGATGACTAGGCCGCTCAATTATCAGAAAA
AGCCTTCAAGTGGACGATTGTATAAACTCTGTATAGGAAATATCCTAAT
TTTGTAAAGACAGCCTCGAATCGGTACCAACAGTATAATAATAGTCTTGA
AAAGGTCAATGAGCCTTGAAAAACAGGCGATCTATTTGCAATTAGACCGA
GTAAGAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAACTTGAT
AGTATTTATCAGCTTGGTATGAAATATGCTAAAAGTGTGATGCCTGAGCT
GAATAGTTATCTAATGAAA

SEQ ID NO. 7708

STRAIN M781

CCTATGTTGTCTGTTGGTTTGTAGTTTGTAG
AGGGTGGCGGAATGAGAGGTCTTTATACTGCTGGAGTTTGTAGATGCTTTT
CTAGATGCAGGAATAAAAATAGATGGTATCGTATCTGTCTCTGCGGGTGC
ATTGTTTGGTGTAAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGAT
ACAATAAAAAGTATTTATCCACCCTGAATATATGAGTCTAAGATCATGG
CTTCGAACAGGGAATTTTGTAAATAAAGATTTACCTATTATGAAGTTC
TATGAAATTGGATGTATTTGACGATGAAGCATTAAAAAATCAAGTATTG
ATTTTACGTAGTTGCTACAGAGATGACATCTGGTAAACCTGAATATTT
AAAATTGATAGTGTTTTGAACAAATGGAAATTTTACGTGCTAGTTCAGC
ATTACCAGTAGTCTCAAAGATGGTTGATTGGCAGGGGAAAAAGTACTTAG
ATGGTGGTTTATCTGATAGTATTCCCGTTGATTTTGCCCGTGGTTTAGGA
TTTGACAAGTTGATTGTTGTGATGACTAGGCCGCTCAATTATCAGAAAA
GCCTTCAAGTGGACGATTGTATAAACTCTGTATAGGAAATATCCTAAT
TTGTAAAGACAGCCTCGAATCGGTACCAACAGTATAATAATAGTCTTGAA
AAGGTCAATGAGCCTTGAAAAACAGGCGATCTATTTGCAATTAGACCGAG
TAAGAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAACTTGATA
GTATTTATCAGCTTGGTATGAAATATGCTAAAAGTGTGATGCCTGAGCTG
AATAGTTATCTAATGAAA

Table 77: Comparative Sequences relating toSAG2059

SEQ ID NO. 7709

STRAIN CJB110

CCTATGTTGTCTGTTGGTTTAGTTTTA
GAGGGTGGCGGAATGAGAGGTCCTTATACTGCTGGAGTTTTAGATGCTTT
TCTAGATGCAGGAATAAAAAATAGATGGTATCGTATCTGTCTCTGCTGGTG
CATTGTTTGGTGTTAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGA
TACAATAAAAAAGTATTTATCCACCCTAAATATATGAGTCTAAGGTCATG
GTTTCGAACAGGGAAATTTTGTAAATAAAGATTTACCTATTATGAAGTTC
CTATGAAATTTGGATGTATTTGACGATGAAGCATTTAAAAAATCAAGTATT
GATTTTACGTAGTTGCTACAGAGATGACATCTGGTAAACCTGAATATTT
TAAAAATTGATAGTGTTTTGAACAAATGGAAATTTTACGTGCTAGTTTCAG
CATTACCAAGTAGTCTCAAAGATGGTTGATTGGCAGGGGAAAAAGTACTTA
GATGGTGGTTTATCTGATAGTATTTCCCGTTGATTTTGGCCGTGGTTTAGG
ATTTGACAAAGTTGATTGTTGTGATGACTAGGCCGCTCAATTATCAGAAAA
AGCCTTCAAGTGGACGATTGTATAAACTCTGTATAGGAAATATCCTAAT
TTTGTAAGACAGCCTCGAATCGGTACCAACAGTATAATAATAGTCTTGA
AAAGGTCATGAGCCTTGAAAAACAGGCGATCTATTTGCAATTAGACCGA
GTAAGAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAACTTGAT
AGTATTTATCAGCTTGGTATGAAAGATGCTAAAAGTGTGATGCCTGAGCT
GAATAGTTATCTAATGAAA

SEQ ID NO. 7710

STRAIN 1169NT

CCTATGTTGTCTGTTGGTTTAGTTTTAGAGGGTG
GCGGAATGAGAGGTCCTTATACTGCTGGAGTTTTAGATGCTTTTCTAGAT
GCAGGAATAAAAAATAGATGGTATCGTATCTGTCTCTGCGGGTGCATTGTT
TGGTGTAAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGATACAATA
AAAAGTATTTATCCACCCTAAATATATGAGTCTAAGATCATGGCTTCGA
ACAGGGAAATTTTGTAAATAAAGATTTACCTATTATGAAGTTCCTATGAA
ATTGGATGTATTTGACGATGAAGCATTTAAAAAATCAAGTATTGATTTTT
ACGCAGTTGCTACAGAGATGACATCTGGTAAACCTGAATATTTTAAAT
GATAGTGTCTTTGAACAAATGGAAATTTTACGTGCTAGTTTCAGCATTACC
AGTAGTCTCAAAGATGGTTGATTGGCAGGGGAAAAAGTACTTAGATGGTG
GTTTATCTGATAGTATCCCGTTGATTTTGGCCGTGGTTTAGGATTTGAC
AAGTTGATTGTTGTGATGACTAGGCCGCTCAATTATCAGAAAAAGCCTTC
AAGTGGACGATTGTATAAACTCTGTATAGGAAATATCCTAATTTTGTA
AGACAGCCTCGAATCGGTACCAACAGTATAATAATAGCCTTGAAAAGGTC
ATGAGCCTTGAAAAACAGGCGATCTATTTGCAATTAGGCCGAGTAAAG
CTTGGTTATTGTCCGCTTAGAGAAGAATCCGGATAAACTTGATAGTATT
ATCAGCTTGGTATGAAAGATGCTAAAAGTGTGATGCCTGAGCTGAATAGT
TATCTAATGAAA

SEQ ID NO. 7711

STRAIN JM9130013

CCTATGTTGTCTGTTGGTTTAGTTTTAGAG
GGTGGCGGAATGAGAGGTCCTTATACTGCTGGAGTTTTAGATGCTTTTCT
AGATGCAGGAATAAAAGTAGATGGTATCATATCTGTCTCTGCTGGTGCAT
TGTTTGGTGTTAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGATAC
AATAAAAAAGTATTTATCCACCCTAAATATATGAGTCTAAGGTCATGGCT
TCGAACAGGGAAATTTTGTAAATAAAGATTTACCTATTATGAAGTTCCTA
TGAAATTGGATGTATTTGACGATGAAGCATTTAAAAAATCAAGTATTGAT
TTTTACGCAGTTGCTACAGAGATGACATCTGGTAAACCTGAGTATTTTAA
AATTGATAGTGTTTTTGAACAAATGGAAATTTTACGTGCTAGTTTCAGCAT
TACCAGTAGTCTCAAAGATGGTTGTTTGGCAGGGGAAAAAGTACTTAGAT
GGTGGTTTATCTGATAGTATTTCCCGTTGATTTTGGCCGTGGTTTAGGATT
TGACAAGTTGATTGTTGTGATGACTAGGCCGCTCAATTATCAGAAAAAGC
CTTCAAGTGGACGATTGTATAAACTCTGTATAGGAAATATCCTAATTTT
GTAAAGACAGCCTCGAACCAGGTACCAACAGTATAATAATAGCCTTGAAAA
GGTCATGAGCCTTGAAAAACAGGCGATCTATTTGCAATTAGACCAAGTA
AGAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAACTTGATAGT
ATTTATCAGCTTGGTATGAAAGATGCTAAAAGTGGGATGCCTGAGCTGAA
TAGTTATCTAATGAAA

PRETTY of: /biotmp/msa47199.2{*} February 19, 2003 05:51 ..

	1				50
msa47199.2{394_A909}	---CCTATGT	TGTCTGTTGG	TTTAGTTTTA	GAGGGTGGCG	GAATGAGAGG
msa47199.2{394_H36B}	---CCTATGT	TGTCTGTTGG	TTTAGTTTTA	GAGGGTGGCG	GAATGAGAGG
msa47199.2{394_JM9130013}	---CCTATGT	TGTCTGTTGG	TTTAGTTTTA	GAGGGTGGCG	GAATGAGAGG
msa47199.2{394_090}	---CCTATGT	TGTCTGTTGG	TTTAGTTTTA	GAGGGTGGCG	GAATGAGAGG
msa47199.2{394_18RS21}	---CCTATGT	TGTCTGTTGG	TTTAGTTTTA	GAGGGTGGCG	GAATGAGAGG
msa47199.2{394_2603}	ttgCCTATGT	TGTCTGTTGG	TTTAGTTTTA	GAGGGTGGCG	GAATGAGAGG
msa47199.2{394_CJB110}	---CCTATGT	TGTCTGTTGG	TTTAGTTTTA	GAGGGTGGCG	GAATGAGAGG
msa47199.2{394_COH1}	---CCTATGT	TGTCTGTTGG	TTTAGTTTTA	GAGGGTGGCG	GAATGAGAGG
msa47199.2{394_M732}	---CCTATGT	TGTCTGTTGG	TTTAGTTTTA	GAGGGTGGCG	GAATGAGAGG
msa47199.2{394_M781}	---CCTATGT	TGTCTGTTGG	TTTAGTTTTA	GAGGGTGGCG	GAATGAGAGG
msa47199.2{394_1169NT}	---CCTATGT	TGTCTGTTGG	TTTAGTTTTA	GAGGGTGGCG	GAATGAGAGG
Consensus	*****	*****	*****	*****	*****
	51				100
msa47199.2{394_A909}	TCCTTATACT	GCTGGAGTTT	TAGATGCTTT	TCTAGATGCA	GGAATAAAAg
msa47199.2{394_H36B}	TCCTTATACT	GCTGGAGTTT	TAGATGCTTT	TCTAGATGCA	GGAATAAAAg
msa47199.2{394_JM9130013}	TCCTTATACT	GCTGGAGTTT	TAGATGCTTT	TCTAGATGCA	GGAATAAAAg

Table 77: Comparative Sequences relating toSAG2059

msa47199.2{394_090}	TCTTTATACT	GCTGGAGTTT	TAGATGCTTT	TCTAGATGCA	GGAATAAAAA
msa47199.2{394_18RS21}	TCTTTATACT	GCTGGAGTTT	TAGATGCTTT	TCTAGATGCA	GGAATAAAAA
msa47199.2{394_2603}	TCTTTATACT	GCTGGAGTTT	TAGATGCTTT	TCTAGATGCA	GGAATAAAAA
msa47199.2{394_CJB110}	TCTTTATACT	GCTGGAGTTT	TAGATGCTTT	TCTAGATGCA	GGAATAAAAA
msa47199.2{394_COH1}	TCTTTATACT	GCTGGAGTTT	TAGATGCTTT	TCTAGATGCA	GGAATAAAAA
msa47199.2{394_M732}	TCTTTATACT	GCTGGAGTTT	TAGATGCTTT	TCTAGATGCA	GGAATAAAAA
msa47199.2{394_M781}	TCTTTATACT	GCTGGAGTTT	TAGATGCTTT	TCTAGATGCA	GGAATAAAAA
msa47199.2{394_1169NT}	TCTTTATACT	GCTGGAGTTT	TAGATGCTTT	TCTAGATGCA	GGAATAAAAA
Consensus	*****	*****	*****	*****	*****
101					
msa47199.2{394_A909}	TAGATGGTAT	CaTATCTGTC	TCTGCTGGTG	CATTGTTTGG	TGTTAATTTT
msa47199.2{394_H36B}	TAGATGGTAT	CaTATCTGTC	TCTGCTGGTG	CATTGTTTGG	TGTTAATTTT
msa47199.2{394_JM9130013}	TAGATGGTAT	CaTATCTGTC	TCTGCTGGTG	CATTGTTTGG	TGTTAATTTT
msa47199.2{394_090}	TAGATGGTAT	CgTATCTGTC	TCTGCTGGTG	CATTGTTTGG	TGTTAATTTT
msa47199.2{394_18RS21}	TAGATGGTAT	CgTATCTGTC	TCTGCTGGTG	CATTGTTTGG	TGTTAATTTT
msa47199.2{394_2603}	TAGATGGTAT	CgTATCTGTC	TCTGCTGGTG	CATTGTTTGG	TGTTAATTTT
msa47199.2{394_CJB110}	TAGATGGTAT	CgTATCTGTC	TCTGCTGGTG	CATTGTTTGG	TGTTAATTTT
msa47199.2{394_COH1}	TAGATGGTAT	CgTATCTGTC	TCTGCTGGTG	CATTGTTTGG	TGTTAATTTT
msa47199.2{394_M732}	TAGATGGTAT	CgTATCTGTC	TCTGCTGGTG	CATTGTTTGG	TGTTAATTTT
msa47199.2{394_M781}	TAGATGGTAT	CgTATCTGTC	TCTGCTGGTG	CATTGTTTGG	TGTTAATTTT
msa47199.2{394_1169NT}	TAGATGGTAT	CgTATCTGTC	TCTGCTGGTG	CATTGTTTGG	TGTTAATTTT
Consensus	*****	*-*****	*****-****	*****	*****
151					
msa47199.2{394_A909}	GTATCTAGAC	AACGAGAGAG	GGCTTTGCGA	TACAATAAAA	AGTATTTATC
msa47199.2{394_H36B}	GTATCTAGAC	AACGAGAGAG	GGCTTTGCGA	TACAATAAAA	AGTATTTATC
msa47199.2{394_JM9130013}	GTATCTAGAC	AACGAGAGAG	GGCTTTGCGA	TACAATAAAA	AGTATTTATC
msa47199.2{394_090}	GTATCTAGAC	AACGAGAGAG	GGCTTTGCGA	TACAATAAAA	AGTATTTATC
msa47199.2{394_18RS21}	GTATCTAGAC	AACGAGAGAG	GGCTTTGCGA	TACAATAAAA	AGTATTTATC
msa47199.2{394_2603}	GTATCTAGAC	AACGAGAGAG	GGCTTTGCGA	TACAATAAAA	AGTATTTATC
msa47199.2{394_CJB110}	GTATCTAGAC	AACGAGAGAG	GGCTTTGCGA	TACAATAAAA	AGTATTTATC
msa47199.2{394_COH1}	GTATCTAGAC	AACGAGAGAG	GGCTTTGCGA	TACAATAAAA	AGTATTTATC
msa47199.2{394_M732}	GTATCTAGAC	AACGAGAGAG	GGCTTTGCGA	TACAATAAAA	AGTATTTATC
msa47199.2{394_M781}	GTATCTAGAC	AACGAGAGAG	GGCTTTGCGA	TACAATAAAA	AGTATTTATC
msa47199.2{394_1169NT}	GTATCTAGAC	AACGAGAGAG	GGCTTTGCGA	TACAATAAAA	AGTATTTATC
Consensus	*****	*****	*****	*****	*****
201					
msa47199.2{394_A909}	CCACCCTaAA	TATATGAGTC	TAAGgTCATG	GcTTCGAACA	GCGAATTTTG
msa47199.2{394_H36B}	CCACCCTaAA	TATATGAGTC	TAAGgTCATG	GcTTCGAACA	GCGAATTTTG
msa47199.2{394_JM9130013}	CCACCCTaAA	TATATGAGTC	TAAGgTCATG	GcTTCGAACA	GCGAATTTTG
msa47199.2{394_090}	CCACCCTaAA	TATATGAGTC	TAAGgTCATG	GtTTCGAACA	GCGAATTTTG
msa47199.2{394_18RS21}	CCACCCTaAA	TATATGAGTC	TAAGgTCATG	GtTTCGAACA	GCGAATTTTG
msa47199.2{394_2603}	CCACCCTaAA	TATATGAGTC	TAAGgTCATG	GtTTCGAACA	GCGAATTTTG
msa47199.2{394_CJB110}	CCACCCTaAA	TATATGAGTC	TAAGgTCATG	GtTTCGAACA	GCGAATTTTG
msa47199.2{394_COH1}	CCACCCTgAA	TATATGAGTC	TAAGaTCATG	GcTTCGAACA	GCGAATTTTG
msa47199.2{394_M732}	CCACCCTgAA	TATATGAGTC	TAAGaTCATG	GcTTCGAACA	GCGAATTTTG
msa47199.2{394_M781}	CCACCCTgAA	TATATGAGTC	TAAGaTCATG	GcTTCGAACA	GCGAATTTTG
msa47199.2{394_1169NT}	CCACCCTaAA	TATATGAGTC	TAAGaTCATG	GcTTCGAACA	GCGAATTTTG
Consensus	*****-**	*****	****-*****	*-*****	*****
251					
msa47199.2{394_A909}	TTAATAAAGA	TTTCACCTAT	TATGAAGTTC	CTATGAAATT	GGATGTATTT
msa47199.2{394_H36B}	TTAATAAAGA	TTTCACCTAT	TATGAAGTTC	CTATGAAATT	GGATGTATTT
msa47199.2{394_JM9130013}	TTAATAAAGA	TTTCACCTAT	TATGAAGTTC	CTATGAAATT	GGATGTATTT
msa47199.2{394_090}	TTAATAAAGA	TTTCACCTAT	TATGAAGTTC	CTATGAAATT	GGATGTATTT
msa47199.2{394_18RS21}	TTAATAAAGA	TTTCACCTAT	TATGAAGTTC	CTATGAAATT	GGATGTATTT
msa47199.2{394_2603}	TTAATAAAGA	TTTCACCTAT	TATGAAGTTC	CTATGAAATT	GGATGTATTT
msa47199.2{394_CJB110}	TTAATAAAGA	TTTCACCTAT	TATGAAGTTC	CTATGAAATT	GGATGTATTT
msa47199.2{394_COH1}	TTAATAAAGA	TTTCACCTAT	TATGAAGTTC	CTATGAAATT	GGATGTATTT
msa47199.2{394_M732}	TTAATAAAGA	TTTCACCTAT	TATGAAGTTC	CTATGAAATT	GGATGTATTT
msa47199.2{394_M781}	TTAATAAAGA	TTTCACCTAT	TATGAAGTTC	CTATGAAATT	GGATGTATTT
msa47199.2{394_1169NT}	TTAATAAAGA	TTTCACCTAT	TATGAAGTTC	CTATGAAATT	GGATGTATTT
Consensus	*****	*****	*****	*****	*****
301					
msa47199.2{394_A909}	GACGATGAAG	CATTTAAAAA	ATCAAGTATT	GATTTTTACG	cAGTTGCTAC
msa47199.2{394_H36B}	GACGATGAAG	CATTTAAAAA	ATCAAGTATT	GATTTTTACG	cAGTTGCTAC
msa47199.2{394_JM9130013}	GACGATGAAG	CATTTAAAAA	ATCAAGTATT	GATTTTTACG	cAGTTGCTAC
msa47199.2{394_090}	GACGATGAAG	CATTTAAAAA	ATCAAGTATT	GATTTTTACG	tAGTTGCTAC
msa47199.2{394_18RS21}	GACGATGAAG	CATTTAAAAA	ATCAAGTATT	GATTTTTACG	tAGTTGCTAC
msa47199.2{394_2603}	GACGATGAAG	CATTTAAAAA	ATCAAGTATT	GATTTTTACG	tAGTTGCTAC
msa47199.2{394_CJB110}	GACGATGAAG	CATTTAAAAA	ATCAAGTATT	GATTTTTACG	tAGTTGCTAC
msa47199.2{394_COH1}	GACGATGAAG	CATTTAAAAA	ATCAAGTATT	GATTTTTACG	tAGTTGCTAC
msa47199.2{394_M732}	GACGATGAAG	CATTTAAAAA	ATCAAGTATT	GATTTTTACG	tAGTTGCTAC
msa47199.2{394_M781}	GACGATGAAG	CATTTAAAAA	ATCAAGTATT	GATTTTTACG	tAGTTGCTAC
msa47199.2{394_1169NT}	GACGATGAAG	CATTTAAAAA	ATCAAGTATT	GATTTTTACG	cAGTTGCTAC
Consensus	*****	*****	*****	*****	-*****
351					
msa47199.2{394_A909}	AGAGATGACA	TCTGGTAAAC	CTGAgTATTT	TAAAATTGAT	AGTGTtTTTG
msa47199.2{394_H36B}	AGAGATGACA	TCTGGTAAAC	CTGAgTATTT	TAAAATTGAT	AGTGTtTTTG

Table 77: Comparative Sequences relating toSAG2059

msa47199.2{394_JM9130013}	AGAGATGACA	TCTGGTAAAC	CTGAaTATTT	TAAAATTGAT	AGTGTtTTTG
msa47199.2{394_090}	AGAGATGACA	TCTGGTAAAC	CTGAaTATTT	TAAAATTGAT	AGTGTtTTTG
msa47199.2{394_18RS21}	AGAGATGACA	TCTGGTAAAC	CTGAaTATTT	TAAAATTGAT	AGTGTtTTTG
msa47199.2{394_2603}	AGAGATGACA	TCTGGTAAAC	CTGAaTATTT	TAAAATTGAT	AGTGTtTTTG
msa47199.2{394_CJB110}	AGAGATGACA	TCTGGTAAAC	CTGAaTATTT	TAAAATTGAT	AGTGTtTTTG
msa47199.2{394_COH1}	AGAGATGACA	TCTGGTAAAC	CTGAaTATTT	TAAAATTGAT	AGTGTtTTTG
msa47199.2{394_M732}	AGAGATGACA	TCTGGTAAAC	CTGAaTATTT	TAAAATTGAT	AGTGTtTTTG
msa47199.2{394_M781}	AGAGATGACA	TCTGGTAAAC	CTGAaTATTT	TAAAATTGAT	AGTGTtTTTG
msa47199.2{394_1169NT}	AGAGATGACA	TCTGGTAAAC	CTGAaTATTT	TAAAATTGAT	AGTGTtTTTG
Consensus	*****	*****	*****	*****	*****
401					
msa47199.2{394_A909}	AACAAATGGA	AATTTTACGT	GCTAGTTCAG	CATTACCAGT	AGTCTCAAAG
msa47199.2{394_H36B}	AACAAATGGA	AATTTTACGT	GCTAGTTCAG	CATTACCAGT	AGTCTCAAAG
msa47199.2{394_JM9130013}	AACAAATGGA	AATTTTACGT	GCTAGTTCAG	CATTACCAGT	AGTCTCAAAG
msa47199.2{394_090}	AACAAATGGA	AATTTTACGT	GCTAGTTCAG	CATTACCAGT	AGTCTCAAAG
msa47199.2{394_18RS21}	AACAAATGGA	AATTTTACGT	GCTAGTTCAG	CATTACCAGT	AGTCTCAAAG
msa47199.2{394_2603}	AACAAATGGA	AATTTTACGT	GCTAGTTCAG	CATTACCAGT	AGTCTCAAAG
msa47199.2{394_CJB110}	AACAAATGGA	AATTTTACGT	GCTAGTTCAG	CATTACCAGT	AGTCTCAAAG
msa47199.2{394_COH1}	AACAAATGGA	AATTTTACGT	GCTAGTTCAG	CATTACCAGT	AGTCTCAAAG
msa47199.2{394_M732}	AACAAATGGA	AATTTTACGT	GCTAGTTCAG	CATTACCAGT	AGTCTCAAAG
msa47199.2{394_M781}	AACAAATGGA	AATTTTACGT	GCTAGTTCAG	CATTACCAGT	AGTCTCAAAG
msa47199.2{394_1169NT}	AACAAATGGA	AATTTTACGT	GCTAGTTCAG	CATTACCAGT	AGTCTCAAAG
Consensus	*****	*****	*****	*****	*****
451					
msa47199.2{394_A909}	ATGGTTGtTT	GGCAGGGGAA	AAAGTACTTA	GATGGTGGTT	TATCTGATAG
msa47199.2{394_H36B}	ATGGTTGtTT	GGCAGGGGAA	AAAGTACTTA	GATGGTGGTT	TATCTGATAG
msa47199.2{394_JM9130013}	ATGGTTGtTT	GGCAGGGGAA	AAAGTACTTA	GATGGTGGTT	TATCTGATAG
msa47199.2{394_090}	ATGGTTGtTT	GGCAGGGGAA	AAAGTACTTA	GATGGTGGTT	TATCTGATAG
msa47199.2{394_18RS21}	ATGGTTGtTT	GGCAGGGGAA	AAAGTACTTA	GATGGTGGTT	TATCTGATAG
msa47199.2{394_2603}	ATGGTTGtTT	GGCAGGGGAA	AAAGTACTTA	GATGGTGGTT	TATCTGATAG
msa47199.2{394_CJB110}	ATGGTTGtTT	GGCAGGGGAA	AAAGTACTTA	GATGGTGGTT	TATCTGATAG
msa47199.2{394_COH1}	ATGGTTGtTT	GGCAGGGGAA	AAAGTACTTA	GATGGTGGTT	TATCTGATAG
msa47199.2{394_M732}	ATGGTTGtTT	GGCAGGGGAA	AAAGTACTTA	GATGGTGGTT	TATCTGATAG
msa47199.2{394_M781}	ATGGTTGtTT	GGCAGGGGAA	AAAGTACTTA	GATGGTGGTT	TATCTGATAG
msa47199.2{394_1169NT}	ATGGTTGtTT	GGCAGGGGAA	AAAGTACTTA	GATGGTGGTT	TATCTGATAG
Consensus	*****	*****	*****	*****	*****
501					
msa47199.2{394_A909}	TATtCCCGTT	GATTTTGCCC	GTGGTTTAGG	ATTTGACAAG	TTGATTGTTG
msa47199.2{394_H36B}	TATtCCCGTT	GATTTTGCCC	GTGGTTTAGG	ATTTGACAAG	TTGATTGTTG
msa47199.2{394_JM9130013}	TATtCCCGTT	GATTTTGCCC	GTGGTTTAGG	ATTTGACAAG	TTGATTGTTG
msa47199.2{394_090}	TATtCCCGTT	GATTTTGCCC	GTGGTTTAGG	ATTTGACAAG	TTGATTGTTG
msa47199.2{394_18RS21}	TATtCCCGTT	GATTTTGCCC	GTGGTTTAGG	ATTTGACAAG	TTGATTGTTG
msa47199.2{394_2603}	TATtCCCGTT	GATTTTGCCC	GTGGTTTAGG	ATTTGACAAG	TTGATTGTTG
msa47199.2{394_CJB110}	TATtCCCGTT	GATTTTGCCC	GTGGTTTAGG	ATTTGACAAG	TTGATTGTTG
msa47199.2{394_COH1}	TATtCCCGTT	GATTTTGCCC	GTGGTTTAGG	ATTTGACAAG	TTGATTGTTG
msa47199.2{394_M732}	TATtCCCGTT	GATTTTGCCC	GTGGTTTAGG	ATTTGACAAG	TTGATTGTTG
msa47199.2{394_M781}	TATtCCCGTT	GATTTTGCCC	GTGGTTTAGG	ATTTGACAAG	TTGATTGTTG
msa47199.2{394_1169NT}	TATtCCCGTT	GATTTTGCCC	GTGGTTTAGG	ATTTGACAAG	TTGATTGTTG
Consensus	*****	*****	*****	*****	*****
551					
msa47199.2{394_A909}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAAG	TGGACGATTG
msa47199.2{394_H36B}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAAG	TGGACGATTG
msa47199.2{394_JM9130013}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAAG	TGGACGATTG
msa47199.2{394_090}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAAG	TGGACGATTG
msa47199.2{394_18RS21}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAAG	TGGACGATTG
msa47199.2{394_2603}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAAG	TGGACGATTG
msa47199.2{394_CJB110}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAAG	TGGACGATTG
msa47199.2{394_COH1}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAAG	TGGACGATTG
msa47199.2{394_M732}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAAG	TGGACGATTG
msa47199.2{394_M781}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAAG	TGGACGATTG
msa47199.2{394_1169NT}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAAG	TGGACGATTG
Consensus	*****	*****	*****	*****	*****
601					
msa47199.2{394_A909}	TATAAACTC	TGTATAGGAA	ATATCCTAAT	TTTGTAAGA	CAGCCTCGAA
msa47199.2{394_H36B}	TATAAACTC	TGTATAGGAA	ATATCCTAAT	TTTGTAAGA	CAGCCTCGAA
msa47199.2{394_JM9130013}	TATAAACTC	TGTATAGGAA	ATATCCTAAT	TTTGTAAGA	CAGCCTCGAA
msa47199.2{394_090}	TATAAACTC	TGTATAGGAA	ATATCCTAAT	TTTGTAAGA	CAGCCTCGAA
msa47199.2{394_18RS21}	TATAAACTC	TGTATAGGAA	ATATCCTAAT	TTTGTAAGA	CAGCCTCGAA
msa47199.2{394_2603}	TATAAACTC	TGTATAGGAA	ATATCCTAAT	TTTGTAAGA	CAGCCTCGAA
msa47199.2{394_CJB110}	TATAAACTC	TGTATAGGAA	ATATCCTAAT	TTTGTAAGA	CAGCCTCGAA
msa47199.2{394_COH1}	TATAAACTC	TGTATAGGAA	ATATCCTAAT	TTTGTAAGA	CAGCCTCGAA
msa47199.2{394_M732}	TATAAACTC	TGTATAGGAA	ATATCCTAAT	TTTGTAAGA	CAGCCTCGAA
msa47199.2{394_M781}	TATAAACTC	TGTATAGGAA	ATATCCTAAT	TTTGTAAGA	CAGCCTCGAA
msa47199.2{394_1169NT}	TATAAACTC	TGTATAGGAA	ATATCCTAAT	TTTGTAAGA	CAGCCTCGAA
Consensus	*****	*****	*****	*****	*****
651					
msa47199.2{394_A909}	cCGGTACCAA	CAGTATAATA	ATAGcCTTGA	AAAGGTCATG	AGCCTTGAAA
700					

Table 77: Comparative Sequences relating to SAG2059

msa47199.2{394_H36B}	cCGGTACCAA	CAGTATAATA	ATAGcCTTGA	AAAGGTCATG	AGCCTTGAAA
msa47199.2{394_JM9130013}	cCGGTACCAA	CAGTATAATA	ATAGcCTTGA	AAAGGTCATG	AGCCTTGAAA
msa47199.2{394_090}	tCGGTACCAA	CAGTATAATA	ATAGtCTTGA	AAAGGTCATG	AGCCTTGAAA
msa47199.2{394_18RS21}	tCGGTACCAA	CAGTATAATA	ATAGtCTTGA	AAAGGTCATG	AGCCTTGAAA
msa47199.2{394_2603}	tCGGTACCAA	CAGTATAATA	ATAGtCTTGA	AAAGGTCATG	AGCCTTGAAA
msa47199.2{394_CJB110}	tCGGTACCAA	CAGTATAATA	ATAGtCTTGA	AAAGGTCATG	AGCCTTGAAA
msa47199.2{394_COH1}	tCGGTACCAA	CAGTATAATA	ATAGtCTTGA	AAAGGTCATG	AGCCTTGAAA
msa47199.2{394_M732}	tCGGTACCAA	CAGTATAATA	ATAGtCTTGA	AAAGGTCATG	AGCCTTGAAA
msa47199.2{394_M781}	tCGGTACCAA	CAGTATAATA	ATAGtCTTGA	AAAGGTCATG	AGCCTTGAAA
msa47199.2{394_1169NT}	tCGGTACCAA	CAGTATAATA	ATAGcCTTGA	AAAGGTCATG	AGCCTTGAAA
Consensus	*****	*****	*****	*****	*****
701					
msa47199.2{394_A909}	AAACAGGCGA	TCTATTTGCA	ATTAGaCCaA	GTAAGAGCTT	GGTTATTGgC
msa47199.2{394_H36B}	AAACAGGCGA	TCTATTTGCA	ATTAGaCCaA	GTAAGAGCTT	GGTTATTGgC
msa47199.2{394_JM9130013}	AAACAGGCGA	TCTATTTGCA	ATTAGaCCaA	GTAAGAGCTT	GGTTATTGgC
msa47199.2{394_090}	AAACAGGCGA	TCTATTTGCA	ATTAGaCCgA	GTAAGAGCTT	GGTTATTGgC
msa47199.2{394_18RS21}	AAACAGGCGA	TCTATTTGCA	ATTAGaCCgA	GTAAGAGCTT	GGTTATTGgC
msa47199.2{394_2603}	AAACAGGCGA	TCTATTTGCA	ATTAGaCCgA	GTAAGAGCTT	GGTTATTGgC
msa47199.2{394_CJB110}	AAACAGGCGA	TCTATTTGCA	ATTAGaCCgA	GTAAGAGCTT	GGTTATTGgC
msa47199.2{394_COH1}	AAACAGGCGA	TCTATTTGCA	ATTAGaCCgA	GTAAGAGCTT	GGTTATTGgC
msa47199.2{394_M732}	AAACAGGCGA	TCTATTTGCA	ATTAGaCCgA	GTAAGAGCTT	GGTTATTGgC
msa47199.2{394_M781}	AAACAGGCGA	TCTATTTGCA	ATTAGaCCgA	GTAAGAGCTT	GGTTATTGgC
msa47199.2{394_1169NT}	AAACAGGCGA	TCTATTTGCA	ATTAGgCCgA	GTAaAGCTT	GGTTATTGtC
Consensus	*****	*****	*****	*****	*****
751					
msa47199.2{394_A909}	CGCTTAGAGA	AGAATCCGGA	TAAACTTGAT	AGTATTTATC	AGCTTGGTAT
msa47199.2{394_H36B}	CGCTTAGAGA	AGAATCCGGA	TAAACTTGAT	AGTATTTATC	AGCTTGGTAT
msa47199.2{394_JM9130013}	CGCTTAGAGA	AGAATCCGGA	TAAACTTGAT	AGTATTTATC	AGCTTGGTAT
msa47199.2{394_090}	CGCTTAGAGA	AGAATCCGGA	TAAACTTGAT	AGTATTTATC	AGCTTGGTAT
msa47199.2{394_18RS21}	CGCTTAGAGA	AGAATCCGGA	TAAACTTGAT	AGTATTTATC	AGCTTGGTAT
msa47199.2{394_2603}	CGCTTAGAGA	AGAATCCGGA	TAAACTTGAT	AGTATTTATC	AGCTTGGTAT
msa47199.2{394_CJB110}	CGCTTAGAGA	AGAATCCGGA	TAAACTTGAT	AGTATTTATC	AGCTTGGTAT
msa47199.2{394_COH1}	CGCTTAGAGA	AGAATCCGGA	TAAACTTGAT	AGTATTTATC	AGCTTGGTAT
msa47199.2{394_M732}	CGCTTAGAGA	AGAATCCGGA	TAAACTTGAT	AGTATTTATC	AGCTTGGTAT
msa47199.2{394_M781}	CGCTTAGAGA	AGAATCCGGA	TAAACTTGAT	AGTATTTATC	AGCTTGGTAT
msa47199.2{394_1169NT}	CGCTTAGAGA	AGAATCCGGA	TAAACTTGAT	AGTATTTATC	AGCTTGGTAT
Consensus	*****	*****	*****	*****	*****
801					
msa47199.2{394_A909}	GAAAGATGCT	AAAAGTGgGA	TGCCTGAGCT	GAATAGTTAT	CTAATGAAA
msa47199.2{394_H36B}	GAAAGATGCT	AAAAGTGgGA	TGCCTGAGCT	GAATAGTTAT	CTAATGAAA
msa47199.2{394_JM9130013}	GAAAGATGCT	AAAAGTGgGA	TGCCTGAGCT	GAATAGTTAT	CTAATGAAA
msa47199.2{394_090}	GAAAGATGCT	AAAAGTGtGA	TGCCTGAGCT	GAATAGTTAT	CTAATGAAA
msa47199.2{394_18RS21}	GAAAGATGCT	AAAAGTGtGA	TGCCTGAGCT	GAATAGTTAT	CTAATGAAA
msa47199.2{394_2603}	GAAAGATGCT	AAAAGTGtGA	TGCCTGAGCT	GAATAGTTAT	CTAATGAAA
msa47199.2{394_CJB110}	GAAAGATGCT	AAAAGTGtGA	TGCCTGAGCT	GAATAGTTAT	CTAATGAAA
msa47199.2{394_COH1}	GAAAtATGCT	AAAAGTGtGA	TGCCTGAGCT	GAATAGTTAT	CTAATGAAA
msa47199.2{394_M732}	GAAAtATGCT	AAAAGTGtGA	TGCCTGAGCT	GAATAGTTAT	CTAATGAAA
msa47199.2{394_M781}	GAAAtATGCT	AAAAGTGtGA	TGCCTGAGCT	GAATAGTTAT	CTAATGAAA
msa47199.2{394_1169NT}	GAAAGATGCT	AAAAGTGtGA	TGCCTGAGCT	GAATAGTTAT	CTAATGAAA
Consensus	*****	*****	*****	*****	*****

SEQ ID NO. 7712

STRAIN 2603 frame: 1

PMLSVGLVLEGGMRGLYTAGVLDAGIKIDGIVSVSAGALFGVNFVSRQRERALRY
 NKKYLSHPKYMSLRSWFRTGNFVNKDFTYYEVPMKLDVFDDEAFKKSSIDFYVVATEMTS
 GKPEYFKIDSVEQMEILRASSALPVVSKMVDWQGGKYLDDGLSDSIPVDFARGLGFDKL
 IVVMTRPLNYQKKPSSGRLYKTLRKYPNFVKTSNRYQQYNNLSLEKVMSEKLTGDLFAI
 RPSKSLVIGRLEKNPDKLDSIYQLGMKDAKSVMPPELNSYLMK

SEQ ID NO. 7713

STRAIN 090 frame: 1

PMLSVGLVLEGGMRGLYTAGVLDAGIKIDGIVSVSAGALFGVNFVSRQRERALRY
 NKKYLSHPKYMSLRSWFRTGNFVNKDFTYYEVPMKLDVFDDEAFKKSSIDFYVVATEMTS
 GKPEYFKIDSVEQMEILRASSALPVVSKMVDWQGGKYLDDGLSDSIPVDFARGLGFDKL
 IVVMTRPLNYQKKPSSGRLYKTLRKYPNFVKTSNRYQQYNNLSLEKVMSEKLTGDLFAI
 RPSKSLVIGRLEKNPDKLDSIYQLGMKDAKSVMPPELNSYLMK

SEQ ID NO. 7714

STRAIN A909 frame: 1

PMLSVGLVLEGGMRGLYTAGVLDAGIKVDGII SVSAGALFGVNFVSRQRERALRY
 NKKYLSHPKYMSLRSWLRTGNFVNKDFTYYEVPMKLDVFDDEAFKKSSIDFYAVATEMTS
 GKPEYFKIDSVEQMEILRASSALPVVSKMVVWQGGKYLDDGLSDSIPVDFARGLGFDKL
 IVVMTRPLNYQKKPSSGRLYKTLRKYPNFVKTSNRYQQYNNLSLEKVMSEKLTGDLFAI
 RPSKSLVIGRLEKNPDKLDSIYQLGMKDAKSGMPELNSYLMK

SEQ ID NO. 7715

STRAIN H36B frame: 1

PMLSVGLVLEGGMRGLYTAGVLDAGIKVDGII SVSAGALFGVNFVSRQRERALRY
 NKKYLSHPKYMSLRSWLRTGNFVNKDFTYYEVPMKLDVFDDEAFKKSSIDFYAVATEMTS

Table 77: Comparative Sequences relating to SAG2059

GKPEYFKIDSVFEQMEILRASSALPVVSKMVDWQKKYLDGGLSDSIPVDFARGLGFDKL
 IVVMTRPLNYQKKPSSGRLYKTLRKYPNFVKTSNRYQQYNNSLEKMSLEKTGDLFAI
 RPSKSLVIGRLEKNPDKLDSIYQLGMKDAKSGMPELNSYLMK

SEQ ID NO. 7716

STRAIN 18RS21 frame: 1

PMLSVGLVLEGGMRGLYTAGVLDAGIKIDGIVSVSAGALFGVNFVSRQRERLRY
 NKKYLSHPKYMRLRSWRTGNFVNKDFTYYEVPKLDVDFDEAFKKSSIDFYVVATEMTS
 GKPEYFKIDSVFEQMEILRASSALPVVSKMVDWQKKYLDGGLSDSIPVDFARGLGFDKL
 IVVMTRPLNYQKKPSSGRLYKTLRKYPNFVKTSNRYQQYNNSLEKMSLEKTGDLFAI
 RPSKSLVIGRLEKNPDKLDSIYQLGMKDAKSVMPPELNSYLMK

SEQ ID NO. 7717

STRAIN M732 frame: 1

PMLSVGLVLEGGMRGLYTAGVLDAGIKIDGIVSVSAGALFGVNFVSRQRERLRY
 NKKYLSHPKYMRLRSWRTGNFVNKDFTYYEVPKLDVDFDEAFKKSSIDFYVVATEMTS
 GKPEYFKIDSVFEQMEILRASSALPVVSKMVDWQKKYLDGGLSDSIPVDFARGLGFDKL
 IVVMTRPLNYQKKPSSGRLYKTLRKYPNFVKTSNRYQQYNNSLEKMSLEKTGDLFAI
 RPSKSLVIGRLEKNPDKLDSIYQLGMKYAKSVMPPELNSYLMK

SEQ ID NO. 7718

STRAIN COH1 frame: 1

PMLSVGLVLEGGMRGLYTAGVLDAGIKIDGIVSVSAGALFGVNFVSRQRERLRY
 NKKYLSHPKYMRLRSWRTGNFVNKDFTYYEVPKLDVDFDEAFKKSSIDFYVVATEMTS
 GKPEYFKIDSVFEQMEILRASSALPVVSKMVDWQKKYLDGGLSDSIPVDFARGLGFDKL
 IVVMTRPLNYQKKPSSGRLYKTLRKYPNFVKTSNRYQQYNNSLEKMSLEKTGDLFAI
 RPSKSLVIGRLEKNPDKLDSIYQLGMKYAKSVMPPELNSYLMK

SEQ ID NO. 7719

STRAIN M781 frame: 1

PMLSVGLVLEGGMRGLYTAGVLDAGIKIDGIVSVSAGALFGVNFVSRQRERLRY
 NKKYLSHPKYMRLRSWRTGNFVNKDFTYYEVPKLDVDFDEAFKKSSIDFYVVATEMTS
 GKPEYFKIDSVFEQMEILRASSALPVVSKMVDWQKKYLDGGLSDSIPVDFARGLGFDKL
 IVVMTRPLNYQKKPSSGRLYKTLRKYPNFVKTSNRYQQYNNSLEKMSLEKTGDLFAI
 RPSKSLVIGRLEKNPDKLDSIYQLGMKYAKSVMPPELNSYLMK

SEQ ID NO. 7720

STRAIN CJB110 frame: 1

PMLSVGLVLEGGMRGLYTAGVLDAGIKIDGIVSVSAGALFGVNFVSRQRERLRY
 NKKYLSHPKYMRLRSWRTGNFVNKDFTYYEVPKLDVDFDEAFKKSSIDFYVVATEMTS
 GKPEYFKIDSVFEQMEILRASSALPVVSKMVDWQKKYLDGGLSDSIPVDFARGLGFDKL
 IVVMTRPLNYQKKPSSGRLYKTLRKYPNFVKTSNRYQQYNNSLEKMSLEKTGDLFAI
 RPSKSLVIGRLEKNPDKLDSIYQLGMKDAKSVMPPELNSYLMK

SEQ ID NO. 7721

STRAIN JM9130013 frame: 1

PMLSVGLVLEGGMRGLYTAGVLDAGIKVDGII SVSAGALFGVNFVSRQRERLRY
 NKKYLSHPKYMRLRSWRTGNFVNKDFTYYEVPKLDVDFDEAFKKSSIDFYAVATEMTS
 GKPEYFKIDSVFEQMEILRASSALPVVSKMVDWQKKYLDGGLSDSIPVDFARGLGFDKL
 IVVMTRPLNYQKKPSSGRLYKTLRKYPNFVKTSNRYQQYNNSLEKMSLEKTGDLFAI
 RPSKSLVIGRLEKNPDKLDSIYQLGMKDAKSGMPELNSYLMK

SEQ ID NO. 7722

STRAIN 1169NT frame: 1

PMLSVGLVLEGGMRGLYTAGVLDAGIKIDGIVSVSAGALFGVNFVSRQRERLRY
 NKKYLSHPKYMRLRSWRTGNFVNKDFTYYEVPKLDVDFDEAFKKSSIDFYAVATEMTS
 GKPEYFKIDSVFEQMEILRASSALPVVSKMVDWQKKYLDGGLSDSIPVDFARGLGFDKL
 IVVMTRPLNYQKKPSSGRLYKTLRKYPNFVKTSNRYQQYNNSLEKMSLEKTGDLFAI
 RPSKSLVIVRLEKNPDKLDSIYQLGMKDAKSVMPPELNSYLMK

	1		50
msa47322.2{394_A909}	PMLSVGLVLE	GGGMRGLYTA	GVLDAGFLDAG IKvDGIISVS AGALFGVNFV
msa47322.2{394_H36B}	PMLSVGLVLE	GGGMRGLYTA	GVLDAGFLDAG IKvDGIISVS AGALFGVNFV
msa47322.2{394_JM9130013}	PMLSVGLVLE	GGGMRGLYTA	GVLDAGFLDAG IKvDGIISVS AGALFGVNFV
msa47322.2{394_090}	PMLSVGLVLE	GGGMRGLYTA	GVLDAGFLDAG IKIDGIvSVS AGALFGVNFV
msa47322.2{394_1169NT}	PMLSVGLVLE	GGGMRGLYTA	GVLDAGFLDAG IKIDGIvSVS AGALFGVNFV
msa47322.2{394_18RS21}	PMLSVGLVLE	GGGMRGLYTA	GVLDAGFLDAG IKIDGIvSVS AGALFGVNFV
msa47322.2{394_2603}	PMLSVGLVLE	GGGMRGLYTA	GVLDAGFLDAG IKIDGIvSVS AGALFGVNFV
msa47322.2{394_CJB110}	PMLSVGLVLE	GGGMRGLYTA	GVLDAGFLDAG IKIDGIvSVS AGALFGVNFV
msa47322.2{394_COH1}	PMLSVGLVLE	GGGMRGLYTA	GVLDAGFLDAG IKIDGIvSVS AGALFGVNFV
msa47322.2{394_M732}	PMLSVGLVLE	GGGMRGLYTA	GVLDAGFLDAG IKIDGIvSVS AGALFGVNFV
msa47322.2{394_M781}	PMLSVGLVLE	GGGMRGLYTA	GVLDAGFLDAG IKIDGIvSVS AGALFGVNFV
Consensus	*****	*****	***** **-***-*** *****
	51		100
msa47322.2{394_A909}	SRQRERLRY	NKKYLSHPkY	MSLRSLWRTG NFNKDFTYY EVPMKLDVFD
msa47322.2{394_H36B}	SRQRERLRY	NKKYLSHPkY	MSLRSLWRTG NFNKDFTYY EVPMKLDVFD
msa47322.2{394_JM9130013}	SRQRERLRY	NKKYLSHPkY	MSLRSLWRTG NFNKDFTYY EVPMKLDVFD
msa47322.2{394_090}	SRQRERLRY	NKKYLSHPkY	MSLRSLWRTG NFNKDFTYY EVPMKLDVFD
msa47322.2{394_1169NT}	SRQRERLRY	NKKYLSHPkY	MSLRSLWRTG NFNKDFTYY EVPMKLDVFD
msa47322.2{394_18RS21}	SRQRERLRY	NKKYLSHPkY	MSLRSLWRTG NFNKDFTYY EVPMKLDVFD

Table 77: Comparative Sequences relating toSAG2059

msa47322.2{394_2603}	SRQRERALRY	NKKYLSHPkY	MSLRSWfRTG	NFVNKDFTYY	EVPMKLDVFD
msa47322.2{394_CJB110}	SRQRERALRY	NKKYLSHPkY	MSLRSWfRTG	NFVNKDFTYY	EVPMKLDVFD
msa47322.2{394_COH1}	SRQRERALRY	NKKYLSHPeY	MSLRSWlRTG	NFVNKDFTYY	EVPMKLDVFD
msa47322.2{394_M732}	SRQRERALRY	NKKYLSHPeY	MSLRSWlRTG	NFVNKDFTYY	EVPMKLDVFD
msa47322.2{394_M781}	SRQRERALRY	NKKYLSHPeY	MSLRSWlRTG	NFVNKDFTYY	EVPMKLDVFD
Consensus	*****	*****-*	*****-***	*****	*****
101					
msa47322.2{394_A909}	DEAFKKSSID	FYavATEMTS	GKPEYFKIDS	VFEQMEILRA	SSALPVVSKM
msa47322.2{394_H36B}	DEAFKKSSID	FYavATEMTS	GKPEYFKIDS	VFEQMEILRA	SSALPVVSKM
msa47322.2{394_JM9130013}	DEAFKKSSID	FYavATEMTS	GKPEYFKIDS	VFEQMEILRA	SSALPVVSKM
msa47322.2{394_090}	DEAFKKSSID	FYvVATEMTS	GKPEYFKIDS	VFEQMEILRA	SSALPVVSKM
msa47322.2{394_1169NT}	DEAFKKSSID	FYavATEMTS	GKPEYFKIDS	VFEQMEILRA	SSALPVVSKM
msa47322.2{394_18RS21}	DEAFKKSSID	FYvVATEMTS	GKPEYFKIDS	VFEQMEILRA	SSALPVVSKM
msa47322.2{394_2603}	DEAFKKSSID	FYvVATEMTS	GKPEYFKIDS	VFEQMEILRA	SSALPVVSKM
msa47322.2{394_CJB110}	DEAFKKSSID	FYvVATEMTS	GKPEYFKIDS	VFEQMEILRA	SSALPVVSKM
msa47322.2{394_COH1}	DEAFKKSSID	FYvVATEMTS	GKPEYFKIDS	VFEQMEILRA	SSALPVVSKM
msa47322.2{394_M732}	DEAFKKSSID	FYvVATEMTS	GKPEYFKIDS	VFEQMEILRA	SSALPVVSKM
msa47322.2{394_M781}	DEAFKKSSID	FYvVATEMTS	GKPEYFKIDS	VFEQMEILRA	SSALPVVSKM
Consensus	*****	**_*****	*****	*****	*****
151					
msa47322.2{394_A909}	VvWQGKKYLD	GGLSDSIPVD	FARGLGFDKL	IVVMTRPLNY	QKKPSSGRLY
msa47322.2{394_H36B}	VvWQGKKYLD	GGLSDSIPVD	FARGLGFDKL	IVVMTRPLNY	QKKPSSGRLY
msa47322.2{394_JM9130013}	VvWQGKKYLD	GGLSDSIPVD	FARGLGFDKL	IVVMTRPLNY	QKKPSSGRLY
msa47322.2{394_090}	VdWQGKKYLD	GGLSDSIPVD	FARGLGFDKL	IVVMTRPLNY	QKKPSSGRLY
msa47322.2{394_1169NT}	VdWQGKKYLD	GGLSDSIPVD	FARGLGFDKL	IVVMTRPLNY	QKKPSSGRLY
msa47322.2{394_18RS21}	VdWQGKKYLD	GGLSDSIPVD	FARGLGFDKL	IVVMTRPLNY	QKKPSSGRLY
msa47322.2{394_2603}	VdWQGKKYLD	GGLSDSIPVD	FARGLGFDKL	IVVMTRPLNY	QKKPSSGRLY
msa47322.2{394_CJB110}	VdWQGKKYLD	GGLSDSIPVD	FARGLGFDKL	IVVMTRPLNY	QKKPSSGRLY
msa47322.2{394_COH1}	VdWQGKKYLD	GGLSDSIPVD	FARGLGFDKL	IVVMTRPLNY	QKKPSSGRLY
msa47322.2{394_M732}	VdWQGKKYLD	GGLSDSIPVD	FARGLGFDKL	IVVMTRPLNY	QKKPSSGRLY
msa47322.2{394_M781}	VdWQGKKYLD	GGLSDSIPVD	FARGLGFDKL	IVVMTRPLNY	QKKPSSGRLY
Consensus	*-*****	*****	*****	*****	*****
200					
201					
msa47322.2{394_A909}	KTLYRKYPNF	VKTASNRYQQ	YNNsLEKVMS	LEKTGDLFAI	RPSKSLVIgR
msa47322.2{394_H36B}	KTLYRKYPNF	VKTASNRYQQ	YNNsLEKVMS	LEKTGDLFAI	RPSKSLVIgR
msa47322.2{394_JM9130013}	KTLYRKYPNF	VKTASNRYQQ	YNNsLEKVMS	LEKTGDLFAI	RPSKSLVIgR
msa47322.2{394_090}	KTLYRKYPNF	VKTASNRYQQ	YNNsLEKVMS	LEKTGDLFAI	RPSKSLVIgR
msa47322.2{394_1169NT}	KTLYRKYPNF	VKTASNRYQQ	YNNsLEKVMS	LEKTGDLFAI	RPSKSLVIgR
msa47322.2{394_18RS21}	KTLYRKYPNF	VKTASNRYQQ	YNNsLEKVMS	LEKTGDLFAI	RPSKSLVIgR
msa47322.2{394_2603}	KTLYRKYPNF	VKTASNRYQQ	YNNsLEKVMS	LEKTGDLFAI	RPSKSLVIgR
msa47322.2{394_CJB110}	KTLYRKYPNF	VKTASNRYQQ	YNNsLEKVMS	LEKTGDLFAI	RPSKSLVIgR
msa47322.2{394_COH1}	KTLYRKYPNF	VKTASNRYQQ	YNNsLEKVMS	LEKTGDLFAI	RPSKSLVIgR
msa47322.2{394_M732}	KTLYRKYPNF	VKTASNRYQQ	YNNsLEKVMS	LEKTGDLFAI	RPSKSLVIgR
msa47322.2{394_M781}	KTLYRKYPNF	VKTASNRYQQ	YNNsLEKVMS	LEKTGDLFAI	RPSKSLVIgR
Consensus	*****	*****	*****	*****	*****-*
250					
251					
msa47322.2{394_A909}	LEKNPDKLDS	IYQLGMKdAK	SgMPELNSYL	MK	
msa47322.2{394_H36B}	LEKNPDKLDS	IYQLGMKdAK	SgMPELNSYL	MK	
msa47322.2{394_JM9130013}	LEKNPDKLDS	IYQLGMKdAK	SgMPELNSYL	MK	
msa47322.2{394_090}	LEKNPDKLDS	IYQLGMKdAK	SvMPELNSYL	MK	
msa47322.2{394_1169NT}	LEKNPDKLDS	IYQLGMKdAK	SvMPELNSYL	MK	
msa47322.2{394_18RS21}	LEKNPDKLDS	IYQLGMKdAK	SvMPELNSYL	MK	
msa47322.2{394_2603}	LEKNPDKLDS	IYQLGMKdAK	SvMPELNSYL	MK	
msa47322.2{394_CJB110}	LEKNPDKLDS	IYQLGMKdAK	SvMPELNSYL	MK	
msa47322.2{394_COH1}	LEKNPDKLDS	IYQLGMKyAK	SvMPELNSYL	MK	
msa47322.2{394_M732}	LEKNPDKLDS	IYQLGMKyAK	SvMPELNSYL	MK	
msa47322.2{394_M781}	LEKNPDKLDS	IYQLGMKyAK	SvMPELNSYL	MK	
Consensus	*****	*****-*	*-*****	**	
282					

Table 78: Comparative Sequences relating to SAG1016

SEQ ID NO. 7801

STRAIN 2603

ATGAAAGTTTTAGTAGTTGATGATGAACCAGTTGCACGTAACGAATTAATTTACCTTCTT
 AATAAGTATGATTCTAACCTCGTTATAGCAGAGGCGCATGATATGGCTACTGCATTAGCT
 ATTTTACTTAGAGAAACTTTTGATGTAGCACTGTTAGATATCCATCTCAGAGATGATTCT
 GGGTTGCAATTAGCAGAGTATATCAATAAAATGCCCAAACCACCATTATTGATATTTGCG
 ACTGCTTATGATCAATATGCTATTTCAGGCTTTTGAGCATGATGCGCGTGATTATTTGTTA
 AAACCTTATGATTTTGATAGGCTAAAGCAAGCTATGGATAGAGTAAAAGGAGCGCTAAGT
 ACATCTACAATTATAGAGAGCGTAACCTCCGGTCTCTCTTCAAGCAACAGTATCCATTG
 ACAGTAGAAGATCGAATCTATCTGGTGTGCGCGGATGATATCCTTTTGATTGAAGCTATG
 CAAGGAAAACTGATTATACAAACACCTGATAAAAATTATGAAATTGATGGCTCTCTACAA
 CAATGGCAAGATAAACTACCATCATCTCAATTTGTACGGGTACATCGCTCTTACATTGTG
 AACATTAATGCTATTAAAACGATTGAACCTTGGTTTAAACCAACACTTCAGTTACACCTT
 TGTAAATAAAATAACAGTTCCTGTTAGCAGAGCAAATGTAAAACCCCTAAAACAAATGTTA
 GGCATATCTACC

SEQ ID NO. 7802

STRAIN 090

AAAGTTTTAGTAGTTGATGATGAACCAGTTGCACGTAA
 CGAATTAATTTACCTTCTTAATAAGTATGATTCTAACCTCGTTATAGCAG
 AGGCGCATGATATGGCTACTGCATTAGCTATTTTACTTAGAGAAACTTTT
 GATGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTGGGTTGCAATT
 AGCAGAGTATATCAATAAAATGCCCAAACCACCATTATTGATATTTGCGA
 CTGCTTATGATCAATATGCTATTTCAGGCTTTTGAGCATGATGCGCGTGAT
 TATTTGTTAAAACCTTATGATTTTGATAGGCTAAAGCAAGCTATGGATAG
 AGTAAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCGTAACCTCCG
 GTCCTCTCTTCAAGCAACAGTATCCATTGACAGTAGAAGATCGAATCTAT
 CTGGTGTGCGCGGATGATATCCTTTTGATTGAAGCTATGCAAGGAAAACT
 GATTATACAAACACCTGATAAAAATTATGAAATTGATGGCTCTCTACAAC
 AATGGCAAGATAAACTACCATCATCTCAATTTGTACGGGTACATCGCTCT
 TACATTGTGAACATTAATGCTATTAAAACGATTGAACCTTGGTTTAACCA
 AACACTTCAGTTACACCTTTGTAATAAAATAACAGTTCCTGTTAGCAGAG
 CAAATGTAAAACCCCTAAAACAAATGTTAGGCATATCTACC

SEQ ID NO. 7803

STRAIN A909

AAAGTTTTAGTAGTTGATGATGAACCAGTTGCACGTAA
 GAATTAATTTACCTTCTTAATAAGTATGATTCTAACCTCGTTATAGCAGA
 GGCGCATGATATGGCTACTGCATTAGCTATTTTACTTAGAGAAACTTTTG
 ATGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTGGGTTGCAATTA
 GCAGAGTATATCAATAAAATGCCCAAACCACCATTATTGATATTCGCGAC
 TGCTTATGATCAATATGCTATTCAAGCTTTTGAGCATGATGCGCGTGATT
 ATTTGTTAAAACCTTATGAGTTTGATAGGCTAAAGCAAGCTATGGATAGA
 GTAAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCGTAACCTCCGG
 CCTCTCTTCAAGCAACAGTATCCATTGACAGTAGAAGATCGAATCTATC
 TGGTGTGCGCGGATGATATCCTTTTGATTGAAGCTATGCAAGGAAAACTG
 ATTATACAAACACCTGATAAAAATTATGAAATTGATGGCTCTCTACAACA
 ATGGCAAGATAAACTACCATCATCTCAATTTGTACGGGTGCACCGCTCTT
 ACATTGTGAATATTAAATGCTATTAAAACGATTGAACCTTGGTTTAAACAA
 ACCTTCAGTTACACCTTTGTAATAAAATAACAGTTCCTGTTAGCAGAGC
 AAATGTAAAACCCCTAAAACAAATGTTAGGCATATCTACC

SEQ ID NO. 7804

STRAIN H36B

AAAGTTTTAGTAGTTGATGATGAACCAGTTGCACGT
 AACGAATTAATTTACCTTCTTAATAAGTATGATTCTAACCTCGTTATAGC
 AGAGGCGCATGATATGGCTACTGCATTAGCTATTTTACTTAGAGAAACTTT
 TTGATGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTGGGTTGCAA
 TTAGCAGAGTATATCAATAAAATGCCCAAACCACCATTATTGATATTCGC
 GACTGCTTATGATCAATATGCTATTCAAGCTTTTGAGCATGATGCGCGTG
 ATTATTTGTTAAAACCTTATGAGTTTGATAGGCTAAAGCAAGCTATGGAT
 AGAGTAAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCGTAACCTC
 CGGCCCTCTCTTCAAGCAACAGTATCCATTGACAGTAGAAGATCGAATCT
 ATCTGGTGTGCGCGGATGATATCCTTTTGATTGAAGCTATGCAAGGAAAA
 CTGATTATACAAACACCTGATAAAAATTATGAAATTGATGGCTCTCTACA
 ACAATGGCAAGATAAACTACCATCATCTCAATTTGTACGGGTGCACCGCT
 CTACATTGTGAATATTAAATGCTATTAAAACGATTGAACCTTGGTTTAAAC
 CAAACACTTCAGTTACACCTTTGTAATAAAATAACAGTTCCTGTTAGCAG
 AGCAAATGTAAAACCCCTAAAACAAATGTTAGGCATATCTACC

SEQ ID NO. 7805

STRAIN 18RS21

AAAGTTTTAGTAGTTGATGATGAACCAGTTGCACGTAA
 GAATTAATTTACCTTCTTAATAAGTATGATTCTAACCTCGTTATAGCAGA
 GGCGCATGATATGGCTACTGCATTAGCTATTTTACTTAGAGAAACTTTTG
 ATGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTGGGTTGCAATTA
 GCAGAGTATATCAATAAAATGCCCAAACCACCATTATTGATATTTGCGAC
 TGCTTATGATCAATATGCTATTTCAGGCTTTTGAGCATGATGCGCGTGATT
 ATTTGTTAAAACCTTATGAGTTTGATAGGCTAAAGCAAGCTATGGATAGA
 GTAAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCGTAACCTCCGG
 TCCTCTCTTCAAGCAACAGTATCCATTGACAGTAGAAGATCGAATCTATC
 TGGTGTGCGCGGATGATATCCTTTTGATTGAAGCTATGCAAGGAAAACTG

Table 78: Comparative Sequences relating to SAG1016

ATTATACAAACACCTGATAAAAATTATGAAATTGATGGCTCTCTACAACA
 ATGGCAAGATAAACTACCATCATCTCAATTTGTACGGGTACATCGCTCTT
 ACATTGTGAACATTAATGCTATTAAAAACGATTGAACCTTGGTTTAAACAA
 ACACCTTCAGTTACACCTTTGTAATAAAAATAACAGTTCCTGTTAGCAGAGC
 AAATGTAAAACCCCTAAAACAAATGTTAGGCATATCTACC

SEQ ID NO. 7806

STRAIN M732

AAAGTTTTAGTAGTTGATGATGAACCAGTT
 GCACGTAACGAATTAATTTACCTTCTTAATAAGTATGATTCTAACCTCGT
 TATAGCAGAGGCGCATGATATGGCTACTGCATTAGCTATTTTACTTAGAG
 AAACCTTTTGATGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTGGG
 TTGCAATTAGCAGAGTATATCAATAAAATGCCCAAACCACCATTTATTGAT
 ATTTCGCGACTGCTTATGATCAATATGCTATTTCAGGCTTTTGAGCAGGATG
 CGCGTGATTATTTGTTAAAAACCTATGAGTTTGATAGGTTAAAGCAAGCT
 ATGGATAGAGTAAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCGT
 AGCTTCCGGTCCCTCTCTTCAAGCAACAGTATCCATTGACAGTAGAAGATC
 GAATCTATCTGGTGTGCGCGGATGATATCCTTTTGAATTGAAGCTATGCAA
 GGAAACTGATTATACAAACACCTGATAAAAATTATGAAATTGATGGCTC
 TCTACAACAATGGCAAGATAAACTACCATCATCTCAATTTGTACGGGTAC
 ATCGCTCTTACATTGTGAATATTAATGCTATTAAAAACGATTGAACCTTGG
 TTTAAACCAACACTTCAGTTACACCTTTGTAATAAAAATAACAGTTCCTGT
 TAGCAGAGCAAATGTAAAACCCCTAAAACAAATGTTAGGCATATCTACC

SEQ ID NO. 7807

STRAIN COH1

AAAGTTTTAGTAGTTGATGATGAACCAGTTGCACGTA
 ACGAATTAATTTACCTTCTTAATAAGTATGATTCTAACCTCGTTATAGCA
 GAGGCGCATGATATGGCTACTGCATTAGCTATTTTACTTAGAGAACTTT
 TGATGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTGGGTTGCAAT
 TAGCAGAGTATATCAATAAAATGCCCAAACCACCATTTATTGATATTTCGCG
 ACTGCTTATGATCAATATGCTATTTCAGGCTTTTGAGCAGGATGCGCGTGA
 TTATTGTTAAAAACCTATGAGTTTGATAGGTTAAAGCAAGCTATGGATA
 GAGTAAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCGTAGCTTCC
 GGTCTCTCTTCAAGCAACAGTATCCATTGACAGTAGAAGATCGAATCTA
 TCTGGTGTGCGCGGATGATATCCTTTTGAATTGAAGCTATGCAAGGAAAAC
 TGATTATACAAACACCTGATAAAAATTATGAAATTGATGGCTCTCTACAA
 CAATGGCAAGATAAACTACCATCATCTCAATTTGTACGGGTACATCGCTC
 TTACATTGTGAATATTAATGCTATTAAAAACGATTGAACCTTGGTTTAAAC
 AAACACTTCAGTTACACCTTTGTAATAAAAATAACAGTTCCTGTTAGCAGA
 GCAAATGTAAAACCCCTAAAACAAATGTTAGGCATATCTACC

SEQ ID NO. 7808

STRAIN M781

AAAGTTTTAGTAGTTGATGATGAACCAGTTGCACGTAAC
 GAATTAATTTACCTTCTTAATAAGTATGATTCTAACCTCGTTATAGCAGA
 GGCGCATGATATGGCTACTGCATTAGCTATTTTACTTAGAGAACTTTTG
 ATGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTGGGTTGCAATTA
 GCAGAGTATATCAATAAAATGCCCAAACCACCATTTATTGATATTTCGCGAC
 TGCTTATGATCAATATGCTATTTCAGGCTTTTGAGCAGGATGCGCGTGATT
 ATTTGTTAAAAACCTATGAGTTTGATAGGTTAAAGCAAGCTATGGATAGA
 GTAAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCGTAGCTTCCGG
 TCCTCTCTTCAAGCAACAGTATCCATTGACAGTAGAAGATCGAATCTATC
 TGGTGTGCGCGGATGATATCCTTTTGAATTGAAGCTATGCAAGGAAAAC
 ATTATACAAACACCTGATAAAAATTATGAAATTGATGGCTCTCTACAACA
 ATGGCAAGATAAACTACCATCATCTCAATTTGTACGGGTACATCGCTCTT
 ACATTGTGAATATTAATGCTATTAAAAACGATTGAACCTTGGTTTAAACAA
 ACACCTTCAGTTACACCTTTGTAATAAAAATAACAGTTCCTGTTAGCAGAGC
 AAATGTAAAACCCCTAAAACAAATGTTAGGCATATCTACC

SEQ ID NO. 7809

STRAIN CJB110

CTTAATAAGTATGATTCTAACCTCGTTATAGCAGAGGCGCATGATATGGC
 TACTGCATTAGCTATTTTACTTAGAGAACTTTTGATGTAGCACTGTTAG
 ATATCCATCTCAGAGATGATTCTGGGTTGCAATTAGCAGAGTATATCAAT
 AAAATGCCCAAACCACCATTTATTGATATTTCGCGACTGCTTATGATCAATA
 TGCTATTCAAGCTTTTGAGCATGATGCGCGTGATTATTTGTTAAAAACCT
 ATGAGTTTGATAGGCTAAAGCAAGnTATGGATAGAGTAAAAGGAGCGCTA
 AGTACATCTACAATTATAGAGAGCGTAACCTCCGGCCCTCTCTTCAAGCA
 ACAGTATCCATTGACAGTAGAAGATnGAATCTATCTGGTGTGCGCGGATG
 ATATCCTTTTGAATTGAAGCTATGCAAGGAAAACGATTATACAAACACCT
 GATAAAAATTATGAAATTGATGGCTCTCTACAACAATGGCAAGATAAACT
 ACCATCATCTCAATTTGTACGGGTGACCGCTCTTACATTGTGAATATTA
 ATGCTATTAAAAACGATTGAACCTTGGTTTAAACCAACACTTCAGTTACAC
 CTTTGTATAAAAATAACAGTTCCTGTTAGCAGAGCAAATGTAAAACCCCT
 AAAACAAATGTTAGG

SEQ ID NO. 7810

STRAIN 1169NT

AAAGTTTTAGTAGTTGATGATGAACCAG
 TTGCACGTAACGAATTAATTTATCTTCTTAATAAGTATGATTCTAACCTC
 GTTATAGCAGAGGCGCATGATATAGCTACTGCATTAGCTATTTTACTTAG

Table 78: Comparative Sequences relating to SAG1016

AGAAACTTTTGTAGTACTGTTAGATATCCATCTCAGAGATGATTCTG
 GGTGCAATTAGCAGAGTATATCAATAAAATGCCAAACCACCATTATTG
 ATATTGCGGACTGCTTATGATCAATATGCTATTCAAGCTTTTGAGCATGA
 TCGCGGTGATTATTTGTTAAACCCCTATGAGTTTGATAGGCTAAAGCAAG
 CTATGGATAGAGTAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGC
 GTAACCTCCGGCCCTCTCTCAAGCAACAGTATCCATTGACAGTAGAAGA
 TCGAATCTATCTGGTGTGCGCGGATGATATCCTTTTGATTGAAGCTATGC
 AAGGAAACTGATTATACAAACACCTGATAAAATTTATGAAATTGATGGC
 TCTCTACAACAATGGCAAGATAAACTACCATCATCTCAATTTGTACGGGT
 GCACCGCTCTTACATTGTGAATATTAATGCTATTAAACGATTGAACCTT
 GGTTTAACCAACACTTCAGTTACACCTTTGTAATAAAATAACAGTTCCT
 GTTAGCAGAGCAAATGTAAACCCCTAAACAAATGTTAGGCATATCTAC
 C

SEQ ID NO. 7811

STRAIN JM9130013

AAAGTTTGTAGTATTGATGATGAACCAGT

TGCACGTAACGAATTAATTTACCTTCTTAATAAGTATGATTCTAACCTCG
 TTATAGCAGAGGCGCATGATATGGCTACTGCATTAGCTATTTTACTTAGA
 GAAACTTTTGTAGTACTGTTAGATATCCATCTCAGAGATGATTCTGG
 GTTGCAATTAGCAGAGTATATCAATAAAATGCCAAACCACCATTATTGA
 TATTGCGGACTGCTTATGATCAATATGCTATTCAAGCTTTTGAGCATGAT
 GCGCGTGATTATTTGTTAAACCCCTATGAGTTTGATAGGCTAAAGCAAGC
 TATGGATAGAGTAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCG
 TAACTTCCGGCCCTCTCTTCAAGCAACAGTATCCATTGACAGTAGAAGAT
 CGAATCTATCTGGTGTGCGCGGATGATATCCTTTTGATTGAAGCTATGCA
 AGGAAACTGATTATACAAACACCTGATAAAATTTATGAAATTGATGGCT
 CTCTACAACAATGGCAAGATAAACTACCATCATCTCAATTTGTACGGGTG
 CACCGCTCTTACATTGTGAATATTAATGCTATTAAACGATTGAACCTTG
 GTTTAACCAACACTTCAGTTACACCTTTGTAATAAAATAACAGTTCCTG
 TTAGCAGAGCAAATGTAAACCCCTAAACAAATGTTAGGCATATCTACC

MSA Alignment Results: Pretty output

PRETTY of: /biotmp/msa141507.2(*) April 10, 2003 06:36 ..

	1				50
msa141507.2{399_A909}	---aaagttt	tagtagttga	tgatgaacca	ggtgcacgta	acgaattaat
msa141507.2{399_CJB110}	-----	-----	-----	-----	-----
msa141507.2{399_H36B}	---aaagttt	tagtagttga	tgatgaacca	ggtgcacgta	acgaattaat
msa141507.2{399_JM9130013}	---aaagttt	tagtagttga	tgatgaacca	ggtgcacgta	acgaattaat
msa141507.2{399_1169NT}	---aaagttt	tagtagttga	tgatgaacca	ggtgcacgta	acgaattaat
msa141507.2{399_090}	---aaagttt	tagtagttga	tgatgaacca	ggtgcacgta	acgaattaat
msa141507.2{399_18RS21}	---aaagttt	tagtagttga	tgatgaacca	ggtgcacgta	acgaattaat
msa141507.2{399_2603}	atgaaagttt	tagtagttga	tgatgaacca	ggtgcacgta	acgaattaat
msa141507.2{399_COH1}	---aaagttt	tagtagttga	tgatgaacca	ggtgcacgta	acgaattaat
msa141507.2{399_M732}	---aaagttt	tagtagttga	tgatgaacca	ggtgcacgta	acgaattaat
msa141507.2{399_M781}	---aaagttt	tagtagttga	tgatgaacca	ggtgcacgta	acgaattaat
Consensus	***-----	-----	-----	-----	-----
	51				100
msa141507.2{399_A909}	ttaccttCTT	AATAAGTATG	ATTCTAACCT	CGTTATAGCA	GAGGCGCATG
msa141507.2{399_CJB110}	-----CTT	AATAAGTATG	ATTCTAACCT	CGTTATAGCA	GAGGCGCATG
msa141507.2{399_H36B}	ttaccttCTT	AATAAGTATG	ATTCTAACCT	CGTTATAGCA	GAGGCGCATG
msa141507.2{399_JM9130013}	ttaccttCTT	AATAAGTATG	ATTCTAACCT	CGTTATAGCA	GAGGCGCATG
msa141507.2{399_1169NT}	ttatcttCTT	AATAAGTATG	ATTCTAACCT	CGTTATAGCA	GAGGCGCATG
msa141507.2{399_090}	ttaccttCTT	AATAAGTATG	ATTCTAACCT	CGTTATAGCA	GAGGCGCATG
msa141507.2{399_18RS21}	ttaccttCTT	AATAAGTATG	ATTCTAACCT	CGTTATAGCA	GAGGCGCATG
msa141507.2{399_2603}	ttaccttCTT	AATAAGTATG	ATTCTAACCT	CGTTATAGCA	GAGGCGCATG
msa141507.2{399_COH1}	ttaccttCTT	AATAAGTATG	ATTCTAACCT	CGTTATAGCA	GAGGCGCATG
msa141507.2{399_M732}	ttaccttCTT	AATAAGTATG	ATTCTAACCT	CGTTATAGCA	GAGGCGCATG
msa141507.2{399_M781}	ttaccttCTT	AATAAGTATG	ATTCTAACCT	CGTTATAGCA	GAGGCGCATG
Consensus	-----***	*****	*****	*****	*****
	101				150
msa141507.2{399_A909}	ATATgGCTAC	TGCATTAGCT	ATTTTACTTA	GAGAACTTT	TGATGTAGCA
msa141507.2{399_CJB110}	ATATgGCTAC	TGCATTAGCT	ATTTTACTTA	GAGAACTTT	TGATGTAGCA
msa141507.2{399_H36B}	ATATgGCTAC	TGCATTAGCT	ATTTTACTTA	GAGAACTTT	TGATGTAGCA
msa141507.2{399_JM9130013}	ATATgGCTAC	TGCATTAGCT	ATTTTACTTA	GAGAACTTT	TGATGTAGCA
msa141507.2{399_1169NT}	ATATaGCTAC	TGCATTAGCT	ATTTTACTTA	GAGAACTTT	TGATGTAGCA
msa141507.2{399_090}	ATATgGCTAC	TGCATTAGCT	ATTTTACTTA	GAGAACTTT	TGATGTAGCA
msa141507.2{399_18RS21}	ATATgGCTAC	TGCATTAGCT	ATTTTACTTA	GAGAACTTT	TGATGTAGCA
msa141507.2{399_2603}	ATATgGCTAC	TGCATTAGCT	ATTTTACTTA	GAGAACTTT	TGATGTAGCA
msa141507.2{399_COH1}	ATATgGCTAC	TGCATTAGCT	ATTTTACTTA	GAGAACTTT	TGATGTAGCA
msa141507.2{399_M732}	ATATgGCTAC	TGCATTAGCT	ATTTTACTTA	GAGAACTTT	TGATGTAGCA
msa141507.2{399_M781}	ATATgGCTAC	TGCATTAGCT	ATTTTACTTA	GAGAACTTT	TGATGTAGCA
Consensus	****-*****	*****	*****	*****	*****
	151				200
msa141507.2{399_A909}	CTGTTAGATA	TCCATCTCAG	AGATGATTCT	GGGTTGCAAT	TAGCAGAGTA
msa141507.2{399_CJB110}	CTGTTAGATA	TCCATCTCAG	AGATGATTCT	GGGTTGCAAT	TAGCAGAGTA
msa141507.2{399_H36B}	CTGTTAGATA	TCCATCTCAG	AGATGATTCT	GGGTTGCAAT	TAGCAGAGTA
msa141507.2{399_JM9130013}	CTGTTAGATA	TCCATCTCAG	AGATGATTCT	GGGTTGCAAT	TAGCAGAGTA
msa141507.2{399_1169NT}	CTGTTAGATA	TCCATCTCAG	AGATGATTCT	GGGTTGCAAT	TAGCAGAGTA

Table 78: Comparative Sequences relating to SAG1016

msa141507.2{399_090}	CTGTTAGATA	TCCATCTCAG	AGATGATTCT	GGGTTGCAAT	TAGCAGAGTA
msa141507.2{399_18RS21}	CTGTTAGATA	TCCATCTCAG	AGATGATTCT	GGGTTGCAAT	TAGCAGAGTA
msa141507.2{399_2603}	CTGTTAGATA	TCCATCTCAG	AGATGATTCT	GGGTTGCAAT	TAGCAGAGTA
msa141507.2{399_COH1}	CTGTTAGATA	TCCATCTCAG	AGATGATTCT	GGGTTGCAAT	TAGCAGAGTA
msa141507.2{399_M732}	CTGTTAGATA	TCCATCTCAG	AGATGATTCT	GGGTTGCAAT	TAGCAGAGTA
msa141507.2{399_M781}	CTGTTAGATA	TCCATCTCAG	AGATGATTCT	GGGTTGCAAT	TAGCAGAGTA
Consensus	*****	*****	*****	*****	*****
msa141507.2{399_A909}	TATCAATAAA	ATGCCCAAAC	CACCATTATT	GATATTcGCG	ACTGCTTATG
msa141507.2{399_CJB110}	TATCAATAAA	ATGCCCAAAC	CACCATTATT	GATATTcGCG	ACTGCTTATG
msa141507.2{399_H36B}	TATCAATAAA	ATGCCCAAAC	CACCATTATT	GATATTcGCG	ACTGCTTATG
msa141507.2{399_JM9130013}	TATCAATAAA	ATGCCCAAAC	CACCATTATT	GATATTcGCG	ACTGCTTATG
msa141507.2{399_1169NT}	TATCAATAAA	ATGCCCAAAC	CACCATTATT	GATATTcGCG	ACTGCTTATG
msa141507.2{399_090}	TATCAATAAA	ATGCCCAAAC	CACCATTATT	GATATTcGCG	ACTGCTTATG
msa141507.2{399_18RS21}	TATCAATAAA	ATGCCCAAAC	CACCATTATT	GATATTcGCG	ACTGCTTATG
msa141507.2{399_2603}	TATCAATAAA	ATGCCCAAAC	CACCATTATT	GATATTcGCG	ACTGCTTATG
msa141507.2{399_COH1}	TATCAATAAA	ATGCCCAAAC	CACCATTATT	GATATTcGCG	ACTGCTTATG
msa141507.2{399_M732}	TATCAATAAA	ATGCCCAAAC	CACCATTATT	GATATTcGCG	ACTGCTTATG
msa141507.2{399_M781}	TATCAATAAA	ATGCCCAAAC	CACCATTATT	GATATTcGCG	ACTGCTTATG
Consensus	*****	*****	*****	*****	*****
msa141507.2{399_A909}	ATCAATATGC	TATTCaAGCT	TTTGAGCAtG	ATGCGCGTGA	TTATTTGTTA
msa141507.2{399_CJB110}	ATCAATATGC	TATTCaAGCT	TTTGAGCAtG	ATGCGCGTGA	TTATTTGTTA
msa141507.2{399_H36B}	ATCAATATGC	TATTCaAGCT	TTTGAGCAtG	ATGCGCGTGA	TTATTTGTTA
msa141507.2{399_JM9130013}	ATCAATATGC	TATTCaAGCT	TTTGAGCAtG	ATGCGCGTGA	TTATTTGTTA
msa141507.2{399_1169NT}	ATCAATATGC	TATTCaAGCT	TTTGAGCAtG	ATGCGCGTGA	TTATTTGTTA
msa141507.2{399_090}	ATCAATATGC	TATTCaAGCT	TTTGAGCAtG	ATGCGCGTGA	TTATTTGTTA
msa141507.2{399_18RS21}	ATCAATATGC	TATTCaAGCT	TTTGAGCAtG	ATGCGCGTGA	TTATTTGTTA
msa141507.2{399_2603}	ATCAATATGC	TATTCaAGCT	TTTGAGCAtG	ATGCGCGTGA	TTATTTGTTA
msa141507.2{399_COH1}	ATCAATATGC	TATTCaAGCT	TTTGAGCAtG	ATGCGCGTGA	TTATTTGTTA
msa141507.2{399_M732}	ATCAATATGC	TATTCaAGCT	TTTGAGCAtG	ATGCGCGTGA	TTATTTGTTA
msa141507.2{399_M781}	ATCAATATGC	TATTCaAGCT	TTTGAGCAtG	ATGCGCGTGA	TTATTTGTTA
Consensus	*****	*****	*****	*****	*****
msa141507.2{399_A909}	AAACCCTATG	AgTTTGATAG	GcTAAAGCAA	GcTATGGATA	GAGTAAAAGG
msa141507.2{399_CJB110}	AAACCCTATG	AgTTTGATAG	GcTAAAGCAA	GcTATGGATA	GAGTAAAAGG
msa141507.2{399_H36B}	AAACCCTATG	AgTTTGATAG	GcTAAAGCAA	GcTATGGATA	GAGTAAAAGG
msa141507.2{399_JM9130013}	AAACCCTATG	AgTTTGATAG	GcTAAAGCAA	GcTATGGATA	GAGTAAAAGG
msa141507.2{399_1169NT}	AAACCCTATG	AgTTTGATAG	GcTAAAGCAA	GcTATGGATA	GAGTAAAAGG
msa141507.2{399_090}	AAACCCTATG	AtTTTGATAG	GcTAAAGCAA	GcTATGGATA	GAGTAAAAGG
msa141507.2{399_18RS21}	AAACCCTATG	AtTTTGATAG	GcTAAAGCAA	GcTATGGATA	GAGTAAAAGG
msa141507.2{399_2603}	AAACCCTATG	AtTTTGATAG	GcTAAAGCAA	GcTATGGATA	GAGTAAAAGG
msa141507.2{399_COH1}	AAACCCTATG	AgTTTGATAG	GcTAAAGCAA	GcTATGGATA	GAGTAAAAGG
msa141507.2{399_M732}	AAACCCTATG	AgTTTGATAG	GcTAAAGCAA	GcTATGGATA	GAGTAAAAGG
msa141507.2{399_M781}	AAACCCTATG	AgTTTGATAG	GcTAAAGCAA	GcTATGGATA	GAGTAAAAGG
Consensus	*****	*-*****	*-*****	*-*****	*****
msa141507.2{399_A909}	AGCGCTAAGT	ACATCTACAA	TTATAGAGAG	CGTAaCTTCC	GGcCCTCTCT
msa141507.2{399_CJB110}	AGCGCTAAGT	ACATCTACAA	TTATAGAGAG	CGTAaCTTCC	GGcCCTCTCT
msa141507.2{399_H36B}	AGCGCTAAGT	ACATCTACAA	TTATAGAGAG	CGTAaCTTCC	GGcCCTCTCT
msa141507.2{399_JM9130013}	AGCGCTAAGT	ACATCTACAA	TTATAGAGAG	CGTAaCTTCC	GGcCCTCTCT
msa141507.2{399_1169NT}	AGCGCTAAGT	ACATCTACAA	TTATAGAGAG	CGTAaCTTCC	GGcCCTCTCT
msa141507.2{399_090}	AGCGCTAAGT	ACATCTACAA	TTATAGAGAG	CGTAaCTTCC	GGcCCTCTCT
msa141507.2{399_18RS21}	AGCGCTAAGT	ACATCTACAA	TTATAGAGAG	CGTAaCTTCC	GGcCCTCTCT
msa141507.2{399_2603}	AGCGCTAAGT	ACATCTACAA	TTATAGAGAG	CGTAaCTTCC	GGcCCTCTCT
msa141507.2{399_COH1}	AGCGCTAAGT	ACATCTACAA	TTATAGAGAG	CGTAaCTTCC	GGcCCTCTCT
msa141507.2{399_M732}	AGCGCTAAGT	ACATCTACAA	TTATAGAGAG	CGTAaCTTCC	GGcCCTCTCT
msa141507.2{399_M781}	AGCGCTAAGT	ACATCTACAA	TTATAGAGAG	CGTAaCTTCC	GGcCCTCTCT
Consensus	*****	*****	*****	*****	*****
msa141507.2{399_A909}	TCAAGCAACA	GTATCCATTG	ACAGTAGAAG	ATcGAATCTA	TCTGGTGTCTG
msa141507.2{399_CJB110}	TCAAGCAACA	GTATCCATTG	ACAGTAGAAG	ATcGAATCTA	TCTGGTGTCTG
msa141507.2{399_H36B}	TCAAGCAACA	GTATCCATTG	ACAGTAGAAG	ATcGAATCTA	TCTGGTGTCTG
msa141507.2{399_JM9130013}	TCAAGCAACA	GTATCCATTG	ACAGTAGAAG	ATcGAATCTA	TCTGGTGTCTG
msa141507.2{399_1169NT}	TCAAGCAACA	GTATCCATTG	ACAGTAGAAG	ATcGAATCTA	TCTGGTGTCTG
msa141507.2{399_090}	TCAAGCAACA	GTATCCATTG	ACAGTAGAAG	ATcGAATCTA	TCTGGTGTCTG
msa141507.2{399_18RS21}	TCAAGCAACA	GTATCCATTG	ACAGTAGAAG	ATcGAATCTA	TCTGGTGTCTG
msa141507.2{399_2603}	TCAAGCAACA	GTATCCATTG	ACAGTAGAAG	ATcGAATCTA	TCTGGTGTCTG
msa141507.2{399_COH1}	TCAAGCAACA	GTATCCATTG	ACAGTAGAAG	ATcGAATCTA	TCTGGTGTCTG
msa141507.2{399_M732}	TCAAGCAACA	GTATCCATTG	ACAGTAGAAG	ATcGAATCTA	TCTGGTGTCTG
msa141507.2{399_M781}	TCAAGCAACA	GTATCCATTG	ACAGTAGAAG	ATcGAATCTA	TCTGGTGTCTG
Consensus	*****	*****	*****	*****	*****
msa141507.2{399_A909}	GCGGATGATA	TCCTTTTGAT	TGAAGCTATG	CAAGGAAAAC	TGATTATACA
msa141507.2{399_CJB110}	GCGGATGATA	TCCTTTTGAT	TGAAGCTATG	CAAGGAAAAC	TGATTATACA
msa141507.2{399_H36B}	GCGGATGATA	TCCTTTTGAT	TGAAGCTATG	CAAGGAAAAC	TGATTATACA
msa141507.2{399_JM9130013}	GCGGATGATA	TCCTTTTGAT	TGAAGCTATG	CAAGGAAAAC	TGATTATACA

Table 78: Comparative Sequences relating to SAG1016

msa141507.2{399_1169NT}	GCGGATGATA	TCCTTTTGAT	TGAAGCTATG	CAAGGAAAAC	TGATTATACA
msa141507.2{399_090}	GCGGATGATA	TCCTTTTGAT	TGAAGCTATG	CAAGGAAAAC	TGATTATACA
msa141507.2{399_18RS21}	GCGGATGATA	TCCTTTTGAT	TGAAGCTATG	CAAGGAAAAC	TGATTATACA
msa141507.2{399_2603}	GCGGATGATA	TCCTTTTGAT	TGAAGCTATG	CAAGGAAAAC	TGATTATACA
msa141507.2{399_COH1}	GCGGATGATA	TCCTTTTGAT	TGAAGCTATG	CAAGGAAAAC	TGATTATACA
msa141507.2{399_M732}	GCGGATGATA	TCCTTTTGAT	TGAAGCTATG	CAAGGAAAAC	TGATTATACA
msa141507.2{399_M781}	GCGGATGATA	TCCTTTTGAT	TGAAGCTATG	CAAGGAAAAC	TGATTATACA
Consensus	*****	*****	*****	*****	*****
501					
msa141507.2{399_A909}	AACACCTGAT	AAAAATTATG	AAATTGATGG	CTCTCTACAA	CAATGGCAAG
msa141507.2{399_CJB110}	AACACCTGAT	AAAAATTATG	AAATTGATGG	CTCTCTACAA	CAATGGCAAG
msa141507.2{399_H36B}	AACACCTGAT	AAAAATTATG	AAATTGATGG	CTCTCTACAA	CAATGGCAAG
msa141507.2{399_JM9130013}	AACACCTGAT	AAAAATTATG	AAATTGATGG	CTCTCTACAA	CAATGGCAAG
msa141507.2{399_1169NT}	AACACCTGAT	AAAAATTATG	AAATTGATGG	CTCTCTACAA	CAATGGCAAG
msa141507.2{399_090}	AACACCTGAT	AAAAATTATG	AAATTGATGG	CTCTCTACAA	CAATGGCAAG
msa141507.2{399_18RS21}	AACACCTGAT	AAAAATTATG	AAATTGATGG	CTCTCTACAA	CAATGGCAAG
msa141507.2{399_2603}	AACACCTGAT	AAAAATTATG	AAATTGATGG	CTCTCTACAA	CAATGGCAAG
msa141507.2{399_COH1}	AACACCTGAT	AAAAATTATG	AAATTGATGG	CTCTCTACAA	CAATGGCAAG
msa141507.2{399_M732}	AACACCTGAT	AAAAATTATG	AAATTGATGG	CTCTCTACAA	CAATGGCAAG
msa141507.2{399_M781}	AACACCTGAT	AAAAATTATG	AAATTGATGG	CTCTCTACAA	CAATGGCAAG
Consensus	*****	*****	*****	*****	*****
551					
msa141507.2{399_A909}	ATAAACTACC	ATCATCTCAA	TTTGTACGGG	TgCacCGCTC	TTACATTGTG
msa141507.2{399_CJB110}	ATAAACTACC	ATCATCTCAA	TTTGTACGGG	TgCacCGCTC	TTACATTGTG
msa141507.2{399_H36B}	ATAAACTACC	ATCATCTCAA	TTTGTACGGG	TgCacCGCTC	TTACATTGTG
msa141507.2{399_JM9130013}	ATAAACTACC	ATCATCTCAA	TTTGTACGGG	TgCacCGCTC	TTACATTGTG
msa141507.2{399_1169NT}	ATAAACTACC	ATCATCTCAA	TTTGTACGGG	TgCacCGCTC	TTACATTGTG
msa141507.2{399_090}	ATAAACTACC	ATCATCTCAA	TTTGTACGGG	TaCatCGCTC	TTACATTGTG
msa141507.2{399_18RS21}	ATAAACTACC	ATCATCTCAA	TTTGTACGGG	TaCatCGCTC	TTACATTGTG
msa141507.2{399_2603}	ATAAACTACC	ATCATCTCAA	TTTGTACGGG	TaCatCGCTC	TTACATTGTG
msa141507.2{399_COH1}	ATAAACTACC	ATCATCTCAA	TTTGTACGGG	TaCatCGCTC	TTACATTGTG
msa141507.2{399_M732}	ATAAACTACC	ATCATCTCAA	TTTGTACGGG	TaCatCGCTC	TTACATTGTG
msa141507.2{399_M781}	ATAAACTACC	ATCATCTCAA	TTTGTACGGG	TaCatCGCTC	TTACATTGTG
Consensus	*****	*****	*****	*-**-*****	*****
601					
msa141507.2{399_A909}	AAtATTAATG	CTATTAAAAC	GATTGAACCT	TGGTTTAACC	AAACACTTCA
msa141507.2{399_CJB110}	AAtATTAATG	CTATTAAAAC	GATTGAACCT	TGGTTTAACC	AAACACTTCA
msa141507.2{399_H36B}	AAtATTAATG	CTATTAAAAC	GATTGAACCT	TGGTTTAACC	AAACACTTCA
msa141507.2{399_JM9130013}	AAtATTAATG	CTATTAAAAC	GATTGAACCT	TGGTTTAACC	AAACACTTCA
msa141507.2{399_1169NT}	AAtATTAATG	CTATTAAAAC	GATTGAACCT	TGGTTTAACC	AAACACTTCA
msa141507.2{399_090}	AACATTAATG	CTATTAAAAC	GATTGAACCT	TGGTTTAACC	AAACACTTCA
msa141507.2{399_18RS21}	AACATTAATG	CTATTAAAAC	GATTGAACCT	TGGTTTAACC	AAACACTTCA
msa141507.2{399_2603}	AACATTAATG	CTATTAAAAC	GATTGAACCT	TGGTTTAACC	AAACACTTCA
msa141507.2{399_COH1}	AAtATTAATG	CTATTAAAAC	GATTGAACCT	TGGTTTAACC	AAACACTTCA
msa141507.2{399_M732}	AAtATTAATG	CTATTAAAAC	GATTGAACCT	TGGTTTAACC	AAACACTTCA
msa141507.2{399_M781}	AAtATTAATG	CTATTAAAAC	GATTGAACCT	TGGTTTAACC	AAACACTTCA
Consensus	**-*****	*****	*****	*****	*****
651					
msa141507.2{399_A909}	GTTACACCTT	TGTAATAAAA	TAACAGTTCC	TGTTAGCAGA	GCAAATGTAA
msa141507.2{399_CJB110}	GTTACACCTT	TGTAATAAAA	TAACAGTTCC	TGTTAGCAGA	GCAAATGTAA
msa141507.2{399_H36B}	GTTACACCTT	TGTAATAAAA	TAACAGTTCC	TGTTAGCAGA	GCAAATGTAA
msa141507.2{399_JM9130013}	GTTACACCTT	TGTAATAAAA	TAACAGTTCC	TGTTAGCAGA	GCAAATGTAA
msa141507.2{399_1169NT}	GTTACACCTT	TGTAATAAAA	TAACAGTTCC	TGTTAGCAGA	GCAAATGTAA
msa141507.2{399_090}	GTTACACCTT	TGTAATAAAA	TAACAGTTCC	TGTTAGCAGA	GCAAATGTAA
msa141507.2{399_18RS21}	GTTACACCTT	TGTAATAAAA	TAACAGTTCC	TGTTAGCAGA	GCAAATGTAA
msa141507.2{399_2603}	GTTACACCTT	TGTAATAAAA	TAACAGTTCC	TGTTAGCAGA	GCAAATGTAA
msa141507.2{399_COH1}	GTTACACCTT	TGTAATAAAA	TAACAGTTCC	TGTTAGCAGA	GCAAATGTAA
msa141507.2{399_M732}	GTTACACCTT	TGTAATAAAA	TAACAGTTCC	TGTTAGCAGA	GCAAATGTAA
msa141507.2{399_M781}	GTTACACCTT	TGTAATAAAA	TAACAGTTCC	TGTTAGCAGA	GCAAATGTAA
Consensus	*****	*****	*****	*****	*****
701					
msa141507.2{399_A909}	AACCCCTAAA	ACAAATGTTA	GGcatatcta	cc	
msa141507.2{399_CJB110}	AACCCCTAAA	ACAAATGTTA	GG-----	--	
msa141507.2{399_H36B}	AACCCCTAAA	ACAAATGTTA	GGcatatcta	cc	
msa141507.2{399_JM9130013}	AACCCCTAAA	ACAAATGTTA	GGcatatcta	cc	
msa141507.2{399_1169NT}	AACCCCTAAA	ACAAATGTTA	GGcatatcta	cc	
msa141507.2{399_090}	AACCCCTAAA	ACAAATGTTA	GGcatatcta	cc	
msa141507.2{399_18RS21}	AACCCCTAAA	ACAAATGTTA	GGcatatcta	cc	
msa141507.2{399_2603}	AACCCCTAAA	ACAAATGTTA	GGcatatcta	cc	
msa141507.2{399_COH1}	AACCCCTAAA	ACAAATGTTA	GGcatatcta	cc	
msa141507.2{399_M732}	AACCCCTAAA	ACAAATGTTA	GGcatatcta	cc	
msa141507.2{399_M781}	AACCCCTAAA	ACAAATGTTA	GGcatatcta	cc	
Consensus	*****	*****	***-----	--	
732					

SEQ ID NO. 7812

STRAIN 2603 frame: 1

KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALAILLRETFDVALLDIHLRDDSG
 LQLAEYINKMPKPPLLI FATA YDQYAIQAFEHDARDYLLKPYDFDRLKQAMDRVKGALST

Table 78: Comparative Sequences relating to SAG1016

STIIESVTSGPLFKQQYPLTVEDRIYLVSAADDILLIEAMQGKLI IQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRYSYIVNINAIKTI EPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7813

STRAIN 090 frame: 1

KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALA ILLRETFDVALLDIHLRDDSG
LQLAEYINKMPKPPLLI FATAYDQYAIQAFEHDARDYLLKPYDFDRLKQAMDRVKGALST
STIIESVTSGPLFKQQYPLTVEDRIYLVSAADDILLIEAMQGKLI IQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRYSYIVNINAIKTI EPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7814

STRAIN A909 frame: 1

KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALA ILLRETFDVALLDIHLRDDSG
LQLAEYINKMPKPPLLI FATAYDQYAIQAFEHDARDYLLKPYEFDRLKQAMDRVKGALST
STIIESVTSGPLFKQQYPLTVEDRIYLVSAADDILLIEAMQGKLI IQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRYSYIVNINAIKTI EPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7815

STRAIN H36B frame: 1

KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALA ILLRETFDVALLDIHLRDDSG
LQLAEYINKMPKPPLLI FATAYDQYAIQAFEHDARDYLLKPYEFDRLKQAMDRVKGALST
STIIESVTSGPLFKQQYPLTVEDRIYLVSAADDILLIEAMQGKLI IQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRYSYIVNINAIKTI EPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7816

STRAIN 18RS21 frame: 1

KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALA ILLRETFDVALLDIHLRDDSG
LQLAEYINKMPKPPLLI FATAYDQYAIQAFEHDARDYLLKPYDFDRLKQAMDRVKGALST
STIIESVTSGPLFKQQYPLTVEDRIYLVSAADDILLIEAMQGKLI IQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRYSYIVNINAIKTI EPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7817

STRAIN M732 frame: 1

KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALA ILLRETFDVALLDIHLRDDSG
LQLAEYINKMPKPPLLI FATAYDQYAIQAFEQDARDYLLKPYEFDRLKQAMDRVKGALST
STIIESVASGPLFKQQYPLTVEDRIYLVSAADDILLIEAMQGKLI IQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRYSYIVNINAIKTI EPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7818

STRAIN COH1 frame: 1

KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALA ILLRETFDVALLDIHLRDDSG
LQLAEYINKMPKPPLLI FATAYDQYAIQAFEQDARDYLLKPYEFDRLKQAMDRVKGALST
STIIESVASGPLFKQQYPLTVEDRIYLVSAADDILLIEAMQGKLI IQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRYSYIVNINAIKTI EPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7819

STRAIN M781 frame: 1

KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALA ILLRETFDVALLDIHLRDDSG
LQLAEYINKMPKPPLLI FATAYDQYAIQAFEQDARDYLLKPYEFDRLKQAMDRVKGALST
STIIESVASGPLFKQQYPLTVEDRIYLVSAADDILLIEAMQGKLI IQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRYSYIVNINAIKTI EPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7820

STRAIN CJB110 frame: 1

LNKYDSNLVIAEAHDMATALA ILLRETFDVALLDIHLRDDSG LQLAEYINKMPKPPLLI F
ATAYDQYAIQAFEHDARDYLLKPYEFDRLKQXMDRVKGALSTSTIIESVTSGPLFKQQYP
LTVEDXIYLVSAADDILLIEAMQGKLI IQTPDKNYEIDGSLQQWQDKLPSSQFVRVHRYSYI
VNINAIKTI EPWFNQTLQLHLCNKITVPVSRANVKPLKQML

SEQ ID NO. 7821

STRAIN 1169NT frame: 1

KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDIATALA ILLRETFDVALLDIHLRDDSG
LQLAEYINKMPKPPLLI FATAYDQYAIQAFEHDARDYLLKPYEFDRLKQAMDRVKGALST
STIIESVTSGPLFKQQYPLTVEDRIYLVSAADDILLIEAMQGKLI IQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRYSYIVNINAIKTI EPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7822

STRAIN JM9130013 frame: 1

KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALA ILLRETFDVALLDIHLRDDSG
LQLAEYINKMPKPPLLI FATAYDQYAIQAFEHDARDYLLKPYEFDRLKQAMDRVKGALST
STIIESVTSGPLFKQQYPLTVEDRIYLVSAADDILLIEAMQGKLI IQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRYSYIVNINAIKTI EPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

Table 78: Comparative Sequences relating to SAG1016

PRETTY of: /biotmp/msa141801.2{*} April 10, 2003 06:38 ..

	1				50
msa141801.2{399_COH1}	kvlvvddepv	arneliyLLN	KYDSNLVIAE	AHDmATALAI	LLRETFDVAL
msa141801.2{399_M732}	kvlvvddepv	arneliyLLN	KYDSNLVIAE	AHDmATALAI	LLRETFDVAL
msa141801.2{399_M781}	kvlvvddepv	arneliyLLN	KYDSNLVIAE	AHDmATALAI	LLRETFDVAL
msa141801.2{399_090}	kvlvvddepv	arneliyLLN	KYDSNLVIAE	AHDmATALAI	LLRETFDVAL
msa141801.2{399_18RS21}	kvlvvddepv	arneliyLLN	KYDSNLVIAE	AHDmATALAI	LLRETFDVAL
msa141801.2{399_2603}	kvlvvddepv	arneliyLLN	KYDSNLVIAE	AHDmATALAI	LLRETFDVAL
msa141801.2{399_A909}	kvlvvddepv	arneliyLLN	KYDSNLVIAE	AHDmATALAI	LLRETFDVAL
msa141801.2{399_H36B}	kvlvvddepv	arneliyLLN	KYDSNLVIAE	AHDmATALAI	LLRETFDVAL
msa141801.2{399_JM9130013}	kvlvvddepv	arneliyLLN	KYDSNLVIAE	AHDmATALAI	LLRETFDVAL
msa141801.2{399_1169NT}	kvlvvddepv	arneliyLLN	KYDSNLVIAE	AHDmATALAI	LLRETFDVAL
msa141801.2{399_CJB110}	~~~~~	~~~~~LN	KYDSNLVIAE	AHDmATALAI	LLRETFDVAL
Consensus	-----	-----**	*****	***-*****	*****
	51				100
msa141801.2{399_COH1}	LDIHLRDDSG	LQLAEYINKM	PKPPLLI FAF	AYDQYAIQAF	EqDARDYLLK
msa141801.2{399_M732}	LDIHLRDDSG	LQLAEYINKM	PKPPLLI FAF	AYDQYAIQAF	EqDARDYLLK
msa141801.2{399_M781}	LDIHLRDDSG	LQLAEYINKM	PKPPLLI FAF	AYDQYAIQAF	EqDARDYLLK
msa141801.2{399_090}	LDIHLRDDSG	LQLAEYINKM	PKPPLLI FAF	AYDQYAIQAF	EhDARDYLLK
msa141801.2{399_18RS21}	LDIHLRDDSG	LQLAEYINKM	PKPPLLI FAF	AYDQYAIQAF	EhDARDYLLK
msa141801.2{399_2603}	LDIHLRDDSG	LQLAEYINKM	PKPPLLI FAF	AYDQYAIQAF	EhDARDYLLK
msa141801.2{399_A909}	LDIHLRDDSG	LQLAEYINKM	PKPPLLI FAF	AYDQYAIQAF	EhDARDYLLK
msa141801.2{399_H36B}	LDIHLRDDSG	LQLAEYINKM	PKPPLLI FAF	AYDQYAIQAF	EhDARDYLLK
msa141801.2{399_JM9130013}	LDIHLRDDSG	LQLAEYINKM	PKPPLLI FAF	AYDQYAIQAF	EhDARDYLLK
msa141801.2{399_1169NT}	LDIHLRDDSG	LQLAEYINKM	PKPPLLI FAF	AYDQYAIQAF	EhDARDYLLK
msa141801.2{399_CJB110}	LDIHLRDDSG	LQLAEYINKM	PKPPLLI FAF	AYDQYAIQAF	EhDARDYLLK
Consensus	*****	*****	*****	*****	*-*****
	101				150
msa141801.2{399_COH1}	PYdFDRKQa	MDRVKGALST	STIIESVaSG	PLFKQQYPLT	VEDrIYLVSA
msa141801.2{399_M732}	PYdFDRKQa	MDRVKGALST	STIIESVaSG	PLFKQQYPLT	VEDrIYLVSA
msa141801.2{399_M781}	PYdFDRKQa	MDRVKGALST	STIIESVaSG	PLFKQQYPLT	VEDrIYLVSA
msa141801.2{399_090}	PYdFDRKQa	MDRVKGALST	STIIESVtSG	PLFKQQYPLT	VEDrIYLVSA
msa141801.2{399_18RS21}	PYdFDRKQa	MDRVKGALST	STIIESVtSG	PLFKQQYPLT	VEDrIYLVSA
msa141801.2{399_2603}	PYdFDRKQa	MDRVKGALST	STIIESVtSG	PLFKQQYPLT	VEDrIYLVSA
msa141801.2{399_A909}	PYdFDRKQa	MDRVKGALST	STIIESVtSG	PLFKQQYPLT	VEDrIYLVSA
msa141801.2{399_H36B}	PYdFDRKQa	MDRVKGALST	STIIESVtSG	PLFKQQYPLT	VEDrIYLVSA
msa141801.2{399_JM9130013}	PYdFDRKQa	MDRVKGALST	STIIESVtSG	PLFKQQYPLT	VEDrIYLVSA
msa141801.2{399_1169NT}	PYdFDRKQa	MDRVKGALST	STIIESVtSG	PLFKQQYPLT	VEDrIYLVSA
msa141801.2{399_CJB110}	PYdFDRKQx	MDRVKGALST	STIIESVtSG	PLFKQQYPLT	VEDxIYLVSA
Consensus	**~*****-	*****	*****~**	*****	***~*****
	151				200
msa141801.2{399_COH1}	DDILLIEAMQ	GKLI IQTPDK	NYEIDGSLQQ	WQDKLPSSQF	VRVHRSYIVN
msa141801.2{399_M732}	DDILLIEAMQ	GKLI IQTPDK	NYEIDGSLQQ	WQDKLPSSQF	VRVHRSYIVN
msa141801.2{399_M781}	DDILLIEAMQ	GKLI IQTPDK	NYEIDGSLQQ	WQDKLPSSQF	VRVHRSYIVN
msa141801.2{399_090}	DDILLIEAMQ	GKLI IQTPDK	NYEIDGSLQQ	WQDKLPSSQF	VRVHRSYIVN
msa141801.2{399_18RS21}	DDILLIEAMQ	GKLI IQTPDK	NYEIDGSLQQ	WQDKLPSSQF	VRVHRSYIVN
msa141801.2{399_2603}	DDILLIEAMQ	GKLI IQTPDK	NYEIDGSLQQ	WQDKLPSSQF	VRVHRSYIVN
msa141801.2{399_A909}	DDILLIEAMQ	GKLI IQTPDK	NYEIDGSLQQ	WQDKLPSSQF	VRVHRSYIVN
msa141801.2{399_H36B}	DDILLIEAMQ	GKLI IQTPDK	NYEIDGSLQQ	WQDKLPSSQF	VRVHRSYIVN
msa141801.2{399_JM9130013}	DDILLIEAMQ	GKLI IQTPDK	NYEIDGSLQQ	WQDKLPSSQF	VRVHRSYIVN
msa141801.2{399_1169NT}	DDILLIEAMQ	GKLI IQTPDK	NYEIDGSLQQ	WQDKLPSSQF	VRVHRSYIVN
msa141801.2{399_CJB110}	DDILLIEAMQ	GKLI IQTPDK	NYEIDGSLQQ	WQDKLPSSQF	VRVHRSYIVN
Consensus	*****	*****	*****	*****	*****
	201				243
msa141801.2{399_COH1}	INAIKTIEPW	FNQTLQLHLC	NKITVPVSRA	NVKPLKQMLg	ist
msa141801.2{399_M732}	INAIKTIEPW	FNQTLQLHLC	NKITVPVSRA	NVKPLKQMLg	ist
msa141801.2{399_M781}	INAIKTIEPW	FNQTLQLHLC	NKITVPVSRA	NVKPLKQMLg	ist
msa141801.2{399_090}	INAIKTIEPW	FNQTLQLHLC	NKITVPVSRA	NVKPLKQMLg	ist
msa141801.2{399_18RS21}	INAIKTIEPW	FNQTLQLHLC	NKITVPVSRA	NVKPLKQMLg	ist
msa141801.2{399_2603}	INAIKTIEPW	FNQTLQLHLC	NKITVPVSRA	NVKPLKQMLg	ist
msa141801.2{399_A909}	INAIKTIEPW	FNQTLQLHLC	NKITVPVSRA	NVKPLKQMLg	ist
msa141801.2{399_H36B}	INAIKTIEPW	FNQTLQLHLC	NKITVPVSRA	NVKPLKQMLg	ist
msa141801.2{399_JM9130013}	INAIKTIEPW	FNQTLQLHLC	NKITVPVSRA	NVKPLKQMLg	ist
msa141801.2{399_1169NT}	INAIKTIEPW	FNQTLQLHLC	NKITVPVSRA	NVKPLKQMLg	ist
msa141801.2{399_CJB110}	INAIKTIEPW	FNQTLQLHLC	NKITVPVSRA	NVKPLKQML-	---
Consensus	*****	*****	*****	*****-	---

Table 79: Comparative Sequences relating to SAG2150**SEQ ID NO. 7901****STRAIN 2603**

ATGGGAATTGAATTTAAAAATGTAAGTTATACCTATCAAGCCGGCACTCCTTTTGAAGGG
 CGTGCCCTTTTGAAGCTCAATCTGAAAATTGAAGATGCTTCTATACCGCGTTCATTGGG
 CACACAGGTTCTGGAAAATCAACTATTATGCAACTTTTGAATGGTTTACATATTCCTACA
 AAAGGTGAGGTAATTGTCGATGATTTTCTATTAAAGCAGGGGACAAGAACAAGAAATC
 AAATTTATAAGGCAAAAAGTTGGTTTAGTTTTTCAATTTCCAGAAAGTCAGCTTTTGA
 GAGACAGTTTAAAGGATGTTGCTTTTGGACCACAAAATTTGGTATTTCTCAGATTGAA
 GCTGAAAGGCTGGCTGAAGAAAAATTAAGGTTAGTTGGTATCAGTGAGGATTTATTTCGAT
 AAAATCCATTTGAACTTTCTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTTA
 GCGATGGAACCCAAAGTACTAGTACTGGATGAGCCAACAGCTGGACTTGATCCTAAGGGA
 AGAAAAGAATTAATGACTCTTTTAAAAATCTTCATAAAAAAGGAATGACTATCGTCTTA
 GTGACTCACTTAATGGACGATGTAGCGGATTATGCTGACTATGTGTATGTTTAGAAGCA
 GGGAAAGTAACCTTATCAGGACAACCAAAACAGATTTTCAAGAAGTAGAAGCTTTTAGAA
 AGTAAACAATTAGGAGTTCCCAAATCACCAGTTTGTCTCAAAGACTATCTCATAAGGGA
 TTAAATTTACCTAGTTTACCAATTACTATTAACGAATTTGTGGAGGCTATTAAGCATGGA

SEQ ID NO. 7902**STRAIN 090**

GGAATTGAATTTAAAAATGTAAGTTATACCTATCAAGCC
 GGCACCTCCTTTTGAAGGGCGTGCCCTTTTGGACGTCAATCTGAAAAATTGA
 AGATGCTTCTATACCGCGTTCATTGGGCACACAGGTTCTGGAAAATCAA
 CTATTATGCAACTTTTGAATGGTTTACATATTCTACAAAAGGTGAGGTA
 ATTGTCGATGATTTTCTATTAAAGCAGGGGACAAGAACAAGAAATCAA
 ATTTATAAGGCAAAAAGTTGGTTTAGTTTTTCAATTTCCAGAAAGTCAGC
 TTTTGAAGAGACAGTTTAAAGGATGTTGCTTTTGGACCACAAAATTTT
 GGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAAAATTAAGGTT
 AGTTGGTATCAGTGAGGATTTATTGATAAAAAATCCATTTGAACTTTCTG
 GAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTTAGCGATGGAACCC
 AAAGTACTAGTACTGGATGAGCCAACAGCTGGACTTGATCCTAAGGGAAG
 AAAAGAATTAATGACTCTTTTAAAAATCTTCATAAAAAAGGAATGACTA
 TCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTATGCTGACTAT
 GTGTATGTTTTAGAAGCAGGGAAAGTAACCTTATCAGGACAACCAAAACA
 GATTTTTCAAGAAGTAGAAGCTTTAGAAAAGTAAACAATTAGGAGTTCCCA
 AAATCACCAGTTTGTCTCAAAGACTATCTCATAAGGGATTAAATTTACCT
 AGTTTACCAATTACTATTAACGAATTTGTGGAGGCTATTAAGCATGGA

SEQ ID NO. 7903**STRAIN A909**

GGAATTGAATTTAAAAATGTAAGTTATACCTATCAA
 GCCGGCACTCCTTTTGAAGGGCGTGCCCTTTTGGACGTCAATCTGAAAAAT
 TGAAGATGCTTCTATACCGCGTTCATTGGGCACACAGGTTCTGGAAAAT
 CAACTATTATGCAACTTTTGAATGGTTTACATATTCTACAAAAGGTGAG
 GTAATTGTCGATGATTTTCTATTAAAGCAGGGGACAAGAACAAGAAAT
 CAAATTTATAAGGCAAAAAGTTGGTTTAGTTTTTCAATTTCCAGAAAGTC
 AGCTTTTGAAGAGACAGTTTAAAGATGTTGCTTTTGGACCACAAAAT
 TTTGGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAAAATTAAG
 GTTAGTTGGTATCAGTGAGGATTTATTGATAAAAAATCCATTTGAACTTT
 CTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTTAGCGATGGAA
 CCCAAAGTACTAGTACTAGATGAGCCAACAGCTGGACTTGATCCTAAGGG
 AAGAAAAGAATTAATGACTCTTTTAAAAATCTTCATAAAAAAGGAATGA
 CTATCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTATGCTGAC
 TATGTGTATGTTTTAGAAGCAGGGAAAGTAACCTTATCAGGACAACCAAA
 GCAGATTTTCAAGAAGTAGAAGCTTTAGAAAAGTAAACAATTAGGAGTTT
 CCAAATCACCAGTTTGTCTCAAAGGCTATCTCATAAGGGATTAAATTTA
 CCTAGTTTACCAATTACTATTAACGAATTTGTGGAGGCTATTAAGCATGG
 A

SEQ ID NO. 7904**STRAIN H36B**

GGAATTGAATTTAAAAATGTAAGTTATAC
 CTATCAAGCCGGCACTCCTTTTGAAGGGCGTGCCCTTTTGGACGTCAATC
 TGAATAATTGAAGATGCTTCTATACCGCGTTCATTGGGCACACAGGTTCT
 GGAAAATCAACTATTATGCAACTTTTGAATGGTTTACATATTCCTACAAA
 AGGTGAGGTAATTGTCGATGATTTTCTATTAAAGCAGGGGACAAGAACA
 AAGAAATCAAAATTTATAAGGCAAAAAGTTGGTTTAGTTTTTCAATTTCCA
 GAAAGTCAGCTTTTGAAGAGACAGTTTAAAGATGTTGCTTTTGGACC
 ACAAATTTTGGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAA
 AATTAAGGTTAGTTGGTATCAGTGAGGATTTATTGATAAAAAATCCATTT
 GAACTTTCTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTTAGC
 CATGGAACCCAAAGTACTAGTACTAGATGAGCCAACAGCTGGACTTGATC
 CTAAGGGAAGAAAAGAATTAATGACTCTTTTAAAAATCTTCATAAAAAA
 GGAATGACTATCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTA
 TGCTGACTATGTGTATGTTTTAGAAGCAGGGAAAGTAACCTTATCAGGAC
 AACCAAGCAGATTTTCAAGAAGTAGAAGCTTTAGAAAAGTAAACAATTA
 GGAGTTCCCAAATCACCAGTTTGTCTCAAAGGCTATCTCATAAGGGATT
 AAATTTACCTAGTTTACCAATTACTATTAACGAATTTGTGGAGGCTATTA
 AGCATGGA

SEQ ID NO. 7905**STRAIN 18RS21**

GGAATTGAATTTAAAAATGTAAGTTATAC
 CTATCAAGCCGGCACTCCTTTTGAAGGGCGTGCCCTTTTGGACGTCAATC

Table 79: Comparative Sequences relating to SAG2150

TGAAAATTGAAGATGCTTCCTATACCGCGTTTCATTGGGCACACAGGTTCT
 GGAAAATCAACTATTATGCAACTTTTGAATGGTTTACATATTCCTACAAA
 AGGTGAGGTAATTGTGCGATGATTTTCTATTAAAGCAGGGGACAAGAACA
 AAGAAATCAAATTTATAAGGCAAAAAGTTGGTTTAGTTTTCATTTCCA
 GAAAGTCAGCTTTTGAAGAGACAGTTTTAAAGGATGTTGCTTTTGGACC
 ACAAATTTTGGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAA
 AATTAAGGTTAGTTGGTATCAGTGAGGATTTATTGATAAAAAATCCATTT
 GAACTTTCTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTTAGC
 GATGGAACCCAAAGTACTAGTACTGGATGAGCCAACAGCTGGACTTGATC
 CTAAGGGAAGAAAAGAATTAATGACTCTTTTAAAAATCTTCATAAAAAA
 GGAATGACTATCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTA
 TGCTGACTATGTGTATGTTTTAGAAGCAGGGAAAGTAACCTTATCAGGAC
 AACCAAAACAGATTTTCAAGAAGTAGAAGTTTAAAGTAACAATTA
 GGAGTTCCCAAAATCACCAAGTTTGCTCAAAGACTATCTCATAAGGGATT
 AAATTTACCTAGTTTACCAATTACTATTAACGAATTTGTGGAGGCTATTA
 AGCATGGA

SEQ ID NO. 7906

STRAIN M732

GGAATTGAATTTAAAAATGTAAGTTATAC
 CTATCAAGCCGGCACTCCTTTTGAAGGGCGTGCCCTTTTGGACGTCAATC
 TGAAAATTGAAGATGTTTCTATACCGCGTTTCATTGGGCACACAGGTTCT
 GGAAAATCAACTATTATGCAACTTTTGAATGGTTTACATATTCCTACAAA
 AGGTGAGGTAATTGTGCGATGATTTTCTATTAAAGCAGGGGACAAGAACA
 AAGAAATCAAATTTATAAGGCAAAAAGTTGGTTTAGTTTTCATTTCCA
 GAAAGTCAGCTTTTGAAGAGACAGTTTTAAAGGATGTTGCTTTTGGACC
 ACAAATTTTGGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAA
 AATTAAGGTTAGTTGGTATCAGTGAGGATTTATTGATAAAAAATCCATTT
 GAACTTTCTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTTAGC
 GATGGAACCCAAAGTACTAGTACTGGATGAGCCAACAGCTGGACTTGATC
 CTAAGGGAAGAAAAGAATTAATGACTCTTTTAAAAATCTTCATAAAAAA
 GGAATGACTATCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTA
 TGCTGACTATGTGTATGTTTTAGAAGCAGGGAAAGTAACCTTATCAGGAC
 AACCAAAACAGATTTTCAAGAAGTAGAAGTTTAAAGTAACAATTA
 GGAGTTCCCAAAATCACCAAGTTTGCTCAAAGACTATCTCATAAGGGATT
 AAATTTACCTAGTTTACCAATTACTATTAACGAATTTGTGGAGGCTATTA
 AGCATGGA

SEQ ID NO. 7907

STRAIN COH1

GGAATTGAATTTAAAAATGTAAGTTATACCTATCAAGCC
 GGCACCTCCTTTTGAAGGGCGTGCCCTTTTGGACGTCAATCTGAAAATTGA
 AGATGTTTCTATACCGCGTTTCATTGGGCACACAGGTTCTGGAAAATCAA
 CTATTATGCAACTTTTGAATGGTTTACATATTCCTACAAAAGGTGAGGTA
 ATTGTGCGATGATTTTCTATTAAAGCAGGGGACAAGAACAAGAAATCAA
 ATTTATAAGGCAAAAAGTTGGTTTAGTTTTCATTTCCAGAAAGTCAGC
 TTTTGAAGAGACAGTTTTAAAGGATGTTGCTTTTGGACCACAAAATTTT
 GGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAAAATTAAGGTT
 AGTTGGTATCAGTGAGGATTTATTGATAAAAAATCCATTTGAACTTTCTG
 GAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTAGCGATGGAACCC
 AAAGTACTAGTACTGGATGAGCCAACAGCTGGACTTGATCCTAAGGGAAG
 AAAAGAATTAATGACTCTTTTAAAAATCTTCATAAAAAAGGAATGACTA
 TCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTTAGCTGACTAT
 GTGTATGTTTTAGAAGCAGGGAAAGTAACCTTATCAGGACAACCAAAACA
 GATTTTTCAAGAAGTAGAAGTTTAAAGTAACAATTAGGAGTTCCCA
 AAATCACCAAGTTTGCTCAAAGACTATCTCATAAGGGATTAAATTTACCT
 AGTTTACCAATTACTATTAACGAATTTGTGGAGGCTATTAAGCATGGA

SEQ ID NO. 7908

STRAIN M781

GGAATTGAATTTAAAAATGTAAGTTATAC
 CTATCAAGCCGGCACTCCTTTTGAAGGGCGTGCCCTTTTGGACGTCAATC
 TGAAAATTGAAGATGTTTCTATACCGCGTTTCATTGGGCACACAGGTTCT
 GGAAAATCAACTATTATGCAACTTTTGAATGGTTTACATATTCCTACAAA
 AGGTGAGGTAATTGTGCGATGATTTTCTATTAAAGCAGGGGACAAGAACA
 AAGAAATCAAATTTATAAGGCAAAAAGTTGGTTTAGTTTTCATTTCCA
 GAAAGTCAGCTTTTGAAGAGACAGTTTTAAAGGATGTTGCTTTTGGACC
 ACAAATTTTGGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAA
 AATTAAGGTTAGTTGGTATCAGTGAGGATTTATTGATAAAAAATCCATTT
 GAACTTTCTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTTAGC
 GATGGAACCCAAAGTACTAGTACTGGATGAGCCAACAGCTGGACTTGATC
 CTAAGGGAAGAAAAGAATTAATGACTCTTTTAAAAATCTTCATAAAAAA
 GGAATGACTATCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTA
 TGCTGACTATGTGTATGTTTTAGAAGCAGGGAAAGTAACCTTATCAGGAC
 AACCAAAACAGATTTTCAAGAAGTAGAAGTTTAAAGTAACAATTA
 GGAGTTCCCAAAATCACCAAGTTTGCTCAAAGACTATCTCATAAGGGATT
 AAATTTACCTAGTTTACCAATTACTATTAACGAATTTGTGGAGGCTATTA
 AGCATGGA

SEQ ID NO. 7909

STRAIN CJB110

GGAATTGAATTTAAAAATGTAAGTTATAC
 CTATCAAGCCGGCACTCCTTTTGAAGGGCGTGCCCTTTTGGACGTCAATC

Table 79: Comparative Sequences relating to SAG2150

TGAAAATTGAAGATGCTTCCTATACCGCGTTCATTGGGCACACAGGTTCT
 GGAAAATCAACTATTATGCAACTTTTGAATGGTTTACATATTCCTACAAA
 AGGTGAGGTAATTTGTCGATGATTTTCTATTAAAGCAGGGGACAAGAACA
 AAGAAATCAAATTTATAAGGCAAAAAGTTGGTTTGTAGTTTTCAATTTCCA
 GAAAGTCAGCTTTTGAAGAGACAGTTTAAAGGATGTTGCTTTTGGACC
 ACAAATTTTGGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAA
 AATTAAGGTTAGTTGGTATCAGTGAGGATTTATTTCGATAAAAATCCATTT
 GAACTTTCTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTTAGC
 GATGGAACCCAAAGTACTAGTACTGGATGAGCCAACAGCTGGACTTGATC
 CTAAGGGAAGAAAAGAATTAATGACTCTTTTAAAAATCTTCATAAAAAA
 GGAATGACTATCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTA
 TGCTGACTATGTGTATGTTTGAAGCAGGGAAAGTAACCTTATCAGGAC
 AACCAAAACAGATTTTCAAGAAGTAGAACTTTGAAGTAACAATTA
 GGAGTTCCCAAAATCACCAGTTTGCTCAAAGACTATCTCATAAGGGATT
 AAATTTACCTAGTTTACCAATTACTATTAACGAATTTGTGGAGGCTATTA
 AGCATGGA

SEQ ID NO. 7910

STRAIN 1169NT

GGAATTGAATTTAAAAATGTAA

GTTATACCTATCAAGCCGGCACTCCTTTTGAAGGGCGTGCCCTTTTGGAC
 GTCAATCTGAAAATTTGAAGATGCTTCCTATACCGCGTTCATTGGGCACAC
 AGGTTCTGAAAATCAACTATTATGCAACTTTTGAATGGTTTACATATTC
 CTACAAAAGGTGAGGTAATTTGTCGATGATTTTCTATTAAAGCAGGGGAC
 AAGAACAAGAAATCAAATTTATAAGGCAAAAAGTTGGTTTGTAGTTTTCA
 ATTTCCAGAAAGTCAGCTTTTGAAGAGACAGTTTAAAGGATGTTGCTT
 TTGGACCACAAAATTTTGGTATTTCTCAGATTGAAGCTGAAAGGCTGGCT
 GAAGAAAATTAAGGTTAGTTGGTATCAGTGAGGATTTATTTCGATAAAAA
 TCCATTTGAATTTCTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTA
 TTTTAGCGATGGAACCCAAAGTACTAGTACTGGATGAGCCAACAGCTGGA
 CTTGATCCTAAGGGAAGAAAAGAATTAATGACTCTTTTAAAAATCTTCA
 TAAAAAAGGAATGACTATCGTCTTAGTGACTCACTTAATGGACGATGTAG
 CGGATTATGCTGACTATGTGTATGTTTGAAGCAGGGAAAGTAACCTTA
 TCAGGACAACCAAAACAGATTTTCAAGAAGTAGAACTTTGAAGTAAGTAA
 ACAATTAGGAGTTCCCAAAATCACCAGTTTGCTCAAAGACTATCTCATA
 AGGGATTAAATTTACCTAGTTTACCAATTACTATTAACGAATTTGTGGAG
 GCTATTAAGCATGGA

SEQ ID NO. 7911

STRAIN JM9130013

GGAATTGAATTTAAAAATGTAAGTT

ATACCTATCAAGCCGGCACTCCTTTTGAAGGGCGTGCCCTTTTGGACGTT
 AATCTGAAAATTTGAAGATGCTTCCTATACCGCATTCATTGGGCACACAGG
 TTCTGAAAATCAACTATTATGCAACTTTTGAATGGTTTACATATTCCTA
 CAAAAGGTGAGGTAATTTGTCGATGATTTTCTATTAAAGCAGGGGACAAG
 AACAAAGAAATCAAATTTATAAGGCAAAAAGTTGGTTTGTAGTTTTCAAT
 TCCAGAAAGTCAGCTTTTGAAGAGACAGTTTAAAGGATGTTGCTTTTG
 GACCACAAAATTTTGGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAA
 GAAAAATTAAGGTTAGTTGGTATTAGTGAGGATTTATTTCGATAAAAATCC
 ATTTGAATTTCTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTT
 TAGCGATGGAACCCAAAGTACTAGTACTGGATGAGCCAACAGCTGGACTT
 GATCCTAAGGGAAGAAAAGAATTAATGACTCTTTTAAAAATCTTCATAA
 AAAAGGAATGACTATCGTCTTAGTGACTCACTTAATGGACGATGTAGCGG
 ATTATGCTGACTATGTGTATGTTTGAAGCAGGGAAAGTAACCTTATCA
 GGACAACCAAAACAGATTTTCAAGAAGTAGAACTTTGAAGTAACA
 ATTAGGAGTTCCCAAAATCACCAGTTTGCTCAAAGACTATCTCATAAGG
 GATTAAATTTACCTAGTTTACCAATTACTATTAACGAATTTGTGGAGGCT
 ATTAAGCATGGA

PRETTY of: /biotmp/msa238454.2{*} May 14, 2003 06:55 ..

	1		50
msa238454.2{401_A909}	---GGAATTG AATTTAAAAA TGTAAGTTAT ACCTATCAAG CCGGCACTCC		
msa238454.2{401_H36B}	---GGAATTG AATTTAAAAA TGTAAGTTAT ACCTATCAAG CCGGCACTCC		
msa238454.2{401_090}	---GGAATTG AATTTAAAAA TGTAAGTTAT ACCTATCAAG CCGGCACTCC		
msa238454.2{401_1169NT}	---GGAATTG AATTTAAAAA TGTAAGTTAT ACCTATCAAG CCGGCACTCC		
msa238454.2{401_18RS21}	---GGAATTG AATTTAAAAA TGTAAGTTAT ACCTATCAAG CCGGCACTCC		
msa238454.2{401_2603}	atgGGAATTG AATTTAAAAA TGTAAGTTAT ACCTATCAAG CCGGCACTCC		
msa238454.2{401_CJB110}	---GGAATTG AATTTAAAAA TGTAAGTTAT ACCTATCAAG CCGGCACTCC		
msa238454.2{401_COH1}	---GGAATTG AATTTAAAAA TGTAAGTTAT ACCTATCAAG CCGGCACTCC		
msa238454.2{401_M732}	---GGAATTG AATTTAAAAA TGTAAGTTAT ACCTATCAAG CCGGCACTCC		
msa238454.2{401_M781}	---GGAATTG AATTTAAAAA TGTAAGTTAT ACCTATCAAG CCGGCACTCC		
msa238454.2{401_JM9130013}	---GGAATTG AATTTAAAAA TGTAAGTTAT ACCTATCAAG CCGGCACTCC		
Consensus	*****		
	51		100
msa238454.2{401_A909}	TTTTGAAGGG CGTGCCCTTT TTGACGTcAA TCTGAAAATT GAAGATGcTT		
msa238454.2{401_H36B}	TTTTGAAGGG CGTGCCCTTT TTGACGTcAA TCTGAAAATT GAAGATGcTT		
msa238454.2{401_090}	TTTTGAAGGG CGTGCCCTTT TTGACGTcAA TCTGAAAATT GAAGATGcTT		
msa238454.2{401_1169NT}	TTTTGAAGGG CGTGCCCTTT TTGACGTcAA TCTGAAAATT GAAGATGcTT		
msa238454.2{401_18RS21}	TTTTGAAGGG CGTGCCCTTT TTGACGTcAA TCTGAAAATT GAAGATGcTT		
msa238454.2{401_2603}	TTTTGAAGGG CGTGCCCTTT TTGACGTcAA TCTGAAAATT GAAGATGcTT		
msa238454.2{401_CJB110}	TTTTGAAGGG CGTGCCCTTT TTGACGTcAA TCTGAAAATT GAAGATGcTT		

Table 79: Comparative Sequences relating to SAG2150

msa238454.2{401_COH1}	TTTTGAAGGG	CGTGCCCTTT	TTGACGTcAA	TCTGAAAATT	GAAGATGtTT
msa238454.2{401_M732}	TTTTGAAGGG	CGTGCCCTTT	TTGACGTcAA	TCTGAAAATT	GAAGATGtTT
msa238454.2{401_M781}	TTTTGAAGGG	CGTGCCCTTT	TTGACGTcAA	TCTGAAAATT	GAAGATGtTT
msa238454.2{401_JM9130013}	TTTTGAAGGG	CGTGCCCTTT	TTGACGTtAA	TCTGAAAATT	GAAGATGcTT
Consensus	*****	*****	*****-*	*****	*****-*
msa238454.2{401_A909}	CCTATACCGC	gTTCATTGGG	CACACAGGTT	CTGGAAAATC	AACTATTATG
msa238454.2{401_H36B}	CCTATACCGC	gTTCATTGGG	CACACAGGTT	CTGGAAAATC	AACTATTATG
msa238454.2{401_090}	CCTATACCGC	gTTCATTGGG	CACACAGGTT	CTGGAAAATC	AACTATTATG
msa238454.2{401_1169NT}	CCTATACCGC	gTTCATTGGG	CACACAGGTT	CTGGAAAATC	AACTATTATG
msa238454.2{401_18RS21}	CCTATACCGC	gTTCATTGGG	CACACAGGTT	CTGGAAAATC	AACTATTATG
msa238454.2{401_2603}	CCTATACCGC	gTTCATTGGG	CACACAGGTT	CTGGAAAATC	AACTATTATG
msa238454.2{401_CJB110}	CCTATACCGC	gTTCATTGGG	CACACAGGTT	CTGGAAAATC	AACTATTATG
msa238454.2{401_COH1}	CCTATACCGC	gTTCATTGGG	CACACAGGTT	CTGGAAAATC	AACTATTATG
msa238454.2{401_M732}	CCTATACCGC	gTTCATTGGG	CACACAGGTT	CTGGAAAATC	AACTATTATG
msa238454.2{401_M781}	CCTATACCGC	gTTCATTGGG	CACACAGGTT	CTGGAAAATC	AACTATTATG
msa238454.2{401_JM9130013}	CCTATACCGC	aTTCATTGGG	CACACAGGTT	CTGGAAAATC	AACTATTATG
Consensus	*****	*****	*****	*****	*****
msa238454.2{401_A909}	CAACTTTTGA	ATGGTTTACA	TATTCCTACA	AAAGGTGAGG	TAATTGTCGA
msa238454.2{401_H36B}	CAACTTTTGA	ATGGTTTACA	TATTCCTACA	AAAGGTGAGG	TAATTGTCGA
msa238454.2{401_090}	CAACTTTTGA	ATGGTTTACA	TATTCCTACA	AAAGGTGAGG	TAATTGTCGA
msa238454.2{401_1169NT}	CAACTTTTGA	ATGGTTTACA	TATTCCTACA	AAAGGTGAGG	TAATTGTCGA
msa238454.2{401_18RS21}	CAACTTTTGA	ATGGTTTACA	TATTCCTACA	AAAGGTGAGG	TAATTGTCGA
msa238454.2{401_2603}	CAACTTTTGA	ATGGTTTACA	TATTCCTACA	AAAGGTGAGG	TAATTGTCGA
msa238454.2{401_CJB110}	CAACTTTTGA	ATGGTTTACA	TATTCCTACA	AAAGGTGAGG	TAATTGTCGA
msa238454.2{401_COH1}	CAACTTTTGA	ATGGTTTACA	TATTCCTACA	AAAGGTGAGG	TAATTGTCGA
msa238454.2{401_M732}	CAACTTTTGA	ATGGTTTACA	TATTCCTACA	AAAGGTGAGG	TAATTGTCGA
msa238454.2{401_M781}	CAACTTTTGA	ATGGTTTACA	TATTCCTACA	AAAGGTGAGG	TAATTGTCGA
msa238454.2{401_JM9130013}	CAACTTTTGA	ATGGTTTACA	TATTCCTACA	AAAGGTGAGG	TAATTGTCGA
Consensus	*****	*****	*****	*****	*****
msa238454.2{401_A909}	TGATTTTTCT	ATTAAAGCAG	GGGACAAGAA	CAAAGAAATC	AAATTTATAA
msa238454.2{401_H36B}	TGATTTTTCT	ATTAAAGCAG	GGGACAAGAA	CAAAGAAATC	AAATTTATAA
msa238454.2{401_090}	TGATTTTTCT	ATTAAAGCAG	GGGACAAGAA	CAAAGAAATC	AAATTTATAA
msa238454.2{401_1169NT}	TGATTTTTCT	ATTAAAGCAG	GGGACAAGAA	CAAAGAAATC	AAATTTATAA
msa238454.2{401_18RS21}	TGATTTTTCT	ATTAAAGCAG	GGGACAAGAA	CAAAGAAATC	AAATTTATAA
msa238454.2{401_2603}	TGATTTTTCT	ATTAAAGCAG	GGGACAAGAA	CAAAGAAATC	AAATTTATAA
msa238454.2{401_CJB110}	TGATTTTTCT	ATTAAAGCAG	GGGACAAGAA	CAAAGAAATC	AAATTTATAA
msa238454.2{401_COH1}	TGATTTTTCT	ATTAAAGCAG	GGGACAAGAA	CAAAGAAATC	AAATTTATAA
msa238454.2{401_M732}	TGATTTTTCT	ATTAAAGCAG	GGGACAAGAA	CAAAGAAATC	AAATTTATAA
msa238454.2{401_M781}	TGATTTTTCT	ATTAAAGCAG	GGGACAAGAA	CAAAGAAATC	AAATTTATAA
msa238454.2{401_JM9130013}	TGATTTTTCT	ATTAAAGCAG	GGGACAAGAA	CAAAGAAATC	AAATTTATAA
Consensus	*****	*****	*****	*****	*****
msa238454.2{401_A909}	GGCAAAAAGT	TGGTTTAGTT	TTTCAATTTT	CAGAAAGTCA	GCTTTTTGAA
msa238454.2{401_H36B}	GGCAAAAAGT	TGGTTTAGTT	TTTCAATTTT	CAGAAAGTCA	GCTTTTTGAA
msa238454.2{401_090}	GGCAAAAAGT	TGGTTTAGTT	TTTCAATTTT	CAGAAAGTCA	GCTTTTTGAA
msa238454.2{401_1169NT}	GGCAAAAAGT	TGGTTTAGTT	TTTCAATTTT	CAGAAAGTCA	GCTTTTTGAA
msa238454.2{401_18RS21}	GGCAAAAAGT	TGGTTTAGTT	TTTCAATTTT	CAGAAAGTCA	GCTTTTTGAA
msa238454.2{401_2603}	GGCAAAAAGT	TGGTTTAGTT	TTTCAATTTT	CAGAAAGTCA	GCTTTTTGAA
msa238454.2{401_CJB110}	GGCAAAAAGT	TGGTTTAGTT	TTTCAATTTT	CAGAAAGTCA	GCTTTTTGAA
msa238454.2{401_COH1}	GGCAAAAAGT	TGGTTTAGTT	TTTCAATTTT	CAGAAAGTCA	GCTTTTTGAA
msa238454.2{401_M732}	GGCAAAAAGT	TGGTTTAGTT	TTTCAATTTT	CAGAAAGTCA	GCTTTTTGAA
msa238454.2{401_M781}	GGCAAAAAGT	TGGTTTAGTT	TTTCAATTTT	CAGAAAGTCA	GCTTTTTGAA
msa238454.2{401_JM9130013}	GGCAAAAAGT	TGGTTTAGTT	TTTCAATTTT	CAGAAAGTCA	GCTTTTTGAA
Consensus	*****	*****	*****	*****	*****
msa238454.2{401_A909}	GAGACAGTTT	TAAAGGATGT	TGCTTTTGGA	CCACAAAATT	TTGGTATTTT
msa238454.2{401_H36B}	GAGACAGTTT	TAAAGGATGT	TGCTTTTGGA	CCACAAAATT	TTGGTATTTT
msa238454.2{401_090}	GAGACAGTTT	TAAAGGATGT	TGCTTTTGGA	CCACAAAATT	TTGGTATTTT
msa238454.2{401_1169NT}	GAGACAGTTT	TAAAGGATGT	TGCTTTTGGA	CCACAAAATT	TTGGTATTTT
msa238454.2{401_18RS21}	GAGACAGTTT	TAAAGGATGT	TGCTTTTGGA	CCACAAAATT	TTGGTATTTT
msa238454.2{401_2603}	GAGACAGTTT	TAAAGGATGT	TGCTTTTGGA	CCACAAAATT	TTGGTATTTT
msa238454.2{401_CJB110}	GAGACAGTTT	TAAAGGATGT	TGCTTTTGGA	CCACAAAATT	TTGGTATTTT
msa238454.2{401_COH1}	GAGACAGTTT	TAAAGGATGT	TGCTTTTGGA	CCACAAAATT	TTGGTATTTT
msa238454.2{401_M732}	GAGACAGTTT	TAAAGGATGT	TGCTTTTGGA	CCACAAAATT	TTGGTATTTT
msa238454.2{401_M781}	GAGACAGTTT	TAAAGGATGT	TGCTTTTGGA	CCACAAAATT	TTGGTATTTT
msa238454.2{401_JM9130013}	GAGACAGTTT	TAAAGGATGT	TGCTTTTGGA	CCACAAAATT	TTGGTATTTT
Consensus	*****	*****	*****	*****	*****
msa238454.2{401_A909}	TCAGATTGAA	GCTGAAAGGC	TGGCTGAAGA	AAAATTAAGG	TTAGTTGGTA
msa238454.2{401_H36B}	TCAGATTGAA	GCTGAAAGGC	TGGCTGAAGA	AAAATTAAGG	TTAGTTGGTA
msa238454.2{401_090}	TCAGATTGAA	GCTGAAAGGC	TGGCTGAAGA	AAAATTAAGG	TTAGTTGGTA
msa238454.2{401_1169NT}	TCAGATTGAA	GCTGAAAGGC	TGGCTGAAGA	AAAATTAAGG	TTAGTTGGTA
msa238454.2{401_18RS21}	TCAGATTGAA	GCTGAAAGGC	TGGCTGAAGA	AAAATTAAGG	TTAGTTGGTA
msa238454.2{401_2603}	TCAGATTGAA	GCTGAAAGGC	TGGCTGAAGA	AAAATTAAGG	TTAGTTGGTA

Table 79: Comparative Sequences relating to SAG2150

msa238454.2{401_CJB110}	TCAGATTGAA	GCTGAAAGGC	TGGCTGAAGA	AAAATTAAGG	TTAGTTGGTA
msa238454.2{401_COH1}	TCAGATTGAA	GCTGAAAGGC	TGGCTGAAGA	AAAATTAAGG	TTAGTTGGTA
msa238454.2{401_M732}	TCAGATTGAA	GCTGAAAGGC	TGGCTGAAGA	AAAATTAAGG	TTAGTTGGTA
msa238454.2{401_M781}	TCAGATTGAA	GCTGAAAGGC	TGGCTGAAGA	AAAATTAAGG	TTAGTTGGTA
msa238454.2{401_JM9130013}	TCAGATTGAA	GCTGAAAGGC	TGGCTGAAGA	AAAATTAAGG	TTAGTTGGTA
Consensus	*****	*****	*****	*****	*****
401					
msa238454.2{401_A909}	TcAGTGAGGA	TTTATTCGAT	AAAAATCCAT	TTGAACTTTC	TGGAGGGCAG
msa238454.2{401_H36B}	TcAGTGAGGA	TTTATTCGAT	AAAAATCCAT	TTGAACTTTC	TGGAGGGCAG
msa238454.2{401_090}	TcAGTGAGGA	TTTATTCGAT	AAAAATCCAT	TTGAACTTTC	TGGAGGGCAG
msa238454.2{401_1169NT}	TcAGTGAGGA	TTTATTCGAT	AAAAATCCAT	TTGAACTTTC	TGGAGGGCAG
msa238454.2{401_18RS21}	TcAGTGAGGA	TTTATTCGAT	AAAAATCCAT	TTGAACTTTC	TGGAGGGCAG
msa238454.2{401_2603}	TcAGTGAGGA	TTTATTCGAT	AAAAATCCAT	TTGAACTTTC	TGGAGGGCAG
msa238454.2{401_CJB110}	TcAGTGAGGA	TTTATTCGAT	AAAAATCCAT	TTGAACTTTC	TGGAGGGCAG
msa238454.2{401_COH1}	TcAGTGAGGA	TTTATTCGAT	AAAAATCCAT	TTGAACTTTC	TGGAGGGCAG
msa238454.2{401_M732}	TcAGTGAGGA	TTTATTCGAT	AAAAATCCAT	TTGAACTTTC	TGGAGGGCAG
msa238454.2{401_M781}	TcAGTGAGGA	TTTATTCGAT	AAAAATCCAT	TTGAACTTTC	TGGAGGGCAG
msa238454.2{401_JM9130013}	TcAGTGAGGA	TTTATTCGAT	AAAAATCCAT	TTGAACTTTC	TGGAGGGCAG
Consensus	*_*_*_*_*_*_*_*	*****	*****	*****	*****
451					
msa238454.2{401_A909}	ATGAGGCGGG	TTGCTATAGC	TGGTATTTTA	GCGATGGAAC	CCAAAGTACT
msa238454.2{401_H36B}	ATGAGGCGGG	TTGCTATAGC	TGGTATTTTA	GCGATGGAAC	CCAAAGTACT
msa238454.2{401_090}	ATGAGGCGGG	TTGCTATAGC	TGGTATTTTA	GCGATGGAAC	CCAAAGTACT
msa238454.2{401_1169NT}	ATGAGGCGGG	TTGCTATAGC	TGGTATTTTA	GCGATGGAAC	CCAAAGTACT
msa238454.2{401_18RS21}	ATGAGGCGGG	TTGCTATAGC	TGGTATTTTA	GCGATGGAAC	CCAAAGTACT
msa238454.2{401_2603}	ATGAGGCGGG	TTGCTATAGC	TGGTATTTTA	GCGATGGAAC	CCAAAGTACT
msa238454.2{401_CJB110}	ATGAGGCGGG	TTGCTATAGC	TGGTATTTTA	GCGATGGAAC	CCAAAGTACT
msa238454.2{401_COH1}	ATGAGGCGGG	TTGCTATAGC	TGGTATTTTA	GCGATGGAAC	CCAAAGTACT
msa238454.2{401_M732}	ATGAGGCGGG	TTGCTATAGC	TGGTATTTTA	GCGATGGAAC	CCAAAGTACT
msa238454.2{401_M781}	ATGAGGCGGG	TTGCTATAGC	TGGTATTTTA	GCGATGGAAC	CCAAAGTACT
msa238454.2{401_JM9130013}	ATGAGGCGGG	TTGCTATAGC	TGGTATTTTA	GCGATGGAAC	CCAAAGTACT
Consensus	*****	*****	*****	*****	*****
501					
msa238454.2{401_A909}	AGTACTgAT	GAGCCAACAG	CTGGACTTGA	TCCTAAGGGA	AGAAAAGAAT
msa238454.2{401_H36B}	AGTACTgAT	GAGCCAACAG	CTGGACTTGA	TCCTAAGGGA	AGAAAAGAAT
msa238454.2{401_090}	AGTACTgAT	GAGCCAACAG	CTGGACTTGA	TCCTAAGGGA	AGAAAAGAAT
msa238454.2{401_1169NT}	AGTACTgAT	GAGCCAACAG	CTGGACTTGA	TCCTAAGGGA	AGAAAAGAAT
msa238454.2{401_18RS21}	AGTACTgAT	GAGCCAACAG	CTGGACTTGA	TCCTAAGGGA	AGAAAAGAAT
msa238454.2{401_2603}	AGTACTgAT	GAGCCAACAG	CTGGACTTGA	TCCTAAGGGA	AGAAAAGAAT
msa238454.2{401_CJB110}	AGTACTgAT	GAGCCAACAG	CTGGACTTGA	TCCTAAGGGA	AGAAAAGAAT
msa238454.2{401_COH1}	AGTACTgAT	GAGCCAACAG	CTGGACTTGA	TCCTAAGGGA	AGAAAAGAAT
msa238454.2{401_M732}	AGTACTgAT	GAGCCAACAG	CTGGACTTGA	TCCTAAGGGA	AGAAAAGAAT
msa238454.2{401_M781}	AGTACTgAT	GAGCCAACAG	CTGGACTTGA	TCCTAAGGGA	AGAAAAGAAT
msa238454.2{401_JM9130013}	AGTACTgAT	GAGCCAACAG	CTGGACTTGA	TCCTAAGGGA	AGAAAAGAAT
Consensus	*****_***	*****	*****	*****	*****
551					
msa238454.2{401_A909}	TAATGACTCT	TTTTAAAAAT	CTTCATAAAA	AAGGAATGAC	TATCGTCTTA
msa238454.2{401_H36B}	TAATGACTCT	TTTTAAAAAT	CTTCATAAAA	AAGGAATGAC	TATCGTCTTA
msa238454.2{401_090}	TAATGACTCT	TTTTAAAAAT	CTTCATAAAA	AAGGAATGAC	TATCGTCTTA
msa238454.2{401_1169NT}	TAATGACTCT	TTTTAAAAAT	CTTCATAAAA	AAGGAATGAC	TATCGTCTTA
msa238454.2{401_18RS21}	TAATGACTCT	TTTTAAAAAT	CTTCATAAAA	AAGGAATGAC	TATCGTCTTA
msa238454.2{401_2603}	TAATGACTCT	TTTTAAAAAT	CTTCATAAAA	AAGGAATGAC	TATCGTCTTA
msa238454.2{401_CJB110}	TAATGACTCT	TTTTAAAAAT	CTTCATAAAA	AAGGAATGAC	TATCGTCTTA
msa238454.2{401_COH1}	TAATGACTCT	TTTTAAAAAT	CTTCATAAAA	AAGGAATGAC	TATCGTCTTA
msa238454.2{401_M732}	TAATGACTCT	TTTTAAAAAT	CTTCATAAAA	AAGGAATGAC	TATCGTCTTA
msa238454.2{401_M781}	TAATGACTCT	TTTTAAAAAT	CTTCATAAAA	AAGGAATGAC	TATCGTCTTA
msa238454.2{401_JM9130013}	TAATGACTCT	TTTTAAAAAT	CTTCATAAAA	AAGGAATGAC	TATCGTCTTA
Consensus	*****	*****	*****	*****	*****
601					
msa238454.2{401_A909}	GTGACTCACT	TAATGGACGA	TGTAGCGGAT	TATGCTGACT	ATGTGTATGT
msa238454.2{401_H36B}	GTGACTCACT	TAATGGACGA	TGTAGCGGAT	TATGCTGACT	ATGTGTATGT
msa238454.2{401_090}	GTGACTCACT	TAATGGACGA	TGTAGCGGAT	TATGCTGACT	ATGTGTATGT
msa238454.2{401_1169NT}	GTGACTCACT	TAATGGACGA	TGTAGCGGAT	TATGCTGACT	ATGTGTATGT
msa238454.2{401_18RS21}	GTGACTCACT	TAATGGACGA	TGTAGCGGAT	TATGCTGACT	ATGTGTATGT
msa238454.2{401_2603}	GTGACTCACT	TAATGGACGA	TGTAGCGGAT	TATGCTGACT	ATGTGTATGT
msa238454.2{401_CJB110}	GTGACTCACT	TAATGGACGA	TGTAGCGGAT	TATGCTGACT	ATGTGTATGT
msa238454.2{401_COH1}	GTGACTCACT	TAATGGACGA	TGTAGCGGAT	TATGCTGACT	ATGTGTATGT
msa238454.2{401_M732}	GTGACTCACT	TAATGGACGA	TGTAGCGGAT	TATGCTGACT	ATGTGTATGT
msa238454.2{401_M781}	GTGACTCACT	TAATGGACGA	TGTAGCGGAT	TATGCTGACT	ATGTGTATGT
msa238454.2{401_JM9130013}	GTGACTCACT	TAATGGACGA	TGTAGCGGAT	TATGCTGACT	ATGTGTATGT
Consensus	*****	*****	*****	*****	*****
651					
msa238454.2{401_A909}	TTTAGAAGCA	GGGAAAGTAA	CCTTATCAGG	ACAACCAAa	CAGATTTTTC
msa238454.2{401_H36B}	TTTAGAAGCA	GGGAAAGTAA	CCTTATCAGG	ACAACCAAa	CAGATTTTTC
msa238454.2{401_090}	TTTAGAAGCA	GGGAAAGTAA	CCTTATCAGG	ACAACCAAa	CAGATTTTTC
msa238454.2{401_1169NT}	TTTAGAAGCA	GGGAAAGTAA	CCTTATCAGG	ACAACCAAa	CAGATTTTTC
msa238454.2{401_18RS21}	TTTAGAAGCA	GGGAAAGTAA	CCTTATCAGG	ACAACCAAa	CAGATTTTTC

Table 79: Comparative Sequences relating to SAG2150

msa238454.2{401_2603}	TTTAGAAGCA	GGGAAAGTAA	CCTTATCAGG	ACAACCAAAa	CAGATTTTTC
msa238454.2{401_CJB110}	TTTAGAAGCA	GGGAAAGTAA	CCTTATCAGG	ACAACCAAAa	CAGATTTTTC
msa238454.2{401_COH1}	TTTAGAAGCA	GGGAAAGTAA	CCTTATCAGG	ACAACCAAAa	CAGATTTTTC
msa238454.2{401_M732}	TTTAGAAGCA	GGGAAAGTAA	CCTTATCAGG	ACAACCAAAa	CAGATTTTTC
msa238454.2{401_M781}	TTTAGAAGCA	GGGAAAGTAA	CCTTATCAGG	ACAACCAAAa	CAGATTTTTC
msa238454.2{401_JM9130013}	TTTAGAAGCA	GGGAAAGTAA	CCTTATCAGG	ACAACCAAAa	CAGATTTTTC
Consensus	*****	*****	*****	*****	*****
701					
msa238454.2{401_A909}	AAGAAGTAGA	ACTTTTAGAA	AGTAAACAAT	TAGGAGTTCC	CAAAATCACC
msa238454.2{401_H36B}	AAGAAGTAGA	ACTTTTAGAA	AGTAAACAAT	TAGGAGTTCC	CAAAATCACC
msa238454.2{401_090}	AAGAAGTAGA	ACTTTTAGAA	AGTAAACAAT	TAGGAGTTCC	CAAAATCACC
msa238454.2{401_1169NT}	AAGAAGTAGA	ACTTTTAGAA	AGTAAACAAT	TAGGAGTTCC	CAAAATCACC
msa238454.2{401_18RS21}	AAGAAGTAGA	ACTTTTAGAA	AGTAAACAAT	TAGGAGTTCC	CAAAATCACC
msa238454.2{401_2603}	AAGAAGTAGA	ACTTTTAGAA	AGTAAACAAT	TAGGAGTTCC	CAAAATCACC
msa238454.2{401_CJB110}	AAGAAGTAGA	ACTTTTAGAA	AGTAAACAAT	TAGGAGTTCC	CAAAATCACC
msa238454.2{401_COH1}	AAGAAGTAGA	ACTTTTAGAA	AGTAAACAAT	TAGGAGTTCC	CAAAATCACC
msa238454.2{401_M732}	AAGAAGTAGA	ACTTTTAGAA	AGTAAACAAT	TAGGAGTTCC	CAAAATCACC
msa238454.2{401_M781}	AAGAAGTAGA	ACTTTTAGAA	AGTAAACAAT	TAGGAGTTCC	CAAAATCACC
msa238454.2{401_JM9130013}	AAGAAGTAGA	ACTTTTAGAA	AGTAAACAAT	TAGGAGTTCC	CAAAATCACC
Consensus	*****	*****	*****	*****	*****
751					
msa238454.2{401_A909}	AAGTTTGCTC	AAAGgCTATC	TCATAAGGGA	TTAAATTTAC	CTAGTTTACC
msa238454.2{401_H36B}	AAGTTTGCTC	AAAGgCTATC	TCATAAGGGA	TTAAATTTAC	CTAGTTTACC
msa238454.2{401_090}	AAGTTTGCTC	AAAGaCTATC	TCATAAGGGA	TTAAATTTAC	CTAGTTTACC
msa238454.2{401_1169NT}	AAGTTTGCTC	AAAGaCTATC	TCATAAGGGA	TTAAATTTAC	CTAGTTTACC
msa238454.2{401_18RS21}	AAGTTTGCTC	AAAGaCTATC	TCATAAGGGA	TTAAATTTAC	CTAGTTTACC
msa238454.2{401_2603}	AAGTTTGCTC	AAAGaCTATC	TCATAAGGGA	TTAAATTTAC	CTAGTTTACC
msa238454.2{401_CJB110}	AAGTTTGCTC	AAAGaCTATC	TCATAAGGGA	TTAAATTTAC	CTAGTTTACC
msa238454.2{401_COH1}	AAGTTTGCTC	AAAGaCTATC	TCATAAGGGA	TTAAATTTAC	CTAGTTTACC
msa238454.2{401_M732}	AAGTTTGCTC	AAAGaCTATC	TCATAAGGGA	TTAAATTTAC	CTAGTTTACC
msa238454.2{401_M781}	AAGTTTGCTC	AAAGaCTATC	TCATAAGGGA	TTAAATTTAC	CTAGTTTACC
msa238454.2{401_JM9130013}	AAGTTTGCTC	AAAGaCTATC	TCATAAGGGA	TTAAATTTAC	CTAGTTTACC
Consensus	*****	*****	*****	*****	*****
801					
msa238454.2{401_A909}	AATTACTATT	AACGAATTTG	TGGAGGCTAT	TAAGCATGGA	
msa238454.2{401_H36B}	AATTACTATT	AACGAATTTG	TGGAGGCTAT	TAAGCATGGA	
msa238454.2{401_090}	AATTACTATT	AACGAATTTG	TGGAGGCTAT	TAAGCATGGA	
msa238454.2{401_1169NT}	AATTACTATT	AACGAATTTG	TGGAGGCTAT	TAAGCATGGA	
msa238454.2{401_18RS21}	AATTACTATT	AACGAATTTG	TGGAGGCTAT	TAAGCATGGA	
msa238454.2{401_2603}	AATTACTATT	AACGAATTTG	TGGAGGCTAT	TAAGCATGGA	
msa238454.2{401_CJB110}	AATTACTATT	AACGAATTTG	TGGAGGCTAT	TAAGCATGGA	
msa238454.2{401_COH1}	AATTACTATT	AACGAATTTG	TGGAGGCTAT	TAAGCATGGA	
msa238454.2{401_M732}	AATTACTATT	AACGAATTTG	TGGAGGCTAT	TAAGCATGGA	
msa238454.2{401_M781}	AATTACTATT	AACGAATTTG	TGGAGGCTAT	TAAGCATGGA	
msa238454.2{401_JM9130013}	AATTACTATT	AACGAATTTG	TGGAGGCTAT	TAAGCATGGA	
Consensus	*****	*****	*****	*****	
840					

SEQ ID NO. 7912

STRAIN 2603 frame: 1

MGIEFKNVSYTYQAGTPFEGRALFDVNLKIEDASYTAFIGHTGSGKSTIMQLLNLHIPTK
 GEVIVDDFSIKAGDKNKEIKFIRQKVGLVFQFPESQLFEETVLKDVAFGPQNFQISQIEA
 ERLAEKLRVLVGI SEDLFDKNPFELSGGQMRRAIAGILAMEPKVLVLDEPTAGLDPKGR
 KELMTLFLKLNHKKGMTIVLVTHLMDDVADYADYVYVLEAGKVTL SGQPKQIFQEV LLES
 KQLGVPKITKFAQRLSHKGLNLPSLPITINEFVEAIKHG

SEQ ID NO. 7913

STRAIN 090 frame: 1

GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDASYTAFIGHTGSGKSTIMQLLNLHIPTK
 GEVIVDDFSIKAGDKNKEIKFIRQKVGLVFQFPESQLFEETVLKDVAFGPQNFQISQIEA
 ERLAEKLRVLVGI SEDLFDKNPFELSGGQMRRAIAGILAMEPKVLVLDEPTAGLDPKGR
 KELMTLFLKLNHKKGMTIVLVTHLMDDVADYADYVYVLEAGKVTL SGQPKQIFQEV LLES
 KQLGVPKITKFAQRLSHKGLNLPSLPITINEFVEAIKHG

SEQ ID NO. 7914

STRAIN 090 frame: 1

GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDASYTAFIGHTGSGKSTIMQLLNLHIPTK
 GEVIVDDFSIKAGDKNKEIKFIRQKVGLVFQFPESQLFEETVLKDVAFGPQNFQISQIEA
 ERLAEKLRVLVGI SEDLFDKNPFELSGGQMRRAIAGILAMEPKVLVLDEPTAGLDPKGR
 KELMTLFLKLNHKKGMTIVLVTHLMDDVADYADYVYVLEAGKVTL SGQPKQIFQEV LLES
 KQLGVPKITKFAQRLSHKGLNLPSLPITINEFVEAIKHG

SEQ ID NO. 7915

STRAIN H36B frame: 1

GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDASYTAFIGHTGSGKSTIMQLLNLHIPTK
 GEVIVDDFSIKAGDKNKEIKFIRQKVGLVFQFPESQLFEETVLKDVAFGPQNFQISQIEA
 ERLAEKLRVLVGI SEDLFDKNPFELSGGQMRRAIAGILAMEPKVLVLDEPTAGLDPKGR
 KELMTLFLKLNHKKGMTIVLVTHLMDDVADYADYVYVLEAGKVTL SGQPKQIFQEV LLES
 KQLGVPKITKFAQRLSHKGLNLPSLPITINEFVEAIKHG

SEQ ID NO. 7916

Table 79: Comparative Sequences relating to SAG2150

STRAIN 18RS21 frame: 1

GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDASYTAFIGHTGSGKSTIMQLLNGLHIPTK
 GEVIVDDFSIKAGDKNKEIKFIRQKVGLVFQFPESQLFEETVLKDVAFGPQNFQISQIEA
 ERLAEEKLRLVIGISEDLEFDKNPFELSGGQMRRVAIAGILAMEPKVLVLDEPTAGLDPKGR
 KELMTLFFKNLHKKGMTIVLVTHLMDDVADYADYVYVLEAGKVTLSGQPKQIFQEVVELLES
 KQLGVPKITKFAQRLSHKGLNLPSPITINEFVEAIKHG

SEQ ID NO. 7917

STRAIN M732 frame: 1

GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDVSYTAFIGHTGSGKSTIMQLLNGLHIPTK
 GEVIVDDFSIKAGDKNKEIKFIRQKVGLVFQFPESQLFEETVLKDVAFGPQNFQISQIEA
 ERLAEEKLRLVIGISEDLEFDKNPFELSGGQMRRVAIAGILAMEPKVLVLDEPTAGLDPKGR
 KELMTLFFKNLHKKGMTIVLVTHLMDDVADYADYVYVLEAGKVTLSGQPKQIFQEVVELLES
 KQLGVPKITKFAQRLSHKGLNLPSPITINEFVEAIKHG

SEQ ID NO. 7918

STRAIN COH1 frame: 1

GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDVSYTAFIGHTGSGKSTIMQLLNGLHIPTK
 GEVIVDDFSIKAGDKNKEIKFIRQKVGLVFQFPESQLFEETVLKDVAFGPQNFQISQIEA
 ERLAEEKLRLVIGISEDLEFDKNPFELSGGQMRRVAIAGILAMEPKVLVLDEPTAGLDPKGR
 KELMTLFFKNLHKKGMTIVLVTHLMDDVADYADYVYVLEAGKVTLSGQPKQIFQEVVELLES
 KQLGVPKITKFAQRLSHKGLNLPSPITINEFVEAIKHG

SEQ ID NO. 7919

STRAIN M781 frame: 1

GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDVSYTAFIGHTGSGKSTIMQLLNGLHIPTK
 GEVIVDDFSIKAGDKNKEIKFIRQKVGLVFQFPESQLFEETVLKDVAFGPQNFQISQIEA
 ERLAEEKLRLVIGISEDLEFDKNPFELSGGQMRRVAIAGILAMEPKVLVLDEPTAGLDPKGR
 KELMTLFFKNLHKKGMTIVLVTHLMDDVADYADYVYVLEAGKVTLSGQPKQIFQEVVELLES
 KQLGVPKITKFAQRLSHKGLNLPSPITINEFVEAIKHG

SEQ ID NO. 7920

STRAIN CJB110 frame: 1

GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDASYTAFIGHTGSGKSTIMQLLNGLHIPTK
 GEVIVDDFSIKAGDKNKEIKFIRQKVGLVFQFPESQLFEETVLKDVAFGPQNFQISQIEA
 ERLAEEKLRLVIGISEDLEFDKNPFELSGGQMRRVAIAGILAMEPKVLVLDEPTAGLDPKGR
 KELMTLFFKNLHKKGMTIVLVTHLMDDVADYADYVYVLEAGKVTLSGQPKQIFQEVVELLES
 KQLGVPKITKFAQRLSHKGLNLPSPITINEFVEAIKHG

SEQ ID NO. 7921

STRAIN 1169NT frame: 1

GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDASYTAFIGHTGSGKSTIMQLLNGLHIPTK
 GEVIVDDFSIKAGDKNKEIKFIRQKVGLVFQFPESQLFEETVLKDVAFGPQNFQISQIEA
 ERLAEEKLRLVIGISEDLEFDKNPFELSGGQMRRVAIAGILAMEPKVLVLDEPTAGLDPKGR
 KELMTLFFKNLHKKGMTIVLVTHLMDDVADYADYVYVLEAGKVTLSGQPKQIFQEVVELLES
 KQLGVPKITKFAQRLSHKGLNLPSPITINEFVEAIKHG

SEQ ID NO. 7922

STRAIN JM9130013 frame: 1

GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDASYTAFIGHTGSGKSTIMQLLNGLHIPTK
 GEVIVDDFSIKAGDKNKEIKFIRQKVGLVFQFPESQLFEETVLKDVAFGPQNFQISQIEA
 ERLAEEKLRLVIGISEDLEFDKNPFELSGGQMRRVAIAGILAMEPKVLVLDEPTAGLDPKGR
 KELMTLFFKNLHKKGMTIVLVTHLMDDVADYADYVYVLEAGKVTLSGQPKQIFQEVVELLES
 KQLGVPKITKFAQRLSHKGLNLPSPITINEFVEAIKHG

PRETTY of: /biotmp/msa238553.2(*) May 14, 2003 06:55 ..

	1		50
msa238553.2{401_090}	~GIEFKNVSY	TYQAGTPFEG	RALFDVNLKI
msa238553.2{401_1169NT}	~GIEFKNVSY	TYQAGTPFEG	RALFDVNLKI
msa238553.2{401_18RS21}	~GIEFKNVSY	TYQAGTPFEG	RALFDVNLKI
msa238553.2{401_2603}	mGIEFKNVSY	TYQAGTPFEG	RALFDVNLKI
msa238553.2{401_CJB110}	~GIEFKNVSY	TYQAGTPFEG	RALFDVNLKI
msa238553.2{401_H36B}	~GIEFKNVSY	TYQAGTPFEG	RALFDVNLKI
msa238553.2{401_JM9130013}	~GIEFKNVSY	TYQAGTPFEG	RALFDVNLKI
msa238553.2{401_COH1}	~GIEFKNVSY	TYQAGTPFEG	RALFDVNLKI
msa238553.2{401_M732}	~GIEFKNVSY	TYQAGTPFEG	RALFDVNLKI
msa238553.2{401_M781}	~GIEFKNVSY	TYQAGTPFEG	RALFDVNLKI
Consensus	*****	*****	*****
	51		100
msa238553.2{401_090}	QLLNGLHIPT	KGEVIVDDFS	IKAGDKNKEI
msa238553.2{401_1169NT}	QLLNGLHIPT	KGEVIVDDFS	IKAGDKNKEI
msa238553.2{401_18RS21}	QLLNGLHIPT	KGEVIVDDFS	IKAGDKNKEI
msa238553.2{401_2603}	QLLNGLHIPT	KGEVIVDDFS	IKAGDKNKEI
msa238553.2{401_CJB110}	QLLNGLHIPT	KGEVIVDDFS	IKAGDKNKEI
msa238553.2{401_H36B}	QLLNGLHIPT	KGEVIVDDFS	IKAGDKNKEI
msa238553.2{401_JM9130013}	QLLNGLHIPT	KGEVIVDDFS	IKAGDKNKEI
msa238553.2{401_COH1}	QLLNGLHIPT	KGEVIVDDFS	IKAGDKNKEI
msa238553.2{401_M732}	QLLNGLHIPT	KGEVIVDDFS	IKAGDKNKEI
msa238553.2{401_M781}	QLLNGLHIPT	KGEVIVDDFS	IKAGDKNKEI

Table 79: Comparative Sequences relating to SAG2150

Consensus	*****	*****	*****	*****	*****
	101				150
msa238553.2{401_090}	ETVLKDVAFG	PQNFGISQIE	AERLAEEKLR	LVGISED LFD	KNPFELSGGQ
msa238553.2{401_1169NT}	ETVLKDVAFG	PQNFGISQIE	AERLAEEKLR	LVGISED LFD	KNPFELSGGQ
msa238553.2{401_18RS21}	ETVLKDVAFG	PQNFGISQIE	AERLAEEKLR	LVGISED LFD	KNPFELSGGQ
msa238553.2{401_2603}	ETVLKDVAFG	PQNFGISQIE	AERLAEEKLR	LVGISED LFD	KNPFELSGGQ
msa238553.2{401_CJB110}	ETVLKDVAFG	PQNFGISQIE	AERLAEEKLR	LVGISED LFD	KNPFELSGGQ
msa238553.2{401_H36B}	ETVLKDVAFG	PQNFGISQIE	AERLAEEKLR	LVGISED LFD	KNPFELSGGQ
msa238553.2{401_JM9130013}	ETVLKDVAFG	PQNFGISQIE	AERLAEEKLR	LVGISED LFD	KNPFELSGGQ
msa238553.2{401_COH1}	ETVLKDVAFG	PQNFGISQIE	AERLAEEKLR	LVGISED LFD	KNPFELSGGQ
msa238553.2{401_M732}	ETVLKDVAFG	PQNFGISQIE	AERLAEEKLR	LVGISED LFD	KNPFELSGGQ
msa238553.2{401_M781}	ETVLKDVAFG	PQNFGISQIE	AERLAEEKLR	LVGISED LFD	KNPFELSGGQ
Consensus	*****	*****	*****	*****	*****
	151				200
msa238553.2{401_090}	MRRVAIAGIL	AMEPKVLVLD	EPTAGLDPKG	RKELMTLFKN	LHKKGMTIVL
msa238553.2{401_1169NT}	MRRVAIAGIL	AMEPKVLVLD	EPTAGLDPKG	RKELMTLFKN	LHKKGMTIVL
msa238553.2{401_18RS21}	MRRVAIAGIL	AMEPKVLVLD	EPTAGLDPKG	RKELMTLFKN	LHKKGMTIVL
msa238553.2{401_2603}	MRRVAIAGIL	AMEPKVLVLD	EPTAGLDPKG	RKELMTLFKN	LHKKGMTIVL
msa238553.2{401_CJB110}	MRRVAIAGIL	AMEPKVLVLD	EPTAGLDPKG	RKELMTLFKN	LHKKGMTIVL
msa238553.2{401_H36B}	MRRVAIAGIL	AMEPKVLVLD	EPTAGLDPKG	RKELMTLFKN	LHKKGMTIVL
msa238553.2{401_JM9130013}	MRRVAIAGIL	AMEPKVLVLD	EPTAGLDPKG	RKELMTLFKN	LHKKGMTIVL
msa238553.2{401_COH1}	MRRVAIAGIL	AMEPKVLVLD	EPTAGLDPKG	RKELMTLFKN	LHKKGMTIVL
msa238553.2{401_M732}	MRRVAIAGIL	AMEPKVLVLD	EPTAGLDPKG	RKELMTLFKN	LHKKGMTIVL
msa238553.2{401_M781}	MRRVAIAGIL	AMEPKVLVLD	EPTAGLDPKG	RKELMTLFKN	LHKKGMTIVL
Consensus	*****	*****	*****	*****	*****
	201				250
msa238553.2{401_090}	VTHLMDDVAD	YADYVYVLEA	GKVTLSGQPK	QIFQEV ELL E	SKQLGV PKIT
msa238553.2{401_1169NT}	VTHLMDDVAD	YADYVYVLEA	GKVTLSGQPK	QIFQEV ELL E	SKQLGV PKIT
msa238553.2{401_18RS21}	VTHLMDDVAD	YADYVYVLEA	GKVTLSGQPK	QIFQEV ELL E	SKQLGV PKIT
msa238553.2{401_2603}	VTHLMDDVAD	YADYVYVLEA	GKVTLSGQPK	QIFQEV ELL E	SKQLGV PKIT
msa238553.2{401_CJB110}	VTHLMDDVAD	YADYVYVLEA	GKVTLSGQPK	QIFQEV ELL E	SKQLGV PKIT
msa238553.2{401_H36B}	VTHLMDDVAD	YADYVYVLEA	GKVTLSGQPK	QIFQEV ELL E	SKQLGV PKIT
msa238553.2{401_JM9130013}	VTHLMDDVAD	YADYVYVLEA	GKVTLSGQPK	QIFQEV ELL E	SKQLGV PKIT
msa238553.2{401_COH1}	VTHLMDDVAD	YADYVYVLEA	GKVTLSGQPK	QIFQEV ELL E	SKQLGV PKIT
msa238553.2{401_M732}	VTHLMDDVAD	YADYVYVLEA	GKVTLSGQPK	QIFQEV ELL E	SKQLGV PKIT
msa238553.2{401_M781}	VTHLMDDVAD	YADYVYVLEA	GKVTLSGQPK	QIFQEV ELL E	SKQLGV PKIT
Consensus	*****	*****	*****	*****	*****
	251				280
msa238553.2{401_090}	KFAQRLSHKG	LNLPSLPITI	NEFVEAIKHG		
msa238553.2{401_1169NT}	KFAQRLSHKG	LNLPSLPITI	NEFVEAIKHG		
msa238553.2{401_18RS21}	KFAQRLSHKG	LNLPSLPITI	NEFVEAIKHG		
msa238553.2{401_2603}	KFAQRLSHKG	LNLPSLPITI	NEFVEAIKHG		
msa238553.2{401_CJB110}	KFAQRLSHKG	LNLPSLPITI	NEFVEAIKHG		
msa238553.2{401_H36B}	KFAQRLSHKG	LNLPSLPITI	NEFVEAIKHG		
msa238553.2{401_JM9130013}	KFAQRLSHKG	LNLPSLPITI	NEFVEAIKHG		
msa238553.2{401_COH1}	KFAQRLSHKG	LNLPSLPITI	NEFVEAIKHG		
msa238553.2{401_M732}	KFAQRLSHKG	LNLPSLPITI	NEFVEAIKHG		
msa238553.2{401_M781}	KFAQRLSHKG	LNLPSLPITI	NEFVEAIKHG		
Consensus	*****	*****	*****		

Table 80: Comparative Sequences relating to SAG1266

SEQ ID NO. 8001

STRAIN 2603

GTGAACCACTTACTTAACCTCAGTAAAGAAAATATAGCTAAAATAGATTTTGACTTTCTT
 AATGAGGCACCTTAATGCAAATATTCGTTTGAAAGAATTAGTAGATGAACATAAAATTTCA
 AAAGAAGCTGGACAGTAAAGGTTGGTCCAAAAAAGACTCTCGAACGATAAAAAATCTTGATC
 GATGGCCTTATCAATAAACATATAGTTTCCCTAGATCGTGCAGATTATAACATTATCCAA
 GTCATTCCATTTGCTAATGTACATGTACTACTGTTTTTAATACCAGAAAGGGAGAATTCT
 AAAAATTATAGAATATACAACTACAGTGATTATGAAATGGAGTTAATCAATGAGGATAGG
 CAACAATTTTCAAATATGAAACAGTTGATTAGACCAATTGATACTTGTGATATTTTT
 AATATTGATGACTACATTTTCATCATATTTAACAATA

SEQ ID NO. 8002

STRAIN H36B

AACCACTTACTTAACCTCAGTAAAGAAAATATAGCT
 AAAATAGATTTTGACTTTCTTAATGAGGCACCTTAATGCAAATATTCGTTT
 GAAAGAATTAGTAGATGAACATAAAATTTCAAAGAAGCTGGACAGTAAAG
 GTTGGTCCAAAAAAGACTCTCGAACGATAAAAAATCTTGATCGATGGCCTT
 ATCAATAAACATATAGTTTCCCTAGATCGTGCAGATTATAACATTATCCAA
 AGTCATTCCATTTGCTAATGTACATGTACTACTGTTTTTAATACCAGAAA
 GGGAGAATTCTAAAAATTATAGAAATATACAACTACAGTGATTATGAAATG
 GAGTTAATCAATGAGGATAGGCAACAATTTTCAAATATGAAACAGTTGA
 TTTAGACCAATTGATACTTGTGATATTTTTTAATATTGATGACTACATTT
 CATCATATTTAACAATA

SEQ ID NO. 8003

STRAIN 18RS21

AACCACTTACTTAACCTCAGTAAAGAAAATATAG
 CTAAAATAGATTTTGACTTTCTTAATGAGGCACCTTAATGCAAATATTCGTT
 TTGAAAGAATTAGTAGATGAACATAAAATTTCAAAGAAGCTGGACAGTAA
 AGGTTGGTCCAAAAAAGACTCTCGAACGATAAAAAATCTTGATCGATGGCC
 TTATCAATAAACATATAGTTTCCCTAGATCGTGCAGATTATAACATTATC
 CAAGTCATTCCATTTGCTAATGTACATGTACTACTGTTTTTAATACCAGA
 AAGGGAGAATTCTAAAAATTATAGAAATATACAACTACAGTGATTATGAAA
 TGGAGTTAATCAATGAGGATAGGCAACAATTTTCAAATATGAAACAGTT
 GATTTAGACCAATTGATACTTGTGATATTTTTTAATATTGATGACTACAT
 TTCATCATATTTAACAATA

PRETTY of: /biotmp/msa49308.2{*} February 19, 2003 07:45 ..

	1		50
msa49308.2{408_18RS21}	---AACCACT TACTTAACCT CAGTAAAGAA AATATAGCTA AAATAGATTT		
msa49308.2{408_2603}	gtgAACCACT TACTTAACCT CAGTAAAGAA AATATAGCTA AAATAGATTT		
msa49308.2{408_H36B}	---AACCACT TACTTAACCT CAGTAAAGAA AATATAGCTA AAATAGATTT		
Consensus	*****	*****	*****
	51		100
msa49308.2{408_18RS21}	TGACTTTCTT AATGAGGCAC TTAATGCAAA TATTCGTTTG AAAGAATTAG		
msa49308.2{408_2603}	TGACTTTCTT AATGAGGCAC TTAATGCAAA TATTCGTTTG AAAGAATTAG		
msa49308.2{408_H36B}	TGACTTTCTT AATGAGGCAC TTAATGCAAA TATTCGTTTG AAAGAATTAG		
Consensus	*****	*****	*****
	101		150
msa49308.2{408_18RS21}	TAGATGAACT AAAAATTTCA AAAGAAGCTGG ACAGTAAAGG TTGGTCCAAA		
msa49308.2{408_2603}	TAGATGAACT AAAAATTTCA AAAGAAGCTGG ACAGTAAAGG TTGGTCCAAA		
msa49308.2{408_H36B}	TAGATGAACT AAAAATTTCA AAAGAAGCTGG ACAGTAAAGG TTGGTCCAAA		
Consensus	*****	*****	*****
	151		200
msa49308.2{408_18RS21}	AAAGACTCTC GAACGATAAA AATCTTGTAC GATGGCCTTA TCAATAAACA		
msa49308.2{408_2603}	AAAGACTCTC GAACGATAAA AATCTTGTAC GATGGCCTTA TCAATAAACA		
msa49308.2{408_H36B}	AAAGACTCTC GAACGATAAA AATCTTGTAC GATGGCCTTA TCAATAAACA		
Consensus	*****	*****	*****
	201		250
msa49308.2{408_18RS21}	TATAGTTTCC CTAGATCGTG CAGATTATAA CATTATCCAA GTCATTCCAT		
msa49308.2{408_2603}	TATAGTTTCC CTAGATCGTG CAGATTATAA CATTATCCAA GTCATTCCAT		
msa49308.2{408_H36B}	TATAGTTTCC CTAGATCGTG CAGATTATAA CATTATCCAA GTCATTCCAT		
Consensus	*****	*****	*****
	251		300
msa49308.2{408_18RS21}	TTGCTAATGT ACATGTACTA CTGTTTTTAA TACCAGAAAG GGAGAATTCT		
msa49308.2{408_2603}	TTGCTAATGT ACATGTACTA CTGTTTTTAA TACCAGAAAG GGAGAATTCT		
msa49308.2{408_H36B}	TTGCTAATGT ACATGTACTA CTGTTTTTAA TACCAGAAAG GGAGAATTCT		
Consensus	*****	*****	*****
	301		350
msa49308.2{408_18RS21}	AAAAATTATA GAATATACAA CTACAGTGAT TATGAAATGG AGTTAATCAA		
msa49308.2{408_2603}	AAAAATTATA GAATATACAA CTACAGTGAT TATGAAATGG AGTTAATCAA		
msa49308.2{408_H36B}	AAAAATTATA GAATATACAA CTACAGTGAT TATGAAATGG AGTTAATCAA		
Consensus	*****	*****	*****

Table 80: Comparative Sequences relating to SAG1266

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351                                     400
msa49308.2{408_18RS21} TGAGGATAGG CAACAATTTT CAAAATATGA AACAGTTGAT TTAGACCAAT
msa49308.2{408_2603} TGAGGATAGG CAACAATTTT CAAAATATGA AACAGTTGAT TTAGACCAAT
msa49308.2{408_H36B} TGAGGATAGG CAACAATTTT CAAAATATGA AACAGTTGAT TTAGACCAAT
Consensus *****

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401                                     450
msa49308.2{408_18RS21} TGATACTTGT TGATATTTT AATATTGATG ACTACATTTC ATCATATTTA
msa49308.2{408_2603} TGATACTTGT TGATATTTT AATATTGATG ACTACATTTC ATCATATTTA
msa49308.2{408_H36B} TGATACTTGT TGATATTTT AATATTGATG ACTACATTTC ATCATATTTA
Consensus *****

```

```

451
msa49308.2{408_18RS21} ACAATA
msa49308.2{408_2603} ACAATA
msa49308.2{408_H36B} ACAATA
Consensus *****

```

SEQ ID NO. 8004

STRAIN 2603 frame: 1

VNHLNLSKENIAKIDFDLNEALNANIRLKELVDELKISKELDSKGWSKKDSRTIKILY
DGLINKHIVSLDRADYNIQVIPFANVHVLFLIPERENSKNYRIYNYSYEMELINEDR
QQFSKYETVDLDQLILVDIFNIDDISSYLT

SEQ ID NO. 8005

STRAIN H36B frame: 1

NHLNLSKENIAKIDFDLNEALNANIRLKELVDELKISKELDSKGWSKKDSRTIKILYD
GLINKHIVSLDRADYNIQVIPFANVHVLFLIPERENSKNYRIYNYSYEMELINEDRQ
QFSKYETVDLDQLILVDIFNIDDISSYLT

SEQ ID NO. 8006

STRAIN 18RS21 frame: 1

NHLNLSKENIAKIDFDLNEALNANIRLKELVDELKISKELDSKGWSKKDSRTIKILYD
GLINKHIVSLDRADYNIQVIPFANVHVLFLIPERENSKNYRIYNYSYEMELINEDRQ
QFSKYETVDLDQLILVDIFNIDDISSYLT

PRETTY of: /biotmp/msa49418.2{*} February 19, 2003 07:47 ..

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1                                     50
msa49418.2{408_18RS21} -NHLNLSKE NIAKIDFDL NEALNANIRL KELVDELKIS KELDSKGWSK
msa49418.2{408_2603} vNHLNLSKE NIAKIDFDL NEALNANIRL KELVDELKIS KELDSKGWSK
msa49418.2{408_H36B} -NHLNLSKE NIAKIDFDL NEALNANIRL KELVDELKIS KELDSKGWSK
Consensus *****

```

```

51                                     100
msa49418.2{408_18RS21} KDSRTIKILY DGLINKHIVS LDRADYNIQ VIPFANVHVL LFLIPERENS
msa49418.2{408_2603} KDSRTIKILY DGLINKHIVS LDRADYNIQ VIPFANVHVL LFLIPERENS
msa49418.2{408_H36B} KDSRTIKILY DGLINKHIVS LDRADYNIQ VIPFANVHVL LFLIPERENS
Consensus *****

```

```

101                                    150
msa49418.2{408_18RS21} KNYRIYNYS YEMELINEDR QQFSKYETVD LDQLILVDIF NIDDISSYL
msa49418.2{408_2603} KNYRIYNYS YEMELINEDR QQFSKYETVD LDQLILVDIF NIDDISSYL
msa49418.2{408_H36B} KNYRIYNYS YEMELINEDR QQFSKYETVD LDQLILVDIF NIDDISSYL
Consensus *****

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151
msa49418.2{408_18RS21} TI
msa49418.2{408_2603} TI
msa49418.2{408_H36B} TI
Consensus **

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Table 81: Comparative Sequences relating to SAG0011**SEQ ID NO. 8101****STRAIN 090**

AGCAAGCCTAATGTTGTTTCAGTTAAA
 TAATCAATATATTAACGATGAGAATCTAAAAAACGTTACGAAGCTGAGG
 AGTTACGCCGAAAAAATCGTTTAAATGGGTTGGGTTCTTATTTTGTGTCATG
 CTTTTATTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAACTTT
 ACAAGAACGTCGTCAAGAAGTTGTAAAATTAACGAAAGACTATCAGACAT
 TAACTAATAGAACTGAGAACCAGAAGTTGCTAGCAAAACAACATAAAAAAT
 CCAGATTACGTTCAAAAATATGCTCGAGCTAAGTATTATTTCTCTAAGAC
 CGGCGAAATGATTTACCCATTACCAGACCTTTTACCAAAA

SEQ ID NO. 8102**STRAIN A909**

AGCAAGCCTAATGTTGTTTCAGTTAAATAATCAATA
 TATTAACGATGAGAATCTAAAAAACGTTACGAAGCTGAGGAGTTACGCCGAAAAAATCG
 TTTAATGGGTTGGGTTCTTATTTTGTGTCATGCTtttATTATTTTACCCACTTATAATTT
 AGTTAAGAGTTACAGAACTTTACAAGAACGTCGTCAAGAAGTTGTAAAATTAACGAAAGA
 CTATCAGACATTAACATAAGAACTGAGAACCAGAAGTTACTAGCAAAACAACATAAAAAA
 TCCAGATTACGTTCAAAAATATGCTCGAGCTAAGTATTATTTCTCTAAGACCGGCGAAAT
 GATTTACCCATTACCAGACCT

SEQ ID NO. 8103**STRAIN H36B**

AGCAAGCCTAATGTTGTTTCAGTTAAA
 TAATCAATATATTAACGATGAGAATCTAAAAAACGTTACGAAGCTGAGG
 AGTTACGCCGAAAAAATCGTTTAAATGGGTTGGGTTCTTATTTTGTGTCATG
 CTTTTATTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAACTTT
 ACAAGAACGTCGTCAAGAAGTTGTAAAATTAACGAAAGACTATCAGACAT
 TAACTAATAGAACTGAGAACCAGAAGTTACTAGCAAAACAACATAAAAAAT
 CCAGATTACGTTCAAAAATATGCTCGAGCTAAGTATTATTTCTCTAAGAC
 CGGCGAAATGATTTACCCATTACCAGACCTTTTACCAAAA

SEQ ID NO. 8104**STRAIN 18RS21**

AGCAAGCCTAATGTTGTTTCAGTTAAATAATCAATATATTAACGATGAGAATCTAAAAAAA
 CGTTACGAAGCTGAGGAGTTACGCCGAAAAAATCGTTTAAATGGGTTGGGTTCTTATTTT
 GTCATGCTTTTATTTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAACTTTACAA
 GAACGTCGTCAAGAAGTTGTAAAATTAACGAAAGACTATCAGACATTAACATAAGAACT
 GAGAACCAGAAGTTGCTAGCAAAACAACATAAAAAATCCAGATTACGTTCAAAAATATGCT
 CGAGCTAAGTATTATTTCTCTAAGACCGGCGAAATGATTTACCCATTACCAGACCTTTTA
 CCAAAA

SEQ ID NO. 8105**STRAIN M732**

AGCAAGCCTAATGTTGTTTCAGTTAAA
 TAATCAATATATTAACGATGAGAATCTAAAAAACGTTACGAAGCTGAGG
 AGTTACGCCGAAAAAATCGTTTAAATGGGTTGGGTTCTTATTTTGTGTCATG
 CTTTTATTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAACTTT
 ACAAGAACGTCGTCAAGAAGTTGTAAAATTAACGAAAGACTATCAGACAT
 TAACTAATAGAACTGAGAACCAGAAGTTACTAGCAAAACAACATAAAAAAT
 CCAGATTACGTTCAAAAATATGCTCGAGCGAAGTATTATTTCTCTAAGAC
 CGGCGAAATGATTTACCCATTACCAGACCTTTTACCAAAA

SEQ ID NO. 8106**STRAIN COH1**

AGCAAGCCTAATGTTGTTTCAGTTAAATAATC
 AATATATTAACGATGAGAATCTAAAAAACGTTACGAAGCTGAGGAGTTA
 CGCCGAAAAAATCGTTTAAATGGGTTGGGTTCTTATTTTGTGTCATGCTttt
 ATTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAACTTTACAAG
 AACGTCGTCAAGAAGTTGTAAAATTAACGAAAGACTATCAGACATTAAC
 AATAGAACTGAGAACCAGAAGTTACTAGCAAAACAACATAAAAAATCCAGA
 TTACGTTCAAAAATATGCTCGAGCGAAGTATTATTTCTCTAAGACCGGCG
 AAATGATTTACCCATTACCAGACCTTTTACCAAAA

SEQ ID NO. 8107**STRAIN M781**

AGCaAGCCTAATGTTGTTTCAGTT
 AAATAATCAATATATTAACGATGAGAATCTAAAAAACGTTACGAAGCTG
 AGGAGTTACGCCGAAAAAATCGTTTAAATGGGTTGGGTTCTTATTTTGTGTC
 ATGCTTTTATTTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAAC
 TTTACAAGAACGTCGTCAAGAAGTTGTAAAATTAACGAAAGACTATCAGA
 CATTAACATAAGAACTGAGAACCAGAAGTTACTAGCAAAACAACATAAAAA
 AATCCAGATTACGTTCAAAAATATGCTCGAGCGAAGTATTATTTCTCTAA
 GACCGGCGAAATGATTTACCCATTACCAGACCTTTTACCAAAA

SEQ ID NO. 8108**STRAIN CJB110**

AGCAAGCCTAATGTTGTTTCAGTTAAATAATC
 AATATATTAACGATGAGAATCTAAAAAACGTTACGAAGCTGAGGAGTTA
 CGCCGAAAAAATCGTTTAAATGGGTTGGGTTCTTATTTTGTGTCATGCTttt
 ATTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAACTTTACAAG

Table 81: Comparative Sequences relating to SAG0011

AACGTCGTCAAGAAGTTGTAAAATTAACGAAAGACTATCAGACATTAACCT
AATAGAACTGAGAACCAAGATTGCTAGCAAAACAATAAAAAATCCAGA
TTACGTTCAAAAATATGCTCGAGCTAAGTATTATTTCTCTAAGACCGGCG
AAATGATTTACCCATTACCAGACCTTTTACCAAAA

SEQ ID NO. 8109

STRAIN 1169NT

AGCAAGCCTAATGTTGTTTCAGTTAAA
TAATCAATATATTAACGATGAGAATCTAAAAAACGTTACGAAGCTGAGG
AGTTACGCCGAAAAAATCGTTTAAATGGGTTGGGTTCTTATTTTGTTCATG
CTTTTATTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAACTTT
ACAAGAACGTCGTCAAGAAGTTGTAAAATTAACGAAAGACTATCAGACAT
TAATAATAGAACTGAGAACCAGAAAGTTACTAGCAAAACAATAAAAAAT
CCAGATTACGTTCAAAAATATGCTCGAGCTAAGTATTATTTCTCTAAGAC
CGGCGAAATGATTTACCCATTACCAGACCTTTTACCAAAA

SEQ ID NO. 8110

STRAIN JM9130013

AGCAAGCCTAATGTTGTTTCAGTTAAA
TAATCAATATATTAACGATGAGAATCTAAAAAACGTTACGAAGCTGAGG
AGTTACGCCGAAAAAATCGTTTAAATGGGTTGGGTTCTTATTTTGTTCATG
CTTTTATTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAACTTT
ACAAGAACGTCGTCAAGAAGTTGTAAAATTAACGAAAGACTATCAGACAT
TAATAATAGAACTGAGAACCAGAAAGTTACTAGCAAAACAATAAAAAAT
CCAGATTACGTTCAAAAATATGCTCGAGCTAAGTATTATTTCTCTAAGAC
TGGCGAAATGATTTACCCATTACCAGACCTTTTACCAAAA

SEQ ID NO. 8111

STRAIN 2603

agcaagcctaattgttgggttcagttaaataatcaatatattaacgatgagaa
tctaaaaaacggttacgaagctgaggagttacgccgaaaaaatcgtttaa
tgggttgggttcttattttgtcatgcttttatttttaccacttat
aatttagttaagagttacagaactttacaagaacgtcgtcaagaagttgt
aaaattaacgaaagactatcagacattaactaataagaactgagaaccaga
agttgctagcaaaaacaactaaaaaatccagattacgttcaaaaatatgct
cgagctaagtattattttctaaagaccggcgaaatgatttaccattacc
agaccttttaccaaaa

PRETTY of: /biotmp/msa25643.2{*} . April 29, 2002 05:59 ..

	1		50
msa25643.2{418_COH1}	AGCAAGCCTA	ATGTTGTTCA	GTTAAATAAT CAATATATTA ACGATGAGAA
msa25643.2{418_M732}	AGCAAGCCTA	ATGTTGTTCA	GTTAAATAAT CAATATATTA ACGATGAGAA
msa25643.2{418_M781}	AGCAAGCCTA	ATGTTGTTCA	GTTAAATAAT CAATATATTA ACGATGAGAA
msa25643.2{418_JM9130013}	AGCAAGCCTA	ATGTTGTTCA	GTTAAATAAT CAATATATTA ACGATGAGAA
msa25643.2{418_090}	AGCAAGCCTA	ATGTTGTTCA	GTTAAATAAT CAATATATTA ACGATGAGAA
msa25643.2{418_18RS21}	AGCAAGCCTA	ATGTTGTTCA	GTTAAATAAT CAATATATTA ACGATGAGAA
msa25643.2{418_2603}	AGCAAGCCTA	ATGTTGTTCA	GTTAAATAAT CAATATATTA ACGATGAGAA
msa25643.2{418_CJB110}	AGCAAGCCTA	ATGTTGTTCA	GTTAAATAAT CAATATATTA ACGATGAGAA
msa25643.2{418_1169NT}	AGCAAGCCTA	ATGTTGTTCA	GTTAAATAAT CAATATATTA ACGATGAGAA
msa25643.2{418_A909}	AGCAAGCCTA	ATGTTGTTCA	GTTAAATAAT CAATATATTA ACGATGAGAA
msa25643.2{418_H36B}	AGCAAGCCTA	ATGTTGTTCA	GTTAAATAAT CAATATATTA ACGATGAGAA
Consensus	*****	*****	*****
	51		100
msa25643.2{418_COH1}	TCTAAAAAAA	CGTTACGAAG	CTGAGGAGTT ACGCCGAAAA AATCGTTTAA
msa25643.2{418_M732}	TCTAAAAAAA	CGTTACGAAG	CTGAGGAGTT ACGCCGAAAA AATCGTTTAA
msa25643.2{418_M781}	TCTAAAAAAA	CGTTACGAAG	CTGAGGAGTT ACGCCGAAAA AATCGTTTAA
msa25643.2{418_JM9130013}	TCTAAAAAAA	CGTTACGAAG	CTGAGGAGTT ACGCCGAAAA AATCGTTTAA
msa25643.2{418_090}	TCTAAAAAAA	CGTTACGAAG	CTGAGGAGTT ACGCCGAAAA AATCGTTTAA
msa25643.2{418_18RS21}	TCTAAAAAAA	CGTTACGAAG	CTGAGGAGTT ACGCCGAAAA AATCGTTTAA
msa25643.2{418_2603}	TCTAAAAAAA	CGTTACGAAG	CTGAGGAGTT ACGCCGAAAA AATCGTTTAA
msa25643.2{418_CJB110}	TCTAAAAAAA	CGTTACGAAG	CTGAGGAGTT ACGCCGAAAA AATCGTTTAA
msa25643.2{418_1169NT}	TCTAAAAAAA	CGTTACGAAG	CTGAGGAGTT ACGCCGAAAA AATCGTTTAA
msa25643.2{418_A909}	TCTAAAAAAA	CGTTACGAAG	CTGAGGAGTT ACGCCGAAAA AATCGTTTAA
msa25643.2{418_H36B}	TCTAAAAAAA	CGTTACGAAG	CTGAGGAGTT ACGCCGAAAA AATCGTTTAA
Consensus	*****	*****	*****
	101		150
msa25643.2{418_COH1}	TGGGTTGGGT	TCTTATTTT	GTCATGCTTT TATTTATTTT ACCCACTTAT
msa25643.2{418_M732}	TGGGTTGGGT	TCTTATTTT	GTCATGCTTT TATTTATTTT ACCCACTTAT
msa25643.2{418_M781}	TGGGTTGGGT	TCTTATTTT	GTCATGCTTT TATTTATTTT ACCCACTTAT
msa25643.2{418_JM9130013}	TGGGTTGGGT	TCTTATTTT	GTCATGCTTT TATTTATTTT ACCCACTTAT
msa25643.2{418_090}	TGGGTTGGGT	TCTTATTTT	GTCATGCTTT TATTTATTTT ACCCACTTAT
msa25643.2{418_18RS21}	TGGGTTGGGT	TCTTATTTT	GTCATGCTTT TATTTATTTT ACCCACTTAT
msa25643.2{418_2603}	TGGGTTGGGT	TCTTATTTT	GTCATGCTTT TATTTATTTT ACCCACTTAT
msa25643.2{418_CJB110}	TGGGTTGGGT	TCTTATTTT	GTCATGCTTT TATTTATTTT ACCCACTTAT
msa25643.2{418_1169NT}	TGGGTTGGGT	TCTTATTTT	GTCATGCTTT TATTTATTTT ACCCACTTAT
msa25643.2{418_A909}	TGGGTTGGGT	TCTTATTTT	GTCATGCTTT TATTTATTTT ACCCACTTAT
msa25643.2{418_H36B}	TGGGTTGGGT	TCTTATTTT	GTCATGCTTT TATTTATTTT ACCCACTTAT
Consensus	*****	*****	*****

Table 81: Comparative Sequences relating to SAG0011

	151				200
msa25643.2{418_COH1}	AATTTAGTTA	AGAGTTACAG	AACTTTACAA	GAACGTCGTC	AAGAAGTTGT
msa25643.2{418_M732}	AATTTAGTTA	AGAGTTACAG	AACTTTACAA	GAACGTCGTC	AAGAAGTTGT
msa25643.2{418_M781}	AATTTAGTTA	AGAGTTACAG	AACTTTACAA	GAACGTCGTC	AAGAAGTTGT
msa25643.2{418_JM9130013}	AATTTAGTTA	AGAGTTACAG	AACTTTACAA	GAACGTCGTC	AAGAAGTTGT
msa25643.2{418_090}	AATTTAGTTA	AGAGTTACAG	AACTTTACAA	GAACGTCGTC	AAGAAGTTGT
msa25643.2{418_18RS21}	AATTTAGTTA	AGAGTTACAG	AACTTTACAA	GAACGTCGTC	AAGAAGTTGT
msa25643.2{418_2603}	AATTTAGTTA	AGAGTTACAG	AACTTTACAA	GAACGTCGTC	AAGAAGTTGT
msa25643.2{418_CJB110}	AATTTAGTTA	AGAGTTACAG	AACTTTACAA	GAACGTCGTC	AAGAAGTTGT
msa25643.2{418_1169NT}	AATTTAGTTA	AGAGTTACAG	AACTTTACAA	GAACGTCGTC	AAGAAGTTGT
msa25643.2{418_A909}	AATTTAGTTA	AGAGTTACAG	AACTTTACAA	GAACGTCGTC	AAGAAGTTGT
msa25643.2{418_H36B}	AATTTAGTTA	AGAGTTACAG	AACTTTACAA	GAACGTCGTC	AAGAAGTTGT
Consensus	*****	*****	*****	*****	*****
	201				250
msa25643.2{418_COH1}	AAAATTAACG	AAAGACTATC	AGACATTAAC	TAATAGAACT	GAGAACCAGA
msa25643.2{418_M732}	AAAATTAACG	AAAGACTATC	AGACATTAAC	TAATAGAACT	GAGAACCAGA
msa25643.2{418_M781}	AAAATTAACG	AAAGACTATC	AGACATTAAC	TAATAGAACT	GAGAACCAGA
msa25643.2{418_JM9130013}	AAAATTAACG	AAAGACTATC	AGACATTAAC	TAATAGAACT	GAGAACCAGA
msa25643.2{418_090}	AAAATTAACG	AAAGACTATC	AGACATTAAC	TAATAGAACT	GAGAACCAGA
msa25643.2{418_18RS21}	AAAATTAACG	AAAGACTATC	AGACATTAAC	TAATAGAACT	GAGAACCAGA
msa25643.2{418_2603}	AAAATTAACG	AAAGACTATC	AGACATTAAC	TAATAGAACT	GAGAACCAGA
msa25643.2{418_CJB110}	AAAATTAACG	AAAGACTATC	AGACATTAAC	TAATAGAACT	GAGAACCAGA
msa25643.2{418_1169NT}	AAAATTAACG	AAAGACTATC	AGACATTAAC	TAATAGAACT	GAGAACCAGA
msa25643.2{418_A909}	AAAATTAACG	AAAGACTATC	AGACATTAAC	TAATAGAACT	GAGAACCAGA
msa25643.2{418_H36B}	AAAATTAACG	AAAGACTATC	AGACATTAAC	TAATAGAACT	GAGAACCAGA
Consensus	*****	*****	*****	*****	*****
	251				300
msa25643.2{418_COH1}	AGTTaCTAGC	AAAACAACCTA	AAAAATCCAG	ATTACGTTCA	AAAATATGCT
msa25643.2{418_M732}	AGTTaCTAGC	AAAACAACCTA	AAAAATCCAG	ATTACGTTCA	AAAATATGCT
msa25643.2{418_M781}	AGTTaCTAGC	AAAACAACCTA	AAAAATCCAG	ATTACGTTCA	AAAATATGCT
msa25643.2{418_JM9130013}	AGTTaCTAGC	AAAACAACCTA	AAAAATCCAG	ATTACGTTCA	AAAATATGCT
msa25643.2{418_090}	AGTTgCTAGC	AAAACAACCTA	AAAAATCCAG	ATTACGTTCA	AAAATATGCT
msa25643.2{418_18RS21}	AGTTgCTAGC	AAAACAACCTA	AAAAATCCAG	ATTACGTTCA	AAAATATGCT
msa25643.2{418_2603}	AGTTgCTAGC	AAAACAACCTA	AAAAATCCAG	ATTACGTTCA	AAAATATGCT
msa25643.2{418_CJB110}	AGTTgCTAGC	AAAACAACCTA	AAAAATCCAG	ATTACGTTCA	AAAATATGCT
msa25643.2{418_1169NT}	AGTTaCTAGC	AAAACAACCTA	AAAAATCCAG	ATTACGTTCA	AAAATATGCT
msa25643.2{418_A909}	AGTTaCTAGC	AAAACAACCTA	AAAAATCCAG	ATTACGTTCA	AAAATATGCT
msa25643.2{418_H36B}	AGTTaCTAGC	AAAACAACCTA	AAAAATCCAG	ATTACGTTCA	AAAATATGCT
Consensus	****-*****	*****	*****	*****	*****
	301				350
msa25643.2{418_COH1}	CGAGCgAAGT	ATTATTTCTC	TAAGACcGGC	GAAATGATTT	ACCCATTACC
msa25643.2{418_M732}	CGAGCgAAGT	ATTATTTCTC	TAAGACcGGC	GAAATGATTT	ACCCATTACC
msa25643.2{418_M781}	CGAGCgAAGT	ATTATTTCTC	TAAGACcGGC	GAAATGATTT	ACCCATTACC
msa25643.2{418_JM9130013}	CGAGCgAAGT	ATTATTTCTC	TAAGACtGGC	GAAATGATTT	ACCCATTACC
msa25643.2{418_090}	CGAGCtAAGT	ATTATTTCTC	TAAGACcGGC	GAAATGATTT	ACCCATTACC
msa25643.2{418_18RS21}	CGAGCtAAGT	ATTATTTCTC	TAAGACcGGC	GAAATGATTT	ACCCATTACC
msa25643.2{418_2603}	CGAGCtAAGT	ATTATTTCTC	TAAGACcGGC	GAAATGATTT	ACCCATTACC
msa25643.2{418_CJB110}	CGAGCtAAGT	ATTATTTCTC	TAAGACcGGC	GAAATGATTT	ACCCATTACC
msa25643.2{418_1169NT}	CGAGCtAAGT	ATTATTTCTC	TAAGACcGGC	GAAATGATTT	ACCCATTACC
msa25643.2{418_A909}	CGAGCtAAGT	ATTATTTCTC	TAAGACcGGC	GAAATGATTT	ACCCATTACC
msa25643.2{418_H36B}	CGAGCtAAGT	ATTATTTCTC	TAAGACcGGC	GAAATGATTT	ACCCATTACC
Consensus	*****-*****	*****	*****-***	*****	*****
	351		366		
msa25643.2{418_COH1}	AGACCTttta	ccaaaa			
msa25643.2{418_M732}	AGACCTttta	ccaaaa			
msa25643.2{418_M781}	AGACCTttta	ccaaaa			
msa25643.2{418_JM9130013}	AGACCTttta	ccaaaa			
msa25643.2{418_090}	AGACCTttta	ccaaaa			
msa25643.2{418_18RS21}	AGACCTttta	ccaaaa			
msa25643.2{418_2603}	AGACCTttta	ccaaaa			
msa25643.2{418_CJB110}	AGACCTttta	ccaaaa			
msa25643.2{418_1169NT}	AGACCTttta	ccaaaa			
msa25643.2{418_A909}	AGACCT----	-----			
msa25643.2{418_H36B}	AGACCTttta	ccaaaa			
Consensus	*****----	-----			

SEQ ID NO. 8112

STRAIN 090

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLI FVMLLFILPTYNL
 VKSYRTLQERRQEVVKLT KDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYFYSKTGEM
 IYPLPDL LPK

SEQ ID NO. 8113

STRAIN A909

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLI FVMLLFILPTYNL
 VKSYRTLQERRQEVVKLT KDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYFYSKTGEM

Table 81: Comparative Sequences relating to SAG0011

IYPLPD

SEQ ID NO. 8114

STRAIN H36B

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLI FVMLLFILPTYNL
 VKSYRTLQERRQEVVKLT KDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYYFSKTGEM
 IYPLPDLLPK

SEQ ID NO. 8115

STRAIN 18RS21

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLI FVMLLFILPTYNLVKSYRTLQ
 ERRQEVVKLT KDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYYFSKTGEM IYPLPDLL
 PK

SEQ ID NO. 8116

STRAIN M732

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLI FVMLLFILPTYNL
 VKSYRTLQERRQEVVKLT KDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYYFSKTGEM
 IYPLPDLLPK

SEQ ID NO. 8117

STRAIN COH1

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLI FVMLLFILPTYNLVK
 SYRTLQERRQEVVKLT KDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYYFSKTGEM IY
 PLPDLLPK

SEQ ID NO. 8118

STRAIN M781

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLI FVMLLFILPTYN
 LVKSYRTLQERRQEVVKLT KDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYYFSKTGE
 MIYPLPDLLPK

SEQ ID NO. 8119

STRAIN CJB110

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLI FVMLLFILPTYNLVK
 SYRTLQERRQEVVKLT KDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYYFSKTGEM IY
 PLPDLLPK

SEQ ID NO. 8120

STRAIN 1169NT

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLI FVMLLFILPTYNL
 VKSYRTLQERRQEVVKLT KDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYYFSKTGEM
 IYPLPDLLPK

SEQ ID NO. 8121

STRAIN JM9130013

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLI FVMLLFILPTYNL
 VKSYRTLQERRQEVVKLT KDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYYFSKTGEM
 IYPLPDLLPK

SEQ ID NO. 8122

STRAIN 2603

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLI FVMLLFILPTYNLVKSYRTLQ
 ERRQEVVKLT KDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYYFSKTGEM IYPLPDLL
 PK

MSA Alignment Results: Pretty output

PRETTY of: /biotmp/msa20122.2{*} April 29, 2002 06:08 ..

	1		50
msa20122.2{418_090}	SKPNVVQLNN	QYINDENLKK RYEAEELRRK	NRLMGWVLIF VMLLFILPTY
msa20122.2{418_A909}	SKPNVVQLNN	QYINDENLKK RYEAEELRRK	NRLMGWVLIF VMLLFILPTY
msa20122.2{418_1169NT}	SKPNVVQLNN	QYINDENLKK RYEAEELRRK	NRLMGWVLIF VMLLFILPTY
msa20122.2{418_18RS21}	SKPNVVQLNN	QYINDENLKK RYEAEELRRK	NRLMGWVLIF VMLLFILPTY
msa20122.2{418_2603}	SKPNVVQLNN	QYINDENLKK RYEAEELRRK	NRLMGWVLIF VMLLFILPTY
msa20122.2{418_CJB110}	SKPNVVQLNN	QYINDENLKK RYEAEELRRK	NRLMGWVLIF VMLLFILPTY
msa20122.2{418_COH1}	SKPNVVQLNN	QYINDENLKK RYEAEELRRK	NRLMGWVLIF VMLLFILPTY
msa20122.2{418_H36B}	SKPNVVQLNN	QYINDENLKK RYEAEELRRK	NRLMGWVLIF VMLLFILPTY
msa20122.2{418_JM9130013}	SKPNVVQLNN	QYINDENLKK RYEAEELRRK	NRLMGWVLIF VMLLFILPTY
msa20122.2{418_M732}	SKPNVVQLNN	QYINDENLKK RYEAEELRRK	NRLMGWVLIF VMLLFILPTY
msa20122.2{418_M781}	SKPNVVQLNN	QYINDENLKK RYEAEELRRK	NRLMGWVLIF VMLLFILPTY
Consensus	*****	*****	*****
	51		100
msa20122.2{418_090}	NLVKSYRTLQ	ERRQEVVKLT KDYQTLTNRT	ENQKLLAKQL KNPDYVQKYA
msa20122.2{418_A909}	NLVKSYRTLQ	ERRQEVVKLT KDYQTLTNRT	ENQKLLAKQL KNPDYVQKYA

Table 81: Comparative Sequences relating to SAG0011

msa20122.2{418_1169NT}	NLVKSYRTLQ	ERRQEVVKLT	KDYQTLTNRT	ENQKLLAKQL	KNPDYVQKYA
msa20122.2{418_18RS21}	NLVKSYRTLQ	ERRQEVVKLT	KDYQTLTNRT	ENQKLLAKQL	KNPDYVQKYA
msa20122.2{418_2603}	NLVKSYRTLQ	ERRQEVVKLT	KDYQTLTNRT	ENQKLLAKQL	KNPDYVQKYA
msa20122.2{418_CJB110}	NLVKSYRTLQ	ERRQEVVKLT	KDYQTLTNRT	ENQKLLAKQL	KNPDYVQKYA
msa20122.2{418_COH1}	NLVKSYRTLQ	ERRQEVVKLT	KDYQTLTNRT	ENQKLLAKQL	KNPDYVQKYA
msa20122.2{418_H36B}	NLVKSYRTLQ	ERRQEVVKLT	KDYQTLTNRT	ENQKLLAKQL	KNPDYVQKYA
msa20122.2{418_JM9130013}	NLVKSYRTLQ	ERRQEVVKLT	KDYQTLTNRT	ENQKLLAKQL	KNPDYVQKYA
msa20122.2{418_M732}	NLVKSYRTLQ	ERRQEVVKLT	KDYQTLTNRT	ENQKLLAKQL	KNPDYVQKYA
msa20122.2{418_M781}	NLVKSYRTLQ	ERRQEVVKLT	KDYQTLTNRT	ENQKLLAKQL	KNPDYVQKYA
Consensus	*****	*****	*****	*****	*****
	101		122		
msa20122.2{418_090}	RAKYYFSKTG	EMIYPLPD11	pk		
msa20122.2{418_A909}	RAKYYFSKTG	EMIYPLPD--	--		
msa20122.2{418_1169NT}	RAKYYFSKTG	EMIYPLPD11	pk		
msa20122.2{418_18RS21}	RAKYYFSKTG	EMIYPLPD11	pk		
msa20122.2{418_2603}	RAKYYFSKTG	EMIYPLPD11	pk		
msa20122.2{418_CJB110}	RAKYYFSKTG	EMIYPLPD11	pk		
msa20122.2{418_COH1}	RAKYYFSKTG	EMIYPLPD11	pk		
msa20122.2{418_H36B}	RAKYYFSKTG	EMIYPLPD11	pk		
msa20122.2{418_JM9130013}	RAKYYFSKTG	EMIYPLPD11	pk		
msa20122.2{418_M732}	RAKYYFSKTG	EMIYPLPD11	pk		
msa20122.2{418_M781}	RAKYYFSKTG	EMIYPLPD11	pk		
Consensus	*****	*****--	--		

Table 82: Comparative Sequences relating to SAG0165

SEQ ID NO. 8201

STRAIN 2603

ATGAAAAATTTATTGTTAAAAATGTAAGGATAAGAAGGTTAAAGCATTACACTTTTAGAA
 TGTGTTGGTAGCATTGGTTACAATCACAGGAGCTTTACTAGTTTATCAAGGACTGACAAA
 TTGTTGGCTCAACAGATAGTAGTGATGTTCTTCCAGTCAGTCTGAATGGGTGTTATTA
 AcTCAGCAACTAAATGCAGAATTGAAGGCGCTCATCTGGAATATTTAAGACAGAACAAA
 CTTTATTTACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGATTTC
 CGTAAGACAGGTTATGATGGTTCGAGGTTATCAACCAATGGTTTATGGGTTAGACAATTGT
 CAAATGAGTCAGACCAAAGTATGGTAAAACCTGTTTTTTATTTTAAGGACGGGTAAAA
 AGGACATTTTACTATGATTTTAAAGAAGAACTTAA

SEQ ID NO. 8202

STRAIN 090

AATTCTGAAGGCGCTCACTTGGAATATTTAAGACAGAACAAACTTTATTTA
 CGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGATT
 CCGTAAGACAGGTTATGATGGTTCGAGGTTATCAACCAATGGTTTATGGGT
 TAGACAATTGTCAAATGAGTCAAACCAAAGTATGGTAAAACCTGTTTTT
 TATTTTAAGGACGGGTAAAAAGGACATTTTACTATGATTTTAAAGAAGA
 AACT

SEQ ID NO. 8203

STRAIN A909

CAGAATTTGAAGGCGCTCATCTGGAATATTTAAGACAGAACAAACTTTAT
 TTACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGA
 TTTCCGTAAGACAGGTTATGATGGTTCGAGGTTATCAACCAATGGTTTATG
 GGTTAGACAATTGTCAAATGAGTCAAACCAAAGTATGGTAAAACCTGTTT
 TTTTATTTTAAGGACGGGTAAAAAGGACATTTTACTATGATTTTAAAGA
 AGAAACT

SEQ ID NO. 8204

STRAIN H36B

ATGCAGAATTTGAAGGCGCTCATCTGGAATATTTAAGACAGAACAAACTT
 TATTTACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGA
 TGATTTCCGTAAGACAGGTTATGATGGTTCGAGGTTATCAACCAATGGTTT
 ATGGGTTAGACAATTGTCAAATGAGTCAAACCAAAGTATGGTAAAACCTT
 GTTTTTTATTTTAAGGACGGGTAAAAAGGACATTTTACTATGATTTTAA
 AGAAGAACT

SEQ ID NO. 8205

STRAIN 18RS21

AGAATTTGAAGGCGCTCATCTGGAATATTTAAGACAGAACAAACTTTATT
 TACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGAT
 TTCCGTAAGACAGGTTATGATGGTTCGAGGTTATCAACCAATGGTTTATGG
 GTTAGACAATTGTCAAATGAGTCAAACCAAAGTATGGTAAAACCTGTTT
 TTTATTTTAAGGACGGGTAAAAAGGACATTTTACTATGATTTTAAAGAA
 GAAACT

SEQ ID NO. 8206

STRAIN M732

CAGAATTCGAAGGCGCTCACTTGGAATATTTAAGACAGAACAAACTTTAT
 TTACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGA
 TTTCCGTAAGACAGGTTATAATGGTTCGAGGTTATCAACCAATGGTTTATG
 GGTTAGACAATTGTCAAATGAGTCAAACCAAAGTATGGTAAAACCTGTTT
 TTTTATTTTAAGGACGGGTAAAAAGGACATTTTACTATGATTTTAAAGA
 AGAACT

SEQ ID NO. 8207

STRAIN COH1

GAATTCGAAGGCGCTCACTTGGAATATTTAAGACAGAACAAACTTTATTT
 ACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGATT
 TCCGTAAGACAGGTTATAATGGTTCGAGGTTATCAACCAATGGTTTATGGG
 TTAGACAATTGTCAAATGAGTCAAACCAAAGTATGGTAAAACCTGTTTT
 TTATTTTAAGGACGGGTAAAAAGGACATTTTACTATGATTTTAAAGAAG
 AACT

SEQ ID NO. 8208

STRAIN M781

AGAATTCGAAGGCGCTCACTTGGAATATTTAAGACAGAACAAACTTTATT
 TACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGAT
 TTCCGTAAGACAGGTTATAATGGTTCGAGGTTATCAACCAATGGTTTATGG
 GTTAGACAATTGTCAAATGAGTCAAACCAAAGTATGGTAAAACCTGTTT
 TTTATTTTAAGGACGGGTAAAAAGGACATTTTACTATGATTTTAAAGAA
 GAACT

SEQ ID NO. 8209

STRAIN CJB110

GAATTCGAAGGCGCTCACTTGGAATATTTAAGACAGAACAAACTTTATTT
 ACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGATT
 TCCGTAAGACAGGTTATGATGGTTCGAGGTTATCAACCAATGGTTTATGGG
 TTAGACAATTGTCAAATGAGTCAAACCAAAGTATGGTAAAACCTGTTTT
 TTATTTTAAGGACGGGTAAAAAGGACATTTTACTATGATTTTAAAGAAG
 AACT

Table 82: Comparative Sequences relating to SAG0165

SEQ ID NO. 8210

STRAIN 1169NT

TCGAAGGCGCTCACTTGGGAATATTTAAGACAGAACAACTTTATTACGT
 AAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGATTTTCG
 TAAGACAGGTTATGATGGTTCGAGGTTATCAACCAATGGTTTATGGGTTAG
 ACAATTGTCAAATGAGTCAAACCAAAAGTATGGTAAACTTGTTTTTTAT
 TTTAAGGACGGGTTAAAAAGGACATTTTACTATGATTTTAAAGAAGAAAC
 T

SEQ ID NO. 8211

STRAIN JM9130013

TGCAGAATTTGAAGGCGCTCATCTGGAATATTTAAGACAGAACAACTTT
 ATTTACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGAT
 GATTTCCGTAAGACAGGTTATGATGGTTCGAGGTTATCAACCAATGGTTTA
 TGGGTTAGACAAATTGTCAAATGAGTCAAGACCAAAAGTATGGTAAACTTG
 TTTTTATTTTAAAGGACGGGTTAAAAAGGACATTTTACTATGATTTTAA
 GAAGAACT

PRETTY of: /biotmp/msa128189.2{*} February 7, 2003 08:19 ..

	1				50
msa128189.2{6_18RS21}	-----	-----	-----	-----	-----
msa128189.2{6_2603}	atgaaaaatt	tattgttaaa	atgtaaggat	aagaaggtta	aagcatttac
msa128189.2{6_A909}	-----	-----	-----	-----	-----
msa128189.2{6_H36B}	-----	-----	-----	-----	-----
msa128189.2{6_JM9130013}	-----	-----	-----	-----	-----
msa128189.2{6_COH1}	-----	-----	-----	-----	-----
msa128189.2{6_M732}	-----	-----	-----	-----	-----
msa128189.2{6_M781}	-----	-----	-----	-----	-----
msa128189.2{6_090}	-----	-----	-----	-----	-----
msa128189.2{6_CJB110}	-----	-----	-----	-----	-----
msa128189.2{6_1169NT}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	51				100
msa128189.2{6_18RS21}	-----	-----	-----	-----	-----
msa128189.2{6_2603}	acttttagaa	tgtttggttag	cattgggttac	aatcacagga	gctttactag
msa128189.2{6_A909}	-----	-----	-----	-----	-----
msa128189.2{6_H36B}	-----	-----	-----	-----	-----
msa128189.2{6_JM9130013}	-----	-----	-----	-----	-----
msa128189.2{6_COH1}	-----	-----	-----	-----	-----
msa128189.2{6_M732}	-----	-----	-----	-----	-----
msa128189.2{6_M781}	-----	-----	-----	-----	-----
msa128189.2{6_090}	-----	-----	-----	-----	-----
msa128189.2{6_CJB110}	-----	-----	-----	-----	-----
msa128189.2{6_1169NT}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	101				150
msa128189.2{6_18RS21}	-----	-----	-----	-----	-----
msa128189.2{6_2603}	tttatcaagg	actgacaaaa	ttgttggttc	aacagatagt	agtgatgtct
msa128189.2{6_A909}	-----	-----	-----	-----	-----
msa128189.2{6_H36B}	-----	-----	-----	-----	-----
msa128189.2{6_JM9130013}	-----	-----	-----	-----	-----
msa128189.2{6_COH1}	-----	-----	-----	-----	-----
msa128189.2{6_M732}	-----	-----	-----	-----	-----
msa128189.2{6_M781}	-----	-----	-----	-----	-----
msa128189.2{6_090}	-----	-----	-----	-----	-----
msa128189.2{6_CJB110}	-----	-----	-----	-----	-----
msa128189.2{6_1169NT}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	151				200
msa128189.2{6_18RS21}	-----	-----	-----	-----	-----aga
msa128189.2{6_2603}	tcttccagtc	agtctgaatg	gggtgttatta	actcagcaac	taaATGCaga
msa128189.2{6_A909}	-----	-----	-----	-----	-----Caga
msa128189.2{6_H36B}	-----	-----	-----	-----	-----ATGCaga
msa128189.2{6_JM9130013}	-----	-----	-----	-----	-----TGCaga
msa128189.2{6_COH1}	-----	-----	-----	-----	-----ga
msa128189.2{6_M732}	-----	-----	-----	-----	-----Caga
msa128189.2{6_M781}	-----	-----	-----	-----	-----aga
msa128189.2{6_090}	-----	-----	-----	-----	-----a
msa128189.2{6_CJB110}	-----	-----	-----	-----	-----ga
msa128189.2{6_1169NT}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	201				250
msa128189.2{6_18RS21}	atTtGAAGGC	GCTCatcTGG	AATATTTAAG	ACAGAACAAA	CTTTATTTAC
msa128189.2{6_2603}	atTtGAAGGC	GCTCatcTGG	AATATTTAAG	ACAGAACAAA	CTTTATTTAC
msa128189.2{6_A909}	atTtGAAGGC	GCTCatcTGG	AATATTTAAG	ACAGAACAAA	CTTTATTTAC
msa128189.2{6_H36B}	atTtGAAGGC	GCTCatcTGG	AATATTTAAG	ACAGAACAAA	CTTTATTTAC

Table 82: Comparative Sequences relating to SAG0165

msa128189.2{6_JM9130013}	atTtGAAGGC	GCTCAcTGG	AATATTTAAG	ACAGAACAAA	CTTTATTTAC
msa128189.2{6_COH1}	atTcGAAGGC	GCTCAcTGG	AATATTTAAG	ACAGAACAAA	CTTTATTTAC
msa128189.2{6_M732}	atTcGAAGGC	GCTCAcTGG	AATATTTAAG	ACAGAACAAA	CTTTATTTAC
msa128189.2{6_M781}	atTcGAAGGC	GCTCAcTGG	AATATTTAAG	ACAGAACAAA	CTTTATTTAC
msa128189.2{6_090}	atTcGAAGGC	GCTCAcTGG	AATATTTAAG	ACAGAACAAA	CTTTATTTAC
msa128189.2{6_CJB110}	atTcGAAGGC	GCTCAcTGG	AATATTTAAG	ACAGAACAAA	CTTTATTTAC
msa128189.2{6_1169NT}	--TcGAAGGC	GCTCAcTGG	AATATTTAAG	ACAGAACAAA	CTTTATTTAC
Consensus	---*****	*****--***	*****	*****	*****
msa128189.2{6_18RS21}	GTAAGCAAGA	TAAGATTGTA	ACCTTTGGCA	AATCTAATAA	AGATGATTTc
msa128189.2{6_2603}	GTAAGCAAGA	TAAGATTGTA	ACCTTTGGCA	AATCTAATAA	AGATGATTTc
msa128189.2{6_A909}	GTAAGCAAGA	TAAGATTGTA	ACCTTTGGCA	AATCTAATAA	AGATGATTTc
msa128189.2{6_H36B}	GTAAGCAAGA	TAAGATTGTA	ACCTTTGGCA	AATCTAATAA	AGATGATTTc
msa128189.2{6_JM9130013}	GTAAGCAAGA	TAAGATTGTA	ACCTTTGGCA	AATCTAATAA	AGATGATTTc
msa128189.2{6_COH1}	GTAAGCAAGA	TAAGATTGTA	ACCTTTGGCA	AATCTAATAA	AGATGATTTc
msa128189.2{6_M732}	GTAAGCAAGA	TAAGATTGTA	ACCTTTGGCA	AATCTAATAA	AGATGATTTc
msa128189.2{6_M781}	GTAAGCAAGA	TAAGATTGTA	ACCTTTGGCA	AATCTAATAA	AGATGATTTc
msa128189.2{6_090}	GTAAGCAAGA	TAAGATTGTA	ACCTTTGGCA	AATCTAATAA	AGATGATTTc
msa128189.2{6_CJB110}	GTAAGCAAGA	TAAGATTGTA	ACCTTTGGCA	AATCTAATAA	AGATGATTTc
msa128189.2{6_1169NT}	GTAAGCAAGA	TAAGATTGTA	ACCTTTGGCA	AATCTAATAA	AGATGATTTt
Consensus	*****	*****	*****	*****	*****-
msa128189.2{6_18RS21}	CGTAAGACAG	GTTATgATGG	TCGAGGTTAT	CAACCAATGG	TTTATGGGTT
msa128189.2{6_2603}	CGTAAGACAG	GTTATgATGG	TCGAGGTTAT	CAACCAATGG	TTTATGGGTT
msa128189.2{6_A909}	CGTAAGACAG	GTTATgATGG	TCGAGGTTAT	CAACCAATGG	TTTATGGGTT
msa128189.2{6_H36B}	CGTAAGACAG	GTTATgATGG	TCGAGGTTAT	CAACCAATGG	TTTATGGGTT
msa128189.2{6_JM9130013}	CGTAAGACAG	GTTATgATGG	TCGAGGTTAT	CAACCAATGG	TTTATGGGTT
msa128189.2{6_COH1}	CGTAAGACAG	GTTATaATGG	TCGAGGTTAT	CAACCAATGG	TTTATGGGTT
msa128189.2{6_M732}	CGTAAGACAG	GTTATaATGG	TCGAGGTTAT	CAACCAATGG	TTTATGGGTT
msa128189.2{6_M781}	CGTAAGACAG	GTTATaATGG	TCGAGGTTAT	CAACCAATGG	TTTATGGGTT
msa128189.2{6_090}	CGTAAGACAG	GTTATgATGG	TCGAGGTTAT	CAACCAATGG	TTTATGGGTT
msa128189.2{6_CJB110}	CGTAAGACAG	GTTATgATGG	TCGAGGTTAT	CAACCAATGG	TTTATGGGTT
msa128189.2{6_1169NT}	CGTAAGACAG	GTTATgATGG	TCGAGGTTAT	CAACCAATGG	TTTATGGGTT
Consensus	*****	*****-****	*****	*****	*****
msa128189.2{6_18RS21}	AGACAAATTGT	CAAATGAGTC	AgACCAAAAG	TATGGTAAAA	CTTGTTTTTT
msa128189.2{6_2603}	AGACAAATTGT	CAAATGAGTC	AgACCAAAAG	TATGGTAAAA	CTTGTTTTTT
msa128189.2{6_A909}	AGACAAATTGT	CAAATGAGTC	AgACCAAAAG	TATGGTAAAA	CTTGTTTTTT
msa128189.2{6_H36B}	AGACAAATTGT	CAAATGAGTC	AgACCAAAAG	TATGGTAAAA	CTTGTTTTTT
msa128189.2{6_JM9130013}	AGACAAATTGT	CAAATGAGTC	AgACCAAAAG	TATGGTAAAA	CTTGTTTTTT
msa128189.2{6_COH1}	AGACAAATTGT	CAAATGAGTC	AgACCAAAAG	TATGGTAAAA	CTTGTTTTTT
msa128189.2{6_M732}	AGACAAATTGT	CAAATGAGTC	AgACCAAAAG	TATGGTAAAA	CTTGTTTTTT
msa128189.2{6_M781}	AGACAAATTGT	CAAATGAGTC	AgACCAAAAG	TATGGTAAAA	CTTGTTTTTT
msa128189.2{6_090}	AGACAAATTGT	CAAATGAGTC	AaACCAAAAG	TATGGTAAAA	CTTGTTTTTT
msa128189.2{6_CJB110}	AGACAAATTGT	CAAATGAGTC	AaACCAAAAG	TATGGTAAAA	CTTGTTTTTT
msa128189.2{6_1169NT}	AGACAAATTGT	CAAATGAGTC	AaACCAAAAG	TATGGTAAAA	CTTGTTTTTT
Consensus	*****	*****	*-*****	*****	*****
msa128189.2{6_18RS21}	ATTTTAAGGA	CGGGTTAAAA	AGGACATTTT	ACTATGATTT	TAAAGAAGAA
msa128189.2{6_2603}	ATTTTAAGGA	CGGGTTAAAA	AGGACATTTT	ACTATGATTT	TAAAGAAGAA
msa128189.2{6_A909}	ATTTTAAGGA	CGGGTTAAAA	AGGACATTTT	ACTATGATTT	TAAAGAAGAA
msa128189.2{6_H36B}	ATTTTAAGGA	CGGGTTAAAA	AGGACATTTT	ACTATGATTT	TAAAGAAGAA
msa128189.2{6_JM9130013}	ATTTTAAGGA	CGGGTTAAAA	AGGACATTTT	ACTATGATTT	TAAAGAAGAA
msa128189.2{6_COH1}	ATTTTAAGGA	CGGGTTAAAA	AGGACATTTT	ACTATGATTT	TAAAGAAGAA
msa128189.2{6_M732}	ATTTTAAGGA	CGGGTTAAAA	AGGACATTTT	ACTATGATTT	TAAAGAAGAA
msa128189.2{6_M781}	ATTTTAAGGA	CGGGTTAAAA	AGGACATTTT	ACTATGATTT	TAAAGAAGAA
msa128189.2{6_090}	ATTTTAAGGA	CGGGTTAAAA	AGGACATTTT	ACTATGATTT	TAAAGAAGAA
msa128189.2{6_CJB110}	ATTTTAAGGA	CGGGTTAAAA	AGGACATTTT	ACTATGATTT	TAAAGAAGAA
msa128189.2{6_1169NT}	ATTTTAAGGA	CGGGTTAAAA	AGGACATTTT	ACTATGATTT	TAAAGAAGAA
Consensus	*****	*****	*****	*****	*****
msa128189.2{6_18RS21}	ACT---				
msa128189.2{6_2603}	ACTtaa				
msa128189.2{6_A909}	ACT---				
msa128189.2{6_H36B}	ACT---				
msa128189.2{6_JM9130013}	ACT---				
msa128189.2{6_COH1}	ACT---				
msa128189.2{6_M732}	ACT---				
msa128189.2{6_M781}	ACT---				
msa128189.2{6_090}	ACT---				
msa128189.2{6_CJB110}	ACT---				
msa128189.2{6_1169NT}	ACT---				
Consensus	*****				

SEQ ID NO. 8212

STRAIN 2603 frame: 1

MKNLLKCKDKKVKAFITLLECLVALVTITGALLVYQGLTKLLAQQIVVMSSSSQSEWVLL
 TQQLNAEFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNC

Table 82: Comparative Sequences relating to SAG0165

QMSQTKSMVKLVFYFKDGLKRTFYDFKEET.

SEQ ID NO. 8213

STRAIN 090 frame: 3

FEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNCQMSQTKS
MVKLVFYFKDGLKRTFYDFKEET

SEQ ID NO. 8214

STRAIN A909 frame: 3

EFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNCQMSQTK
SMVKLVFYFKDGLKRTFYDFKEET

SEQ ID NO. 8215

STRAIN H36B frame: 3

AEFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNCQMSQT
KSMVKLVFYFKDGLKRTFYDFKEET

SEQ ID NO. 8216

STRAIN 18RS21 frame: 2

EFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNCQMSQTK
SMVKLVFYFKDGLKRTFYDFKEET

SEQ ID NO. 8217

STRAIN M732 frame: 3

EFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYNGRGYQPMVYGLDNCQMSQTK
SMVKLVFYFKDGLKRTFYDFKEET

SEQ ID NO. 8218

STRAIN COH1 frame: 1

EFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYNGRGYQPMVYGLDNCQMSQTK
SMVKLVFYFKDGLKRTFYDFKEET

SEQ ID NO. 8219

STRAIN M781 frame: 2

EFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYNGRGYQPMVYGLDNCQMSQTK
SMVKLVFYFKDGLKRTFYDFKEET

SEQ ID NO. 8220

STRAIN CJB110 frame: 1

EFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNCQMSQTK
SMVKLVFYFKDGLKRTFYDFKEET

SEQ ID NO. 8221

STRAIN 1169NT frame: 3

EGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNCQMSQTKSM
VKLVFYFKDGLKRTFYDFKEET

SEQ ID NO. 8222

STRAIN JM9130013 frame: 2

AEFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNCQMSQT
KSMVKLVFYFKDGLKRTFYDFKEET

PRETTY of: /biotmp/msa128319.2{*} February 7, 2003 08:27 ..

	1				50
msa128319.2{6_090}	-----	-----	-----	-----	-----
msa128319.2{6_1169NT}	-----	-----	-----	-----	-----
msa128319.2{6_18RS21}	-----	-----	-----	-----	-----
msa128319.2{6_2603}	mknlllkckd	kkvkaftlle	clvalvtitg	allvyqgltk	llaqqivvms
msa128319.2{6_H36B}	-----	-----	-----	-----	-----
msa128319.2{6_JM9130013}	-----	-----	-----	-----	-----
msa128319.2{6_A909}	-----	-----	-----	-----	-----
msa128319.2{6_CJB110}	-----	-----	-----	-----	-----
msa128319.2{6_COH1}	-----	-----	-----	-----	-----
msa128319.2{6_M732}	-----	-----	-----	-----	-----
msa128319.2{6_M781}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	51				100
msa128319.2{6_090}	-----	-----fEG	AHLEYLRQNK	LYLRKQDKIV	TFGKSNKDDF
msa128319.2{6_1169NT}	-----	-----EG	AHLEYLRQNK	LYLRKQDKIV	TFGKSNKDDF
msa128319.2{6_18RS21}	-----	-----EfEG	AHLEYLRQNK	LYLRKQDKIV	TFGKSNKDDF
msa128319.2{6_2603}	sssqsewvll	tqqlnAEfEG	AHLEYLRQNK	LYLRKQDKIV	TFGKSNKDDF
msa128319.2{6_H36B}	-----	-----AEfEG	AHLEYLRQNK	LYLRKQDKIV	TFGKSNKDDF
msa128319.2{6_JM9130013}	-----	-----AEfEG	AHLEYLRQNK	LYLRKQDKIV	TFGKSNKDDF
msa128319.2{6_A909}	-----	-----EfEG	AHLEYLRQNK	LYLRKQDKIV	TFGKSNKDDF
msa128319.2{6_CJB110}	-----	-----EfEG	AHLEYLRQNK	LYLRKQDKIV	TFGKSNKDDF
msa128319.2{6_COH1}	-----	-----EfEG	AHLEYLRQNK	LYLRKQDKIV	TFGKSNKDDF
msa128319.2{6_M732}	-----	-----EfEG	AHLEYLRQNK	LYLRKQDKIV	TFGKSNKDDF
msa128319.2{6_M781}	-----	-----EfEG	AHLEYLRQNK	LYLRKQDKIV	TFGKSNKDDF
Consensus	*****	*****-*	*****	*****	*****

Table 82: Comparative Sequences relating to SAG0165

	101			150
msa128319.2{6_090}	RKTGYdGRGY	QPMVYGLDNC	QMSQTKSMVK	LVFYFKDGLK RTFYDFKEE
msa128319.2{6_1169NT}	RKTGYdGRGY	QPMVYGLDNC	QMSQTKSMVK	LVFYFKDGLK RTFYDFKEE
msa128319.2{6_18RS21}	RKTGYdGRGY	QPMVYGLDNC	QMSQTKSMVK	LVFYFKDGLK RTFYDFKEE
msa128319.2{6_2603}	RKTGYdGRGY	QPMVYGLDNC	QMSQTKSMVK	LVFYFKDGLK RTFYDFKEE
msa128319.2{6_H36B}	RKTGYdGRGY	QPMVYGLDNC	QMSQTKSMVK	LVFYFKDGLK RTFYDFKEE
msa128319.2{6_JM9130013}	RKTGYdGRGY	QPMVYGLDNC	QMSQTKSMVK	LVFYFKDGLK RTFYDFKEE
msa128319.2{6_A909}	RKTGYdGRGY	QPMVYGLDNC	QMSQTKSMVK	LVFYFKDGLK RTFYDFKEE
msa128319.2{6_CJB110}	RKTGYdGRGY	QPMVYGLDNC	QMSQTKSMVK	LVFYFKDGLK RTFYDFKEE
msa128319.2{6_COH1}	RKTGYnGRGY	QPMVYGLDNC	QMSQTKSMVK	LVFYFKDGLK RTFYDFKEE
msa128319.2{6_M732}	RKTGYnGRGY	QPMVYGLDNC	QMSQTKSMVK	LVFYFKDGLK RTFYDFKEE
msa128319.2{6_M781}	RKTGYnGRGY	QPMVYGLDNC	QMSQTKSMVK	LVFYFKDGLK RTFYDFKEE
Consensus	*****	*****	*****	*****
	151			
msa128319.2{6_090}	T~			
msa128319.2{6_1169NT}	T~			
msa128319.2{6_18RS21}	T~			
msa128319.2{6_2603}	T~			
msa128319.2{6_H36B}	T~			
msa128319.2{6_JM9130013}	T~			
msa128319.2{6_A909}	T~			
msa128319.2{6_CJB110}	T~			
msa128319.2{6_COH1}	T~			
msa128319.2{6_M732}	T~			
msa128319.2{6_M781}	T~			
Consensus	**			

Table 83: Comparative Sequences relating to SAG0108

SEQ ID NO. 8301

STRAIN 2603

atgaaaaagattcgattatcaaagtttattaaaaatgattggttatttttgttttttaatt
 agtgtagcagctagttttttttttccacgttgcccaagttcgagatgataaatccttt
 atttcaaagtgtcaacgttaagcctggaactctttatatgcttatgataaatcctttgat
 aagctattaaagcaaaaaatagaaatgacaaacaaaaatataaagcaagttgcttggtat
 gttcctgctgttaagaaaactcataagacagctgttgtcgttcatggttttgcaatagc
 aaagagaatatgaaggcatatggttggctgtttcataagttaggatacaatgttcttatg
 cctgacaatattgcacatggtgaaagtcatgggcagttgtaggctatggctggaacgac
 cgcgagaacattatcaaattggacagaaatgatagttgataagaatccatcaagccaaatt
 acttttatttgggtgtttcaatgggtggagcaacagtcagtgatggctagtggtgaaaaatta
 cctagtcaggttggtaatatcattgaagattgagggttattctagtggttgggatgaatta
 aaatttcagggttaagagatgtatggtttaccagccttcccactcttatatgaagtttca
 acaatttctaaaatcagagcaggttttctgtaggacaagcaagtagtgtagaacaattg
 aaaaagaataatttaccagcctcttttatctggtgataaggataattttgttccaaca
 agtatggtttatgacaactataaagctacagcaggttaagaaagagcttttatattgtaaaa
 ggggcaaacatgcgaaatcttttgaaacagagccagaaaaatattgagaaacgtatctct
 agttttttgaaaaaatatgaaaaa

SEQ ID NO. 8302

STRAIN 090

GCTAGTTTTTATTTTTTCCACGTTGCCCAAGTTTCG
 AGATGATAAATCCTTTATTTCAAATGGTCAACGTAAGCCTGGAACTCTT
 TATATGCTTATGATAAATCCTTTGATAAGCTATTAAGCAAAAAATAGAA
 ATGACAAACCAAAATATAAAGCAAGTTGCTTGGTATGTTCTGCTGCTAA
 GAAACTCATAAGACAGCTGTTGTCTGTTTATGGTATGCGAATAGCAAAG
 AGAATATGAAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTT
 cTTATGCTGACAAATATTGCACATGGTGAAGTCAATGGGCAGTTGATAGG
 CTATGGCTGGAACGACCGCGAGAACATTATCAATGGACAGAAATGATAG
 TTGATAAGAATCCATCAAGCCAAATTACTTTaTTTGGTGTTCATGGGT
 GGAGCAACAGTCATGATGGCTAGTGGTGAAGAAATTACCTAGTCAGGTTGT
 TAATATCATTGAAGATTGCGGTTATTCTAGTGTTCGGATGAATFAAAT
 TTCAGGCTAAAGAGATGTATGGTTTACCAGCCTTCCCACTCTTATATGAA
 GTTTCACAATTTCTAAAATCAGAGCAGGTTTTTCGTATGGACAAGCAAG
 TAGTGTCGAACAATTGAAAAGAATAATTACCAGCCCTCTTTATTCATG
 GTGATAAGGATAATTTTGTTCACAAGTATGGTTTATGACAACTATAAA
 GCTACAGCAGGTAAGAAAGAGCTTTATATTGTAAAAGGGGCAAAACATGC
 GAAATCTTTTGAACAGAGCCAGAAAAATATGAGAAACGTATCTCTAGTT
 TTTTGAAGAAATATGAAAAA

SEQ ID NO. 8303

STRAIN A909

AATCCTTTATTTCAAATGGTCAACGTAAGCCTGGAACTCTTTATATGCT
 TATGATAAATCCTTTGATAAGCTATTAAGCAAAAAATAGAAATGACAAA
 CCAAAATATAAAGCAAGTTGCTTGGTATGTTCTGCTGCTAAGAAAACTC
 ATAAGACAGCTGTTGTCTGTTTATGGTATGCGAATAGCAAAGAGAAATATG
 AAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTTCTTATGCC
 TGACAACATTGCACATGGTGAAAGTCATGGGCAGTTGATAGGCTATGGCT
 GGAACGACCGCGAGAACATTATCAAATGGACAGAAATGATAGTTGATAAG
 AATTTCATCAAGCCAAATTACTTTATTTGGTGTTCATGGGTGGAGCAAC
 AGTCATGATGGCTAGTGGTGAAGAAATTACCTAGTCAGGTTGTTAATATCA
 TTGAAGATGCGGTTATTCTGGTGTTCGGATGAATFAAATTTTCAAGCT
 AAAGAGATGTATGGTTTACCAGCCTTCCCACTCTTATATGAAGTTTCAAC
 AATTTCTAAAATCAGAGCAGGTTTTTCGTATGGACAAGCAAGTAGTGTCTG
 AACAAATTGAAAAGAATAATTACCAGCCCTCTTTATTCATGGTGATAAG
 GATAATTTTGTTCACAAGTATGGTTTATGACAACTATAAGCTACAGC
 AGGTAAGAAAGAGCTTTATATTGTAAAAGGGGCAAAACATGCGAAATCTT
 TTGAAGCAGAGCCAGAAAAATATGAGAAACGTATCTCTAGTTTTTTGAAA
 AAATATGAAAAA

SEQ ID NO. 8304

STRAIN H36B

AGTTTTTATTTTTTCCACGTTGCCCAAGTTTCGAGATGATAAATCCTTTAT
 TTCAAATGGTCAACGTAAGCCTGGAACTCTTTATATGCTTATGATAAAT
 CCTTTGATAAGCTATTAAGCAAAAAATAGAAATGACAAACCAAAATATA
 AAGCAAGTTGCTTGGTATGTTCTGCTGCTAAGAAAACTCATAAGACAGC
 TGTTGTCTGTTTATGGTATGCGAATAGCAAAGAGAAATATGAAGGCATATG
 GTTGGCTGTTTCATAAGTTAGGATACAATGTTCTTATGCCTGACAACATT
 GCACATGGTGAAAGTCATGGGCAGTTGATAGGCTATGGCTGGAACGACCG
 CGAGAACATTATCAAATGGACAGAAATGATAGTTGATAAGAAATTCATCAA
 GCCAAATTACTTTATTTGGTGTTCATGGGTGGAGCAACAGTCATGATG
 GCTAGTGGTGAAAAATTACCTAGTCAGGTTGTTAATATCATTGAAGATTG
 CGGTTATTCTGGTGTTCGGATGAATFAAATTTTCAAGGCTAAAGAGATGT
 ATGGTTTACCAGCCTTCCCACTCTTATATGAAGTTTCAACAATTTCTAAA
 ATCAGAGCAGGTTTTTCGTATGGACAAGCAAGTAGTGTGCAACAATTGAA
 AAAGAATAATTTACCAGCCCTCTTTATTCATGGTGATAAGGATAATTTTG
 TTCCAACAAGTATGGTTTATGACAACTATAAGCTACAGCAGGTAAGAAA
 GAGCTTTATATTGTAAAAGGGGCAAAACATGCGAAATCTTTTGAACAGA
 GCCAGAAAAATATGAGAAACGTATCTCTAGTTTTTTGAAAAATATGAAA
 AA

SEQ ID NO. 8305

STRAIN 18RS21

Table 83: Comparative Sequences relating to SAG0108

GCTAGTTTTTATTTTTTCCACGTTGCCCAAGTTCGA
 GATGATAAATCCTTTATTTCAAATGGTCAACGTAAGCCTGGAAACTCTTT
 ATATGCTTATGATAAATCCTTTGATAAGCTATTAAAGCAAAAAATAGAAA
 TGACAAACCAAAATATAAAGCAAGTTGCTTGGTATGTTCCCTGCTGTTAAG
 AAAACTCATAAGACAGCTGTTGTCTGTTTTCATGGTTTTGCGAATAGCAAAGA
 GAATATGAAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTTT
 TTATGCCTGACAATATTGCACATGGTGAAGTCATGGGCAGTTGATAGGC
 TATGGCTGGAACGACCGCGAGAACATTATCAAATGGACAGAAATGATAGT
 TGATAAGAATCCATCAAGCCAAATTACTTTATTTGGTGTTCATGGGTG
 GAGCAACAGTCATGATGGCTAGTGGTGAATAATTACCTAGTCAGGTTGTT
 AATATCATTGAAGATTGCGGTTATTCTAGTGTGGGATGAATTAATAAT
 TCAGGCTAAAGAGATGTATGGTTTACCAGCCTTCCCACTCTTATATGAAG
 TTTCAACAATTTCTAAATCAGAGCAGGTTTTTCGTATGGACAAGCAAGT
 AGTGTGGAACAATTGAAAAAGAATAATTTACCAGCCCTCTTTATTCATGG
 TGATAAGGATAATTTTGTTCACAAGTATGGTTTATGACAACTATAAAG
 CTACAGCAGGTAAGAAAGAGCTTTATATTGTAAAAGGGGCAAAACATGCC
 AATCTTTTGAAGCAGAGCCAGAAAAATATGAGAAACGTATCTCTAGTTT
 TTTGAAAAAATATGAAAAA

SEQ ID NO. 8306**STRAIN M732**

GCTAGTTTTTATTTTTTCCACGTTGCCCAAGTTCGA
 GATGATAAATCCTTTATTTCAAATGGTCAACGTAAGCCTGGAAACTCTTT
 ATATGCTTATGATAAATCCTTTGATAAGCTATTAAAGCAAAAAATAGAAA
 TGACAAACCAAAATATAAAGCAAGTTGCTTGGTATGTTCCCTGCTGCTAAG
 AAAACTCATAAGACAGTTGTTGTCTGTTTTCATGGTTTTGCGAATAGCAAAGA
 GAATATGAAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTTT
 TTATGCCTGACAACATTGCACATGGTGAAGTCATGGGCAGTTGATAGGC
 TATGGCTGGAACGACCGCGAGAACATTATCAAATGGACAGAAATGATAGT
 GGATAAGAATCCATCAAGCCAAATTACTTTATTTGGTGTTCATGGGTG
 GAGCAACAGTCATGATGGCTAGTGGTGAATAATTACCTAGTCAGGTTGTT
 AATATCATTGAAGATTGTGGTTATTCTAGTGTGGGATGAATTAATAAT
 TCAGGCTAAAGAGATGTATGGTTTACCAGCCTTCCCACTCTTATATGAAG
 TTTCAACAATTTCTAAATCAGAGCAGGTTTTTCGTATGGACAAGCAAGT
 AGTGTGGAACAATTGAAAAAGAATAATTTACCAGCCCTCTTTATTCATGG
 TGATAAGGATAATTTTGTTCACAAGTATGGTTTATGACAACTATAAAG
 CTACAGCAGGTAAGAAAGAGCTTTATATTGTAAAAGGGGCAAAACATGCC
 AATCTTTTGAAGCAGAGCCAGAAAAATATGAGAAACGTATCTCTAGTTT
 TTTGAAAAAATATGAAAAA

SEQ ID NO. 8307**STRAIN COH1**

GCTAGTTTTTATTTTTTCCACGTTGCCCAAGTTC
 GAGATGATAAATCCTTTATTTCAAATGGTCAACGTAAGCCTGGAAACTCT
 TTATATGCTTATGATAAATCCTTTGATAAGCTATTAAAGCAAAAAATAGA
 AATGaCAAAACCAAAATATAAAGCAAGTTGCTTGGTATGTTCCCTGCTGCTA
 AGAAAACTCATAAGACAGTTGTTGTCTGTTTTCATGGTTTTGCGAATAGCAA
 GAGAATATGAAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGT
 TCTTATGCCTGACAACATTGCACATGGTGAAGTCATGGGCAGTTGATAG
 GCTATGGCTGGAACGACCGCGAGAACATTATCAAATGGACAGAAATGATA
 GTGGATAAGAATCCATCAAGCCAAATTACTTTATTTGGTGTTCATGGGTG
 TGGAGCAACAGTCATGATGGCTAGTGGTGAATAATTACCTAGTCAGGTTG
 TTAATATCATTGAAGATTGTGGTTATTCTAGTGTGGGATGAATTAATAA
 TTTTCAGGCTAAAGAGATGTATGGTTTACCAGCCTTCCCACTCTTATATGA
 AGTTTCAACAATTTCTAAATCAGAGCAGGTTTTTCGTATGGACAAGCAA
 GTAGTGTGGAACAATTGAAAAAGAATAATTTACCAGCCCTCTTTATTCAT
 GGTGATAAGGATAATTTGTTCACAAGTATGGTTTATGACAACTATAA
 AGCTACAGCAGGTAAGAAAGAGCTTTATATTGTAAAAGGGGCAAAACATG
 CGAAATCTTTTGAAGCAGAGCCAGAAAAATATGAGAAACGTATCTCTAGT
 TTTTGAAAAAAATATGAAAAA

SEQ ID NO. 8308**STRAIN M781**

GCTAGTTTTTATTTTTTCCACGTTGCCCAAGTTCG
 AGATGATAAATCCTTTATTTCAAATGGTCAACGTAAGCCTGGAAACTCTT
 TATATGCTTATGATAAATCCTTTGATAAGCTATTAAAGCAAAAAATAGAA
 ATGACAAACCAAAATATAAAGCAAGTTGCTTGGTATGTTCCCTGCTGCTAA
 GAAAACTCATAAGACAGTTGTTGTCTGTTTTCATGGTTTTGCGAATAGCAAAG
 AGAATATGAAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTT
 CTTATGCCTGACAACATTGCACATGGTGAAGTCATGGGCAGTTGATAGG
 CTATGGCTGGAACGACCGCGAGAACATTATCAAATGGACAGAAATGATAG
 TGGATAAGAATCCATCAAGCCAAATTACTTTATTTGGTGTTCATGGGTG
 GGAGCAACAGTCATGATGGCTAGTGGTGAATAATTACCTAGTCAGGTTGT
 TAATATCATTGAAGATTGTGGTTATTCTAGTGTGGGATGAATTAATAA
 TTTTCAGGCTAAAGAGATGTATGGTTTACCAGCCTTCCCACTCTTATATGA
 TTTTCAGGCTAAAGAGATGTATGGTTTACCAGCCTTCCCACTCTTATATGA
 GTTTCAACAATTTCTAAATCAGAGCAGGTTTTTCGTATGGACAAGCAA
 GTAGTGTGGAACAATTGAAAAAGAATAATTTACCAGCCCTCTTTATTCAT
 GGTGATAAGGATAATTTGTTCACAAGTATGGTTTATGACAACTATAA
 AGCTACAGCAGGTAAGAAAGAGCTTTATATTGTAAAAGGGGCAAAACATG
 CGAAATCTTTTGAAGCAGAGCCAGAAAAATATGAGAAACGTATCTCTAGT
 TTTTGAAAAAAATATGAAAAA

SEQ ID NO. 8309

Table 83: Comparative Sequences relating to SAG0108

STRAIN CJB110

GCTAGTTTTTATTTTTTCCACGTTGCCCAAGTTTCGAG
 ATGATAAATCCTTTATTTCAAATGGTCAACGTAAGCCTGGAAACTCTTTA
 TATGCTTATGATAAATCCTTTGATAAGCTATTAAAGCAAAAAATAGAAAT
 GACAAACCAAAATATAAAGCAAGTTGCTTGGTATGTTCTGCTGCTAAGA
 AAACCTCATAAGACAGCTGTTGTCGTTTCATGGTTTTGCGAATAGCAAAGAG
 AATATGAAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTTcT
 TATGCCCTGACAATATTGCACATGGTGAAAGTCATGGGCAGTTGATAGGCT
 ATGGCTGGAACGACCGCGAGAACATTATCAAATGGACAGAAATGATAGTT
 GATAAGAATCCATCAAGCCAAATTACTTTATTTGGTGTTCATGGGTGG
 AGCAACAGTCATGATGGCTAGTGGTGAAAAATTACCTAGTCAGGTTGTTA
 ATATCATTGAAGATTGCGGTTATTcTAGTGTGTTGGGATgAATTAAAATTT
 CAGGCTAAAGAGATGTATGGTTTACCAGCCTTCCCACTCTTATATGAAGT
 TTCAACAATTTCTAAAATCAGAGCAGGTTTTTCGTATGGACAAGCAAGTA
 gTGTGCAACAATTGAAAAAGAATAATTTACCAGCCCTcTTTATTTCATGGT
 GATAAGGATAAATTTTGTTCACAAGTATGGTTTATGACAACATATAAAGC
 TACAGCAGGTAAGAAAGAGCTTTATATTGTAAAAGGGGCAAAACATGCGA
 AATCTTTTGAAACAGAGCCAGAAAAATATGAGAAACGTATCTCTAGTTT
 TTGAAAAAATATGAAAAA

SEQ ID NO. 8310

STRAIN 1169NT

GCTAGTTTTTATTTTTTCCACGTTGCCCAAGTTTCGA
 GATGATAAATCCTTTATTTCAAATGGTCAACGTAAGCCTGGAAACTCTTT
 ATATGCTTATGATAAATCCTTTGATAAGCTATTAAAGCAAAAAATAGAAA
 TGACAAACCcAAATATAAAGCAAGTTGCTTGGTATGTTCTGCTGCTAAG
 AAAACTCATAAGACAGCTGTTGTCGTTTCATGGTTTTGCGAATAGCAAAGA
 gAATATGAAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTTc
 TTATACCTGACAATATTGCACATGGTGAAAGTCATGGGCAGTTGATAGGC
 TATGGCTGGAACGACCGCGAGAACATTATCAAATGGACAGAAATGATAGT
 TGATAAGAATCCATCAAGCCAAATTACTTTATTTGGTGTTCATGGGTG
 GAGCAACAGTCATGATGGCTAGTGGTGAAAAATTACCTAGTCAGGTTGTT
 AATATCATTGAAGATTgCGGTTATTcTAGTGTGTTGGGATgAATTAAAAT
 TCAGGCTAaAGAGATGTATGGTTTACCAGCCTTCCCACTcTTATATGAAG
 TTTCAACAATTTCTAAAATCAGAGCAGGTTTTTCGTATGGACAAGCAAGT
 AGTGTAGAACAATTGAAAAAGAATAATTTACCAGCCCTCTTTATTTCATGG
 TGATAAGGATAAATTTGTTCACAAGTATGGTTTATGACAACATATAAAG
 CTACAGCAGGTAAGAAAGAGCTTTATATTGTAAAAGGGGCAAAACATGCG
 AAATCTTTTGAAcCAGAGCCAGAAAAATATGAGAAACGTATCTCTAGTTT
 TTTGAAAAAATATGAAAAA

SEQ ID NO. 8311

STRAIN JM9130013

GCTAGTTTTTATTTTTTCCACGTTGCCCAAGTTTCG
 AGATGATAAATCCTTTATTTCAAATGGTCAACGTAAGCCTGGAAACTCTT
 TATATGCTTATGATAAATCCTTTGATAAGCTATTAAAGCAAAAAATAGAA
 ATGaCAAACCAAAATATAAAGCAAGTTGCTTGGTATGTTCTGCTGTTAA
 GAAAACTCATAAGACAGCTGTTGTCGTTTCATGGTTTTGCGAATAGCAAAG
 AGAATATGAAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTT
 CTTATGCCTGACAATATGCACATGGTGAAAGTCATGGGCAGTTGATAGG
 CTATGGCTGGAACGACCGCGAGAACATTATCaAATGGACAGAAATGATAG
 TTGATAAGAATCCATCAAGCCAAATTaCTTTATTTGGTGTTCATGGGT
 GGAGCAACAGTCATGATGGCTAGTGGTGAAAAATTACCTAGTCAGGTTGT
 TAATATCATTGAAGATTGCGGTTATTcTAGTGTGTTGGGATgAATTAAAAT
 TTCAGGCTAAAGAGATGTATGGTTTACCAGCCTTCCCACTCTTATATGAA
 GTTTCAACAATTTCTAAAATCAGAGCAGGTTTTTCGTATGGACAAGCAAG
 TAGTGTGCAACAATTGAAAAAGAATAATTTACCAGCCCTCTTTATTTCATG
 GTGATAAGGATAAATTTGTTCACAAGTATGGTTTATGACAACATATAAA
 GCTACAGCAGGTAAGAAAGAGCTTTATATTGTAAAAGGGGCAAAACATGC
 GAAATCTTTTGAAACAGAGCCAGAAAAATATGAGAAACGTATCTCTAGTT
 TTTTGAAAAAATATGAAAAA

PRETTY of: /biotmp/msa286608.2{*} February 24, 2003 06:26 ..

	1				50
msa286608.2{662_COH1}	-----	-----	-----	-----	-----
msa286608.2{662_M732}	-----	-----	-----	-----	-----
msa286608.2{662_M781}	-----	-----	-----	-----	-----
msa286608.2{662_A909}	-----	-----	-----	-----	-----
msa286608.2{662_H36B}	-----	-----	-----	-----	-----
msa286608.2{662_090}	-----	-----	-----	-----	-----
msa286608.2{662_CJB110}	-----	-----	-----	-----	-----
msa286608.2{662_18RS21}	-----	-----	-----	-----	-----
msa286608.2{662_2603}	atgaaaaaga	ttcgattatc	aaagtttatt	aaaatgattg	ttgttatatt
msa286608.2{662_JM9130013}	-----	-----	-----	-----	-----
msa286608.2{662_1169NT}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	51				100
msa286608.2{662_COH1}	-----g	ctagttttta	ttttttccac	gttgccccag	
msa286608.2{662_M732}	-----g	ctagttttta	ttttttccac	gttgccccag	
msa286608.2{662_M781}	-----g	ctagttttta	ttttttccac	gttgccccag	

Table 83: Comparative Sequences relating to SAG0108

msa286608.2{662_A909}	-----	-----	-----	-----	-----
msa286608.2{662_H36B}	-----	-----	--agtttttta	ttttttccac	gttgccccaaag
msa286608.2{662_090}	-----	-----	ctagtttttta	ttttttccac	gttgccccaaag
msa286608.2{662_CJB110}	-----	-----	ctagtttttta	ttttttccac	gttgccccaaag
msa286608.2{662_18RS21}	-----	-----	ctagtttttta	ttttttccac	gttgccccaaag
msa286608.2{662_2603}	gttttttaatt	agtgtagcag	ctagtttttta	ttttttccac	gttgccccaaag
msa286608.2{662_JM9130013}	-----	-----	ctagtttttta	ttttttccac	gttgccccaaag
msa286608.2{662_1169NT}	-----	-----	ctagtttttta	ttttttccac	gttgccccaaag
Consensus	*****	*****	-----	-----	-----
101					
msa286608.2{662_COH1}	ttcgagatga	taAATCCTTT	ATTTCAAATG	GTCAACGTAA	GCCTGGAAAC
msa286608.2{662_M732}	ttcgagatga	taAATCCTTT	ATTTCAAATG	GTCAACGTAA	GCCTGGAAAC
msa286608.2{662_M781}	ttcgagatga	taAATCCTTT	ATTTCAAATG	GTCAACGTAA	GCCTGGAAAC
msa286608.2{662_A909}	-----	--AATCCTTT	ATTTCAAATG	GTCAACGTAA	GCCTGGAAAC
msa286608.2{662_H36B}	ttcgagatga	taAATCCTTT	ATTTCAAATG	GTCAACGTAA	GCCTGGAAAC
msa286608.2{662_090}	ttcgagatga	taAATCCTTT	ATTTCAAATG	GTCAACGTAA	GCCTGGAAAC
msa286608.2{662_CJB110}	ttcgagatga	taAATCCTTT	ATTTCAAATG	GTCAACGTAA	GCCTGGAAAC
msa286608.2{662_18RS21}	ttcgagatga	taAATCCTTT	ATTTCAAATG	GTCAACGTAA	GCCTGGAAAC
msa286608.2{662_2603}	ttcgagatga	taAATCCTTT	ATTTCAAATG	GTCAACGTAA	GCCTGGAAAC
msa286608.2{662_JM9130013}	ttcgagatga	taAATCCTTT	ATTTCAAATG	GTCAACGTAA	GCCTGGAAAC
msa286608.2{662_1169NT}	ttcgagatga	taAATCCTTT	ATTTCAAATG	GTCAACGTAA	GCCTGGAAAC
Consensus	-----	-----	*****	*****	*****
151					
msa286608.2{662_COH1}	TCCTTTATATG	CTTATGATAA	ATCCTTTGAT	AAGCTATTAA	AGCAAAAAAT
msa286608.2{662_M732}	TCCTTTATATG	CTTATGATAA	ATCCTTTGAT	AAGCTATTAA	AGCAAAAAAT
msa286608.2{662_M781}	TCCTTTATATG	CTTATGATAA	ATCCTTTGAT	AAGCTATTAA	AGCAAAAAAT
msa286608.2{662_A909}	TCCTTTATATG	CTTATGATAA	ATCCTTTGAT	AAGCTATTAA	AGCAAAAAAT
msa286608.2{662_H36B}	TCCTTTATATG	CTTATGATAA	ATCCTTTGAT	AAGCTATTAA	AGCAAAAAAT
msa286608.2{662_090}	TCCTTTATATG	CTTATGATAA	ATCCTTTGAT	AAGCTATTAA	AGCAAAAAAT
msa286608.2{662_CJB110}	TCCTTTATATG	CTTATGATAA	ATCCTTTGAT	AAGCTATTAA	AGCAAAAAAT
msa286608.2{662_18RS21}	TCCTTTATATG	CTTATGATAA	ATCCTTTGAT	AAGCTATTAA	AGCAAAAAAT
msa286608.2{662_2603}	TCCTTTATATG	CTTATGATAA	ATCCTTTGAT	AAGCTATTAA	AGCAAAAAAT
msa286608.2{662_JM9130013}	TCCTTTATATG	CTTATGATAA	ATCCTTTGAT	AAGCTATTAA	AGCAAAAAAT
msa286608.2{662_1169NT}	TCCTTTATATG	CTTATGATAA	ATCCTTTGAT	AAGCTATTAA	AGCAAAAAAT
Consensus	*****	*****	*****	*****	*****
201					
msa286608.2{662_COH1}	AGAAATGACA	AACCAAAATA	TAAAGCAAGT	TGCTTGGTAT	GTTCTGCTG
msa286608.2{662_M732}	AGAAATGACA	AACCAAAATA	TAAAGCAAGT	TGCTTGGTAT	GTTCTGCTG
msa286608.2{662_M781}	AGAAATGACA	AACCAAAATA	TAAAGCAAGT	TGCTTGGTAT	GTTCTGCTG
msa286608.2{662_A909}	AGAAATGACA	AACCAAAATA	TAAAGCAAGT	TGCTTGGTAT	GTTCTGCTG
msa286608.2{662_H36B}	AGAAATGACA	AACCAAAATA	TAAAGCAAGT	TGCTTGGTAT	GTTCTGCTG
msa286608.2{662_090}	AGAAATGACA	AACCAAAATA	TAAAGCAAGT	TGCTTGGTAT	GTTCTGCTG
msa286608.2{662_CJB110}	AGAAATGACA	AACCAAAATA	TAAAGCAAGT	TGCTTGGTAT	GTTCTGCTG
msa286608.2{662_18RS21}	AGAAATGACA	AACCAAAATA	TAAAGCAAGT	TGCTTGGTAT	GTTCTGCTG
msa286608.2{662_2603}	AGAAATGACA	AACCAAAATA	TAAAGCAAGT	TGCTTGGTAT	GTTCTGCTG
msa286608.2{662_JM9130013}	AGAAATGACA	AACCAAAATA	TAAAGCAAGT	TGCTTGGTAT	GTTCTGCTG
msa286608.2{662_1169NT}	AGAAATGACA	AACCAAAATA	TAAAGCAAGT	TGCTTGGTAT	GTTCTGCTG
Consensus	*****	*****	*****	*****	*****
251					
msa286608.2{662_COH1}	cTAAGAAAAC	TCATAAGACA	GtTGTGTGCG	TTCATGGTTT	TGCGAATAGC
msa286608.2{662_M732}	cTAAGAAAAC	TCATAAGACA	GtTGTGTGCG	TTCATGGTTT	TGCGAATAGC
msa286608.2{662_M781}	cTAAGAAAAC	TCATAAGACA	GtTGTGTGCG	TTCATGGTTT	TGCGAATAGC
msa286608.2{662_A909}	cTAAGAAAAC	TCATAAGACA	GtTGTGTGCG	TTCATGGTTT	TGCGAATAGC
msa286608.2{662_H36B}	cTAAGAAAAC	TCATAAGACA	GtTGTGTGCG	TTCATGGTTT	TGCGAATAGC
msa286608.2{662_090}	cTAAGAAAAC	TCATAAGACA	GtTGTGTGCG	TTCATGGTTT	TGCGAATAGC
msa286608.2{662_CJB110}	cTAAGAAAAC	TCATAAGACA	GtTGTGTGCG	TTCATGGTTT	TGCGAATAGC
msa286608.2{662_18RS21}	tTAAGAAAAC	TCATAAGACA	GtTGTGTGCG	TTCATGGTTT	TGCGAATAGC
msa286608.2{662_2603}	tTAAGAAAAC	TCATAAGACA	GtTGTGTGCG	TTCATGGTTT	TGCGAATAGC
msa286608.2{662_JM9130013}	tTAAGAAAAC	TCATAAGACA	GtTGTGTGCG	TTCATGGTTT	TGCGAATAGC
msa286608.2{662_1169NT}	cTAAGAAAAC	TCATAAGACA	GtTGTGTGCG	TTCATGGTTT	TGCGAATAGC
Consensus	-----	*****	*-----	*****	*****
301					
msa286608.2{662_COH1}	AAAGAGAATA	TGAAGGCATA	TGGTTGGCTG	TTTCATAAGT	TAGGATACAA
msa286608.2{662_M732}	AAAGAGAATA	TGAAGGCATA	TGGTTGGCTG	TTTCATAAGT	TAGGATACAA
msa286608.2{662_M781}	AAAGAGAATA	TGAAGGCATA	TGGTTGGCTG	TTTCATAAGT	TAGGATACAA
msa286608.2{662_A909}	AAAGAGAATA	TGAAGGCATA	TGGTTGGCTG	TTTCATAAGT	TAGGATACAA
msa286608.2{662_H36B}	AAAGAGAATA	TGAAGGCATA	TGGTTGGCTG	TTTCATAAGT	TAGGATACAA
msa286608.2{662_090}	AAAGAGAATA	TGAAGGCATA	TGGTTGGCTG	TTTCATAAGT	TAGGATACAA
msa286608.2{662_CJB110}	AAAGAGAATA	TGAAGGCATA	TGGTTGGCTG	TTTCATAAGT	TAGGATACAA
msa286608.2{662_18RS21}	AAAGAGAATA	TGAAGGCATA	TGGTTGGCTG	TTTCATAAGT	TAGGATACAA
msa286608.2{662_2603}	AAAGAGAATA	TGAAGGCATA	TGGTTGGCTG	TTTCATAAGT	TAGGATACAA
msa286608.2{662_JM9130013}	AAAGAGAATA	TGAAGGCATA	TGGTTGGCTG	TTTCATAAGT	TAGGATACAA
msa286608.2{662_1169NT}	AAAGAGAATA	TGAAGGCATA	TGGTTGGCTG	TTTCATAAGT	TAGGATACAA
Consensus	*****	*****	*****	*****	*****
351					
msa286608.2{662_COH1}	TGTTCTTATg	CCTGACAAcA	TTGCACATGG	TGAAAGTCAT	GGGCAGTTGA
msa286608.2{662_M732}	TGTTCTTATg	CCTGACAAcA	TTGCACATGG	TGAAAGTCAT	GGGCAGTTGA

Table 83: Comparative Sequences relating to SAG0108

msa286608.2{662_M781}	TGTTCTTATg	CCTGACAAcA	TTGCACATGG	TGAAAGTCAT	GGGCAGTTGA
msa286608.2{662_A909}	TGTTCTTATg	CCTGACAAcA	TTGCACATGG	TGAAAGTCAT	GGGCAGTTGA
msa286608.2{662_H36B}	TGTTCTTATg	CCTGACAAcA	TTGCACATGG	TGAAAGTCAT	GGGCAGTTGA
msa286608.2{662_090}	TGTTCTTATg	CCTGACAAcA	TTGCACATGG	TGAAAGTCAT	GGGCAGTTGA
msa286608.2{662_CJB110}	TGTTCTTATg	CCTGACAAcA	TTGCACATGG	TGAAAGTCAT	GGGCAGTTGA
msa286608.2{662_18RS21}	TGTTCTTATg	CCTGACAAcA	TTGCACATGG	TGAAAGTCAT	GGGCAGTTGA
msa286608.2{662_2603}	TGTTCTTATg	CCTGACAAcA	TTGCACATGG	TGAAAGTCAT	GGGCAGTTGA
msa286608.2{662_JM9130013}	TGTTCTTATg	CCTGACAAcA	TTGCACATGG	TGAAAGTCAT	GGGCAGTTGA
msa286608.2{662_1169NT}	TGTTCTTATa	CCTGACAAcA	TTGCACATGG	TGAAAGTCAT	GGGCAGTTGA
Consensus	*****-*	*****-*	*****	*****	*****
401					
msa286608.2{662_COH1}	TAGGCTATGG	CTGGAACGAC	CGCGAGAACA	TTATCAAATG	GACAGAAATG
msa286608.2{662_M732}	TAGGCTATGG	CTGGAACGAC	CGCGAGAACA	TTATCAAATG	GACAGAAATG
msa286608.2{662_M781}	TAGGCTATGG	CTGGAACGAC	CGCGAGAACA	TTATCAAATG	GACAGAAATG
msa286608.2{662_A909}	TAGGCTATGG	CTGGAACGAC	CGCGAGAACA	TTATCAAATG	GACAGAAATG
msa286608.2{662_H36B}	TAGGCTATGG	CTGGAACGAC	CGCGAGAACA	TTATCAAATG	GACAGAAATG
msa286608.2{662_090}	TAGGCTATGG	CTGGAACGAC	CGCGAGAACA	TTATCAAATG	GACAGAAATG
msa286608.2{662_CJB110}	TAGGCTATGG	CTGGAACGAC	CGCGAGAACA	TTATCAAATG	GACAGAAATG
msa286608.2{662_18RS21}	TAGGCTATGG	CTGGAACGAC	CGCGAGAACA	TTATCAAATG	GACAGAAATG
msa286608.2{662_2603}	TAGGCTATGG	CTGGAACGAC	CGCGAGAACA	TTATCAAATG	GACAGAAATG
msa286608.2{662_JM9130013}	TAGGCTATGG	CTGGAACGAC	CGCGAGAACA	TTATCAAATG	GACAGAAATG
msa286608.2{662_1169NT}	TAGGCTATGG	CTGGAACGAC	CGCGAGAACA	TTATCAAATG	GACAGAAATG
Consensus	*****	*****	*****	*****	*****
451					
msa286608.2{662_COH1}	ATAGTgGATA	AGAATcCATC	AAGCCAAATT	ACTTTATTTG	GTGTTTCAAT
msa286608.2{662_M732}	ATAGTgGATA	AGAATcCATC	AAGCCAAATT	ACTTTATTTG	GTGTTTCAAT
msa286608.2{662_M781}	ATAGTgGATA	AGAATcCATC	AAGCCAAATT	ACTTTATTTG	GTGTTTCAAT
msa286608.2{662_A909}	ATAGTtGATA	AGAATtCATC	AAGCCAAATT	ACTTTATTTG	GTGTTTCAAT
msa286608.2{662_H36B}	ATAGTtGATA	AGAATtCATC	AAGCCAAATT	ACTTTATTTG	GTGTTTCAAT
msa286608.2{662_090}	ATAGTtGATA	AGAATcCATC	AAGCCAAATT	ACTTTATTTG	GTGTTTCAAT
msa286608.2{662_CJB110}	ATAGTtGATA	AGAATcCATC	AAGCCAAATT	ACTTTATTTG	GTGTTTCAAT
msa286608.2{662_18RS21}	ATAGTtGATA	AGAATcCATC	AAGCCAAATT	ACTTTATTTG	GTGTTTCAAT
msa286608.2{662_2603}	ATAGTtGATA	AGAATcCATC	AAGCCAAATT	ACTTTATTTG	GTGTTTCAAT
msa286608.2{662_JM9130013}	ATAGTtGATA	AGAATcCATC	AAGCCAAATT	ACTTTATTTG	GTGTTTCAAT
msa286608.2{662_1169NT}	ATAGTtGATA	AGAATcCATC	AAGCCAAATT	ACTTTATTTG	GTGTTTCAAT
Consensus	*****-****	*****-****	*****	*****	*****
501					
msa286608.2{662_COH1}	GGGTGGAGCA	ACAGTCATGA	TGGCTAGTGG	TGAAAAATTA	CCTAGTCAGG
msa286608.2{662_M732}	GGGTGGAGCA	ACAGTCATGA	TGGCTAGTGG	TGAAAAATTA	CCTAGTCAGG
msa286608.2{662_M781}	GGGTGGAGCA	ACAGTCATGA	TGGCTAGTGG	TGAAAAATTA	CCTAGTCAGG
msa286608.2{662_A909}	GGGTGGAGCA	ACAGTCATGA	TGGCTAGTGG	TGAAAAATTA	CCTAGTCAGG
msa286608.2{662_H36B}	GGGTGGAGCA	ACAGTCATGA	TGGCTAGTGG	TGAAAAATTA	CCTAGTCAGG
msa286608.2{662_090}	GGGTGGAGCA	ACAGTCATGA	TGGCTAGTGG	TGAAAAATTA	CCTAGTCAGG
msa286608.2{662_CJB110}	GGGTGGAGCA	ACAGTCATGA	TGGCTAGTGG	TGAAAAATTA	CCTAGTCAGG
msa286608.2{662_18RS21}	GGGTGGAGCA	ACAGTCATGA	TGGCTAGTGG	TGAAAAATTA	CCTAGTCAGG
msa286608.2{662_2603}	GGGTGGAGCA	ACAGTCATGA	TGGCTAGTGG	TGAAAAATTA	CCTAGTCAGG
msa286608.2{662_JM9130013}	GGGTGGAGCA	ACAGTCATGA	TGGCTAGTGG	TGAAAAATTA	CCTAGTCAGG
msa286608.2{662_1169NT}	GGGTGGAGCA	ACAGTCATGA	TGGCTAGTGG	TGAAAAATTA	CCTAGTCAGG
Consensus	*****	*****	*****	*****	*****
551					
msa286608.2{662_COH1}	TTGTTAATAT	CATTGAAGAT	TGtGGTTATT	CTaGTGTTTG	GGATGAATTA
msa286608.2{662_M732}	TTGTTAATAT	CATTGAAGAT	TGtGGTTATT	CTaGTGTTTG	GGATGAATTA
msa286608.2{662_M781}	TTGTTAATAT	CATTGAAGAT	TGtGGTTATT	CTaGTGTTTG	GGATGAATTA
msa286608.2{662_A909}	TTGTTAATAT	CATTGAAGAT	TGcGGTTATT	CTgGTGTTTG	GGATGAATTA
msa286608.2{662_H36B}	TTGTTAATAT	CATTGAAGAT	TGcGGTTATT	CTgGTGTTTG	GGATGAATTA
msa286608.2{662_090}	TTGTTAATAT	CATTGAAGAT	TGcGGTTATT	CTaGTGTTTG	GGATGAATTA
msa286608.2{662_CJB110}	TTGTTAATAT	CATTGAAGAT	TGcGGTTATT	CTaGTGTTTG	GGATGAATTA
msa286608.2{662_18RS21}	TTGTTAATAT	CATTGAAGAT	TGcGGTTATT	CTaGTGTTTG	GGATGAATTA
msa286608.2{662_2603}	TTGTTAATAT	CATTGAAGAT	TGcGGTTATT	CTaGTGTTTG	GGATGAATTA
msa286608.2{662_JM9130013}	TTGTTAATAT	CATTGAAGAT	TGcGGTTATT	CTaGTGTTTG	GGATGAATTA
msa286608.2{662_1169NT}	TTGTTAATAT	CATTGAAGAT	TGcGGTTATT	CTaGTGTTTG	GGATGAATTA
Consensus	*****	*****	**--*****	**--*****	*****
601					
msa286608.2{662_COH1}	AAATTTTCAGG	CTAAAGAGAT	GTATGGTTTA	CCAGCCTTCC	CACTCTTATA
msa286608.2{662_M732}	AAATTTTCAGG	CTAAAGAGAT	GTATGGTTTA	CCAGCCTTCC	CACTCTTATA
msa286608.2{662_M781}	AAATTTTCAGG	CTAAAGAGAT	GTATGGTTTA	CCAGCCTTCC	CACTCTTATA
msa286608.2{662_A909}	AAATTTTCAGG	CTAAAGAGAT	GTATGGTTTA	CCAGCCTTCC	CACTCTTATA
msa286608.2{662_H36B}	AAATTTTCAGG	CTAAAGAGAT	GTATGGTTTA	CCAGCCTTCC	CACTCTTATA
msa286608.2{662_090}	AAATTTTCAGG	CTAAAGAGAT	GTATGGTTTA	CCAGCCTTCC	CACTCTTATA
msa286608.2{662_CJB110}	AAATTTTCAGG	CTAAAGAGAT	GTATGGTTTA	CCAGCCTTCC	CACTCTTATA
msa286608.2{662_18RS21}	AAATTTTCAGG	CTAAAGAGAT	GTATGGTTTA	CCAGCCTTCC	CACTCTTATA
msa286608.2{662_2603}	AAATTTTCAGG	CTAAAGAGAT	GTATGGTTTA	CCAGCCTTCC	CACTCTTATA
msa286608.2{662_JM9130013}	AAATTTTCAGG	CTAAAGAGAT	GTATGGTTTA	CCAGCCTTCC	CACTCTTATA
msa286608.2{662_1169NT}	AAATTTTCAGG	CTAAAGAGAT	GTATGGTTTA	CCAGCCTTCC	CACTCTTATA
Consensus	*****	*****	*****	*****	*****
651					
msa286608.2{662_COH1}	TGAAGTTTCA	ACAATTTCTA	AAATCAGAGC	AGGTTTTTCG	TATGGACAAG

Table 83: Comparative Sequences relating to SAG0108

msa286608.2{662_M732}	TGAAGTTTCA	ACAATTTCTA	AAATCAGAGC	AGGTTTTTCG	TATGGACAAG
msa286608.2{662_M781}	TGAAGTTTCA	ACAATTTCTA	AAATCAGAGC	AGGTTTTTCG	TATGGACAAG
msa286608.2{662_A909}	TGAAGTTTCA	ACAATTTCTA	AAATCAGAGC	AGGTTTTTCG	TATGGACAAG
msa286608.2{662_H36B}	TGAAGTTTCA	ACAATTTCTA	AAATCAGAGC	AGGTTTTTCG	TATGGACAAG
msa286608.2{662_090}	TGAAGTTTCA	ACAATTTCTA	AAATCAGAGC	AGGTTTTTCG	TATGGACAAG
msa286608.2{662_CJB110}	TGAAGTTTCA	ACAATTTCTA	AAATCAGAGC	AGGTTTTTCG	TATGGACAAG
msa286608.2{662_18RS21}	TGAAGTTTCA	ACAATTTCTA	AAATCAGAGC	AGGTTTTTCG	TATGGACAAG
msa286608.2{662_2603}	TGAAGTTTCA	ACAATTTCTA	AAATCAGAGC	AGGTTTTTCG	TATGGACAAG
msa286608.2{662_JM9130013}	TGAAGTTTCA	ACAATTTCTA	AAATCAGAGC	AGGTTTTTCG	TATGGACAAG
msa286608.2{662_1169NT}	TGAAGTTTCA	ACAATTTCTA	AAATCAGAGC	AGGTTTTTCG	TATGGACAAG
Consensus	*****	*****	*****	*****	*****
701					
msa286608.2{662_COH1}	CAAGTAGTGT	cGAACAATTG	AAAAAGAATA	ATTTACCAGC	CCTCTTTATT
msa286608.2{662_M732}	CAAGTAGTGT	cGAACAATTG	AAAAAGAATA	ATTTACCAGC	CCTCTTTATT
msa286608.2{662_M781}	CAAGTAGTGT	cGAACAATTG	AAAAAGAATA	ATTTACCAGC	CCTCTTTATT
msa286608.2{662_A909}	CAAGTAGTGT	cGAACAATTG	AAAAAGAATA	ATTTACCAGC	CCTCTTTATT
msa286608.2{662_H36B}	CAAGTAGTGT	cGAACAATTG	AAAAAGAATA	ATTTACCAGC	CCTCTTTATT
msa286608.2{662_090}	CAAGTAGTGT	cGAACAATTG	AAAAAGAATA	ATTTACCAGC	CCTCTTTATT
msa286608.2{662_CJB110}	CAAGTAGTGT	cGAACAATTG	AAAAAGAATA	ATTTACCAGC	CCTCTTTATT
msa286608.2{662_18RS21}	CAAGTAGTGT	cGAACAATTG	AAAAAGAATA	ATTTACCAGC	CCTCTTTATT
msa286608.2{662_2603}	CAAGTAGTGT	cGAACAATTG	AAAAAGAATA	ATTTACCAGC	CCTCTTTATT
msa286608.2{662_JM9130013}	CAAGTAGTGT	cGAACAATTG	AAAAAGAATA	ATTTACCAGC	CCTCTTTATT
msa286608.2{662_1169NT}	CAAGTAGTGT	aGAACAATTG	AAAAAGAATA	ATTTACCAGC	CCTCTTTATT
Consensus	*****	*****	*****	*****	*****
751					
msa286608.2{662_COH1}	CATGGTGATA	AGGATAATTT	TGTTCCAACA	AGTATGGTTT	ATGACAACTA
msa286608.2{662_M732}	CATGGTGATA	AGGATAATTT	TGTTCCAACA	AGTATGGTTT	ATGACAACTA
msa286608.2{662_M781}	CATGGTGATA	AGGATAATTT	TGTTCCAACA	AGTATGGTTT	ATGACAACTA
msa286608.2{662_A909}	CATGGTGATA	AGGATAATTT	TGTTCCAACA	AGTATGGTTT	ATGACAACTA
msa286608.2{662_H36B}	CATGGTGATA	AGGATAATTT	TGTTCCAACA	AGTATGGTTT	ATGACAACTA
msa286608.2{662_090}	CATGGTGATA	AGGATAATTT	TGTTCCAACA	AGTATGGTTT	ATGACAACTA
msa286608.2{662_CJB110}	CATGGTGATA	AGGATAATTT	TGTTCCAACA	AGTATGGTTT	ATGACAACTA
msa286608.2{662_18RS21}	CATGGTGATA	AGGATAATTT	TGTTCCAACA	AGTATGGTTT	ATGACAACTA
msa286608.2{662_2603}	CATGGTGATA	AGGATAATTT	TGTTCCAACA	AGTATGGTTT	ATGACAACTA
msa286608.2{662_JM9130013}	CATGGTGATA	AGGATAATTT	TGTTCCAACA	AGTATGGTTT	ATGACAACTA
msa286608.2{662_1169NT}	CATGGTGATA	AGGATAATTT	TGTTCCAACA	AGTATGGTTT	ATGACAACTA
Consensus	*****	*****	*****	*****	*****
801					
msa286608.2{662_COH1}	TAAAGCTACA	GCAGGTAAGA	AAGAGCTTTA	TATTGTAAAA	GGGGCAAAAC
msa286608.2{662_M732}	TAAAGCTACA	GCAGGTAAGA	AAGAGCTTTA	TATTGTAAAA	GGGGCAAAAC
msa286608.2{662_M781}	TAAAGCTACA	GCAGGTAAGA	AAGAGCTTTA	TATTGTAAAA	GGGGCAAAAC
msa286608.2{662_A909}	TAAAGCTACA	GCAGGTAAGA	AAGAGCTTTA	TATTGTAAAA	GGGGCAAAAC
msa286608.2{662_H36B}	TAAAGCTACA	GCAGGTAAGA	AAGAGCTTTA	TATTGTAAAA	GGGGCAAAAC
msa286608.2{662_090}	TAAAGCTACA	GCAGGTAAGA	AAGAGCTTTA	TATTGTAAAA	GGGGCAAAAC
msa286608.2{662_CJB110}	TAAAGCTACA	GCAGGTAAGA	AAGAGCTTTA	TATTGTAAAA	GGGGCAAAAC
msa286608.2{662_18RS21}	TAAAGCTACA	GCAGGTAAGA	AAGAGCTTTA	TATTGTAAAA	GGGGCAAAAC
msa286608.2{662_2603}	TAAAGCTACA	GCAGGTAAGA	AAGAGCTTTA	TATTGTAAAA	GGGGCAAAAC
msa286608.2{662_JM9130013}	TAAAGCTACA	GCAGGTAAGA	AAGAGCTTTA	TATTGTAAAA	GGGGCAAAAC
msa286608.2{662_1169NT}	TAAAGCTACA	GCAGGTAAGA	AAGAGCTTTA	TATTGTAAAA	GGGGCAAAAC
Consensus	*****	*****	*****	*****	*****
851					
msa286608.2{662_COH1}	ATGCCGAAATC	TTTTGAAACA	GAGCCAGAAA	AATATGAGAA	ACGTATCTCT
msa286608.2{662_M732}	ATGCCGAAATC	TTTTGAAACA	GAGCCAGAAA	AATATGAGAA	ACGTATCTCT
msa286608.2{662_M781}	ATGCCGAAATC	TTTTGAAACA	GAGCCAGAAA	AATATGAGAA	ACGTATCTCT
msa286608.2{662_A909}	ATGCCGAAATC	TTTTGAAACA	GAGCCAGAAA	AATATGAGAA	ACGTATCTCT
msa286608.2{662_H36B}	ATGCCGAAATC	TTTTGAAACA	GAGCCAGAAA	AATATGAGAA	ACGTATCTCT
msa286608.2{662_090}	ATGCCGAAATC	TTTTGAAACA	GAGCCAGAAA	AATATGAGAA	ACGTATCTCT
msa286608.2{662_CJB110}	ATGCCGAAATC	TTTTGAAACA	GAGCCAGAAA	AATATGAGAA	ACGTATCTCT
msa286608.2{662_18RS21}	ATGCCGAAATC	TTTTGAAACA	GAGCCAGAAA	AATATGAGAA	ACGTATCTCT
msa286608.2{662_2603}	ATGCCGAAATC	TTTTGAAACA	GAGCCAGAAA	AATATGAGAA	ACGTATCTCT
msa286608.2{662_JM9130013}	ATGCCGAAATC	TTTTGAAACA	GAGCCAGAAA	AATATGAGAA	ACGTATCTCT
msa286608.2{662_1169NT}	ATGCCGAAATC	TTTTGAAACA	GAGCCAGAAA	AATATGAGAA	ACGTATCTCT
Consensus	*****	*****	*****	*****	*****
901					
msa286608.2{662_COH1}	AGTTTTTTTGA	AAAAATATGA	AAAA		
msa286608.2{662_M732}	AGTTTTTTTGA	AAAAATATGA	AAAA		
msa286608.2{662_M781}	AGTTTTTTTGA	AAAAATATGA	AAAA		
msa286608.2{662_A909}	AGTTTTTTTGA	AAAAATATGA	AAAA		
msa286608.2{662_H36B}	AGTTTTTTTGA	AAAAATATGA	AAAA		
msa286608.2{662_090}	AGTTTTTTTGA	AAAAATATGA	AAAA		
msa286608.2{662_CJB110}	AGTTTTTTTGA	AAAAATATGA	AAAA		
msa286608.2{662_18RS21}	AGTTTTTTTGA	AAAAATATGA	AAAA		
msa286608.2{662_2603}	AGTTTTTTTGA	AAAAATATGA	AAAA		
msa286608.2{662_JM9130013}	AGTTTTTTTGA	AAAAATATGA	AAAA		
msa286608.2{662_1169NT}	AGTTTTTTTGA	AAAAATATGA	AAAA		
Consensus	*****	*****	****		
924					

SEQ ID NO. 8312

Table 83: Comparative Sequences relating to SAG0108**STRAIN 2603 frame: 1**

MKKIRLSKFIKMIIVVILEFLISVAASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFD
 KLLKQKIEMTNQNIKQVAWYVPAVKKTHKTAVVVHGFANSKENMKAYGWL FHKLGYNVLM
 PDNIAHGESHGQLIGYGWNDRENI IKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKL
 PSQVVNI IEDCGYSSVWDELKFKQAKEMYGLPAFPLLYEVSTISKIRAGFSYGQASSVEQL
 KKNL PALFIHGDKDNFVPTSMVYDNYKATAGKKELYIVKGAKHAKSFETEPEKEYEKRISSFLKKYEK

SEQ ID NO. 8313**STRAIN 090 frame: 1**

ASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAWYVPA
 AKKTHKTAVVVHGFANSKENMKAYGWL FHKLGYNVLM PDNIAHGESHGQLIGYGWNDREN
 I IKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLPSQVVNI IEDCGYSSVWDELKFKQ
 AKEMYGLPAFPLLYEVSTISKIRAGFSYGQASSVEQLKKNL PALFIHGDKDNFVPTSMV
 YDNYKATAGKKELYIVKGAKHAKSFETEPEKEYEKRISSFLKKYEK

SEQ ID NO. 8314**STRAIN A909 frame: 3**

SFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAWYVPAKKTHKTAVVVHGFAN
 SKENMKAYGWL FHKLGYNVLM PDNIAHGESHGQLIGYGWNDRENI IKWTEMIVDKNSSS
 QITLFGVSMGGATVMMASGEKLPSQVVNI IEDCGYSGVWDELKFKQAKEMYGLPAFPLLYE
 VSTISKIRAGFSYGQASSVEQLKKNL PALFIHGDKDNFVPTSMVYDNYKATAGKKELYI
 VKGAKHAKSFETEPEKEYEKRISSFLKKYEK

SEQ ID NO. 8315**STRAIN H36B frame: 1**

SFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAWYVPA
 KKTHKTAVVVHGFANSKENMKAYGWL FHKLGYNVLM PDNIAHGESHGQLIGYGWNDRENI
 IKWTEMIVDKNSSSQITLFGVSMGGATVMMASGEKLPSQVVNI IEDCGYSGVWDELKFKQ
 AKEMYGLPAFPLLYEVSTISKIRAGFSYGQASSVEQLKKNL PALFIHGDKDNFVPTSMV
 YDNYKATAGKKELYIVKGAKHAKSFETEPEKEYEKRISSFLKKYEK

SEQ ID NO. 8316**STRAIN 18RS21 frame: 1**

ASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAWYVPA
 VKKTHKTAVVVHGFANSKENMKAYGWL FHKLGYNVLM PDNIAHGESHGQLIGYGWNDREN
 I IKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLPSQVVNI IEDCGYSSVWDELKFKQ
 AKEMYGLPAFPLLYEVSTISKIRAGFSYGQASSVEQLKKNL PALFIHGDKDNFVPTSMV
 YDNYKATAGKKELYIVKGAKHAKSFETEPEKEYEKRISSFLKKYEK

SEQ ID NO. 8317**STRAIN M732 frame: 1**

ASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAWYVPA
 AKKTHKTAVVVHGFANSKENMKAYGWL FHKLGYNVLM PDNIAHGESHGQLIGYGWNDREN
 I IKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLPSQVVNI IEDCGYSSVWDELKFKQ
 AKEMYGLPAFPLLYEVSTISKIRAGFSYGQASSVEQLKKNL PALFIHGDKDNFVPTSMV
 YDNYKATAGKKELYIVKGAKHAKSFETEPEKEYEKRISSFLKKYEK

SEQ ID NO. 8318**STRAIN COH1 frame: 1**

ASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAWYVPA
 AKKTHKTAVVVHGFANSKENMKAYGWL FHKLGYNVLM PDNIAHGESHGQLIGYGWNDREN
 I IKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLPSQVVNI IEDCGYSSVWDELKFKQ
 AKEMYGLPAFPLLYEVSTISKIRAGFSYGQASSVEQLKKNL PALFIHGDKDNFVPTSMV
 YDNYKATAGKKELYIVKGAKHAKSFETEPEKEYEKRISSFLKKYEK

SEQ ID NO. 8319**STRAIN M781 frame: 1**

ASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAWYVPA
 AKKTHKTAVVVHGFANSKENMKAYGWL FHKLGYNVLM PDNIAHGESHGQLIGYGWNDREN
 I IKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLPSQVVNI IEDCGYSSVWDELKFKQ
 AKEMYGLPAFPLLYEVSTISKIRAGFSYGQASSVEQLKKNL PALFIHGDKDNFVPTSMV
 YDNYKATAGKKELYIVKGAKHAKSFETEPEKEYEKRISSFLKKYEK

SEQ ID NO. 8320**STRAIN CJB110 frame: 1**

ASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAWYVPA
 AKKTHKTAVVVHGFANSKENMKAYGWL FHKLGYNVLM PDNIAHGESHGQLIGYGWNDREN
 I IKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLPSQVVNI IEDCGYSSVWDELKFKQ
 AKEMYGLPAFPLLYEVSTISKIRAGFSYGQASSVEQLKKNL PALFIHGDKDNFVPTSMV
 YDNYKATAGKKELYIVKGAKHAKSFETEPEKEYEKRISSFLKKYEK

SEQ ID NO. 8321**STRAIN 1169NT frame: 1**

ASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAWYVPA
 AKKTHKTAVVVHGFANSKENMKAYGWL FHKLGYNVLM PDNIAHGESHGQLIGYGWNDREN
 I IKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLPSQVVNI IEDCGYSSVWDELKFKQ
 AKEMYGLPAFPLLYEVSTISKIRAGFSYGQASSVEQLKKNL PALFIHGDKDNFVPTSMV
 YDNYKATAGKKELYIVKGAKHAKSFETEPEKEYEKRISSFLKKYEK

SEQ ID NO. 8322

Table 83: Comparative Sequences relating to SAG0108

STRAIN JM9130013 frame: 1

ASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAWYVPA
 VKKTHKTAVVVHGFANSKENMKAYGWL FHKLGYNVLM PDNIAHGESHGQLIGYGWNDREN
 I IKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLPSQVVNI IEDCGYSSVWDELKFO
 AKEMYGLPAFPLLYEVSTISKIRAGFSYQASSVEQLKKNLPALEFIHGDKDNFVPTSMV
 YDNYKATAGKKELYIVKGAKHAKSFETEPEKYEKRISFLKKYEK

PRETTY of: /biotmp/msa286876.2{*} February 24, 2003 06:46 ..

	1				50
msa286876.2{662_A909}	-----SF	ISNGQRKPGN			
msa286876.2{662_H36B}	-----SFYFFH	VAQVRDDKSF	ISNGQRKPGN		
msa286876.2{662_COH1}	-----ASFYFFH	VAQVRDDKSF	ISNGQRKPGN		
msa286876.2{662_M732}	-----ASFYFFH	VAQVRDDKSF	ISNGQRKPGN		
msa286876.2{662_M781}	-----ASFYFFH	VAQVRDDKSF	ISNGQRKPGN		
msa286876.2{662_18RS21}	-----ASFYFFH	VAQVRDDKSF	ISNGQRKPGN		
msa286876.2{662_2603}	mkkirlskfi kmivvilfli	svaASFYFFH	VAQVRDDKSF	ISNGQRKPGN	
msa286876.2{662_JM9130013}	-----ASFYFFH	VAQVRDDKSF	ISNGQRKPGN		
msa286876.2{662_090}	-----ASFYFFH	VAQVRDDKSF	ISNGQRKPGN		
msa286876.2{662_CJB110}	-----ASFYFFH	VAQVRDDKSF	ISNGQRKPGN		
msa286876.2{662_1169NT}	-----ASFYFFH	VAQVRDDKSF	ISNGQRKPGN		
Consensus	*****	*****	*****	*****	*****
	51				100
msa286876.2{662_A909}	SLYAYDKSFD	KLLKQKIEMT	NQNIKQVAWY	VPAaKKTHKT	avVVHGFANS
msa286876.2{662_H36B}	SLYAYDKSFD	KLLKQKIEMT	NQNIKQVAWY	VPAaKKTHKT	avVVHGFANS
msa286876.2{662_COH1}	SLYAYDKSFD	KLLKQKIEMT	NQNIKQVAWY	VPAaKKTHKT	vVVHGFANS
msa286876.2{662_M732}	SLYAYDKSFD	KLLKQKIEMT	NQNIKQVAWY	VPAaKKTHKT	vVVHGFANS
msa286876.2{662_M781}	SLYAYDKSFD	KLLKQKIEMT	NQNIKQVAWY	VPAaKKTHKT	vVVHGFANS
msa286876.2{662_18RS21}	SLYAYDKSFD	KLLKQKIEMT	NQNIKQVAWY	VPAvKKTHKT	avVVHGFANS
msa286876.2{662_2603}	SLYAYDKSFD	KLLKQKIEMT	NQNIKQVAWY	VPAvKKTHKT	avVVHGFANS
msa286876.2{662_JM9130013}	SLYAYDKSFD	KLLKQKIEMT	NQNIKQVAWY	VPAvKKTHKT	avVVHGFANS
msa286876.2{662_090}	SLYAYDKSFD	KLLKQKIEMT	NQNIKQVAWY	VPAaKKTHKT	avVVHGFANS
msa286876.2{662_CJB110}	SLYAYDKSFD	KLLKQKIEMT	NQNIKQVAWY	VPAaKKTHKT	avVVHGFANS
msa286876.2{662_1169NT}	SLYAYDKSFD	KLLKQKIEMT	NQNIKQVAWY	VPAaKKTHKT	avVVHGFANS
Consensus	*****	*****	*****	***-*****	-*****
	101				150
msa286876.2{662_A909}	KENMKAYGWL	FHKLGYNVLM	PDNIAHGESH	GQLIGYGWND	RENI IKWTEM
msa286876.2{662_H36B}	KENMKAYGWL	FHKLGYNVLM	PDNIAHGESH	GQLIGYGWND	RENI IKWTEM
msa286876.2{662_COH1}	KENMKAYGWL	FHKLGYNVLM	PDNIAHGESH	GQLIGYGWND	RENI IKWTEM
msa286876.2{662_M732}	KENMKAYGWL	FHKLGYNVLM	PDNIAHGESH	GQLIGYGWND	RENI IKWTEM
msa286876.2{662_M781}	KENMKAYGWL	FHKLGYNVLM	PDNIAHGESH	GQLIGYGWND	RENI IKWTEM
msa286876.2{662_18RS21}	KENMKAYGWL	FHKLGYNVLM	PDNIAHGESH	GQLIGYGWND	RENI IKWTEM
msa286876.2{662_2603}	KENMKAYGWL	FHKLGYNVLM	PDNIAHGESH	GQLIGYGWND	RENI IKWTEM
msa286876.2{662_JM9130013}	KENMKAYGWL	FHKLGYNVLM	PDNIAHGESH	GQLIGYGWND	RENI IKWTEM
msa286876.2{662_090}	KENMKAYGWL	FHKLGYNVLM	PDNIAHGESH	GQLIGYGWND	RENI IKWTEM
msa286876.2{662_CJB110}	KENMKAYGWL	FHKLGYNVLM	PDNIAHGESH	GQLIGYGWND	RENI IKWTEM
msa286876.2{662_1169NT}	KENMKAYGWL	FHKLGYNVLI	PDNIAHGESH	GQLIGYGWND	RENI IKWTEM
Consensus	*****	*****	*****	*****	*****
	151				200
msa286876.2{662_A909}	IVDKNsSSQI	TLFGVSMGGA	TVMMASGEKL	PSQVVNI IED	CGYSgVWDEL
msa286876.2{662_H36B}	IVDKNsSSQI	TLFGVSMGGA	TVMMASGEKL	PSQVVNI IED	CGYSgVWDEL
msa286876.2{662_COH1}	IVDKNpSSQI	TLFGVSMGGA	TVMMASGEKL	PSQVVNI IED	CGYSsVWDEL
msa286876.2{662_M732}	IVDKNpSSQI	TLFGVSMGGA	TVMMASGEKL	PSQVVNI IED	CGYSsVWDEL
msa286876.2{662_M781}	IVDKNpSSQI	TLFGVSMGGA	TVMMASGEKL	PSQVVNI IED	CGYSsVWDEL
msa286876.2{662_18RS21}	IVDKNpSSQI	TLFGVSMGGA	TVMMASGEKL	PSQVVNI IED	CGYSsVWDEL
msa286876.2{662_2603}	IVDKNpSSQI	TLFGVSMGGA	TVMMASGEKL	PSQVVNI IED	CGYSsVWDEL
msa286876.2{662_JM9130013}	IVDKNpSSQI	TLFGVSMGGA	TVMMASGEKL	PSQVVNI IED	CGYSsVWDEL
msa286876.2{662_090}	IVDKNpSSQI	TLFGVSMGGA	TVMMASGEKL	PSQVVNI IED	CGYSsVWDEL
msa286876.2{662_CJB110}	IVDKNpSSQI	TLFGVSMGGA	TVMMASGEKL	PSQVVNI IED	CGYSsVWDEL
msa286876.2{662_1169NT}	IVDKNpSSQI	TLFGVSMGGA	TVMMASGEKL	PSQVVNI IED	CGYSsVWDEL
Consensus	*****	*****	*****	*****	*****
	201				250
msa286876.2{662_A909}	KFQAKEMYGL	PAFPLLYEVS	TISKIRAGFS	YGQASSVEQL	KKNLPALEFI
msa286876.2{662_H36B}	KFQAKEMYGL	PAFPLLYEVS	TISKIRAGFS	YGQASSVEQL	KKNLPALEFI
msa286876.2{662_COH1}	KFQAKEMYGL	PAFPLLYEVS	TISKIRAGFS	YGQASSVEQL	KKNLPALEFI
msa286876.2{662_M732}	KFQAKEMYGL	PAFPLLYEVS	TISKIRAGFS	YGQASSVEQL	KKNLPALEFI
msa286876.2{662_M781}	KFQAKEMYGL	PAFPLLYEVS	TISKIRAGFS	YGQASSVEQL	KKNLPALEFI
msa286876.2{662_18RS21}	KFQAKEMYGL	PAFPLLYEVS	TISKIRAGFS	YGQASSVEQL	KKNLPALEFI
msa286876.2{662_2603}	KFQAKEMYGL	PAFPLLYEVS	TISKIRAGFS	YGQASSVEQL	KKNLPALEFI
msa286876.2{662_JM9130013}	KFQAKEMYGL	PAFPLLYEVS	TISKIRAGFS	YGQASSVEQL	KKNLPALEFI
msa286876.2{662_090}	KFQAKEMYGL	PAFPLLYEVS	TISKIRAGFS	YGQASSVEQL	KKNLPALEFI
msa286876.2{662_CJB110}	KFQAKEMYGL	PAFPLLYEVS	TISKIRAGFS	YGQASSVEQL	KKNLPALEFI
msa286876.2{662_1169NT}	KFQAKEMYGL	PAFPLLYEVS	TISKIRAGFS	YGQASSVEQL	KKNLPALEFI
Consensus	*****	*****	*****	*****	*****
	251				300
msa286876.2{662_A909}	HGDKDNFVPT	SMVYDNYKAT	AGKKELYIVK	GAKHAKSFET	EPEKYEKRIS
msa286876.2{662_H36B}	HGDKDNFVPT	SMVYDNYKAT	AGKKELYIVK	GAKHAKSFET	EPEKYEKRIS
msa286876.2{662_COH1}	HGDKDNFVPT	SMVYDNYKAT	AGKKELYIVK	GAKHAKSFET	EPEKYEKRIS

Table 83: Comparative Sequences relating to SAG0108

msa286876.2{662_M732}	HGDKDNFVPT	SMVYDNYKAT	AGKKELYIVK	GAKHAKSFET	EPEKYEKRIS
msa286876.2{662_M781}	HGDKDNFVPT	SMVYDNYKAT	AGKKELYIVK	GAKHAKSFET	EPEKYEKRIS
msa286876.2{662_18RS21}	HGDKDNFVPT	SMVYDNYKAT	AGKKELYIVK	GAKHAKSFET	EPEKYEKRIS
msa286876.2{662_2603}	HGDKDNFVPT	SMVYDNYKAT	AGKKELYIVK	GAKHAKSFET	EPEKYEKRIS
msa286876.2{662_JM9130013}	HGDKDNFVPT	SMVYDNYKAT	AGKKELYIVK	GAKHAKSFET	EPEKYEKRIS
msa286876.2{662_090}	HGDKDNFVPT	SMVYDNYKAT	AGKKELYIVK	GAKHAKSFET	EPEKYEKRIS
msa286876.2{662_CJB110}	HGDKDNFVPT	SMVYDNYKAT	AGKKELYIVK	GAKHAKSFET	EPEKYEKRIS
msa286876.2{662_1169NT}	HGDKDNFVPT	SMVYDNYKAT	AGKKELYIVK	GAKHAKSFET	EPEKYEKRIS
Consensus	*****	*****	*****	*****	*****
301					
msa286876.2{662_A909}	SFLKKYEK				
msa286876.2{662_H36B}	SFLKKYEK				
msa286876.2{662_COH1}	SFLKKYEK				
msa286876.2{662_M732}	SFLKKYEK				
msa286876.2{662_M781}	SFLKKYEK				
msa286876.2{662_18RS21}	SFLKKYEK				
msa286876.2{662_2603}	SFLKKYEK				
msa286876.2{662_JM9130013}	SFLKKYEK				
msa286876.2{662_090}	SFLKKYEK				
msa286876.2{662_CJB110}	SFLKKYEK				
msa286876.2{662_1169NT}	SFLKKYEK				
Consensus	*****				

Table 84: Comparative Sequences relating to SAG0267

SEQ ID NO. 8401

STRAIN 2603

ATGATGAAAGTTTTAGCCTTTGATACTTCAAGCAAAGCACTATCAGTGGCTGTACTAAAC
 AATATGGAATGTTTAGCGACTGTCACTATCAATATCAAAAAGAATCATAGCATTAAATTTG
 ATGCCAGCCATTGATTTTTTAATGCAATCAATTGATTTAGAACCTCAAGATTTGGACCGT
 ATCGTAGTAGCAGAGGGTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGCTACAGCA
 AAAATGCTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACGCTTTA
 ACAAATGGATTTTCAGAAAATGATTTATTGGTACCCTTATAGATGCACGACGTAATAAT
 GTTTATGTTGGTTTCTATCAAAATGGTGATACTGTTAAACCAGACTGTACACTTCTCTT
 GAAGAAGTCTTACAAGAGGTGGGGAATAAAGCCAAATGTTCAATTTGTCGGAGAGGTTGCA
 GCATTTTTTGGATCAGATTAAGAAAGCCTTACCACATGCTAAAATTACAGAACTTTACCT
 TGTGCAGTAGCAATTGGGCGCAAAGGACAAAAATGAAAAGCGTTAATGTAGATGCGTTT
 GTTCCACGATACTTAAAACGTGTTGAAGCTGAGGAAAATTGGTTAAAAAACCACTGTGAA
 ACGAATACAGAAGAATATATTAAGAGAGTT

SEQ ID NO. 8402

STRAIN 090

AAAGTTTTAGCCTTTGATACTTCAAGCAAAGCACTATCAGTGGCTGTACT
 AAACAATATGGAATGTTTAGCGACTGTCACTATCAATATCAAAAAGAATC
 ATAGCATTAAATTTGATGCCAGCCATTGATTTTTTAATGCAATCAATTGAT
 TTAGAACCTCAAGATTTGGACCGTATCGTAGTGGCAGAGGGTCCAGGATC
 TTATACGGGCTTACGTGTAGCTGTTGCTACAGCAAAAATGCTAGCTTATA
 CGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACGCTTTAACAAAT
 GGATTTTCAGAAAATGATTTGTTGGTACCCTTATAGATGCACGACGTAA
 CAATGTTTATGTTGGTTTCTATCAAAATGGTGATACTGTTAAACCAGACT
 GTCACACTTCTCTTGAAGAAGTCTTACAAGAGGTGGGGAATAAAGCCAAAT
 GTTCATTTTGTGCGAGAGGTTGCAGCATTTTTTGGATCAGATTAAgAAAGC
 CTTACCACATGCTAAAATTACAGAACTTTACCTTGTGCAGTGGCAATTG
 GCGCAAAGGACAAAAATGGAAGCGTTAATGTAGATGCGTTTGTCCA
 CGATACTTAAAACGAGTTGAAGCTGAGGAAAATTGGTTAAAAAACCACTG
 TGAAACGAAT

SEQ ID NO. 8403

STRAIN A909

AAAGTTTTAGCCTTTGATACTTCAAGCAAAGCACTATCAG
 TGGCTGTACTAAACAATATGGAATGTTTAGCGACTGTCACTATCAATATC
 AAAAAGAATCATAGCATTAAATTTGATGCCAGCCATTGATTTTTTAATGCA
 ATCAATTGATTTAGAACCTCAAGATTTGGACCGTATCGTAGTAGCAGAGG
 GTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGCTACAGCAAAAATG
 CTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACGC
 TTTAACAAATGGATTTTCAGAAAATGATTTATTGGTACCCTTATAGATG
 CACGACGTAACAATGTTTATGTTGGTTTCTATCAAAATGGAGATACTGTT
 AAACCAGACTGTCACTTCTCTTGAAGAAGTCTTACAAGAGGTGGGGAA
 TAAAGCCAATGTTTCATTTTGTGCGAgAGGTTGCAGCATTGTTGACCAGA
 tTAAGAAAGTTTTACCACATGCTAAAATTACAGAACTTTACCTTGTGCA
 GtGGCAATTGGGCGCAAAGGACAAAAATGAAAAGCGTTAATGTAGATGC
 GTTTGTTCCACGATACTTAAAACGTGTTGAAGCTGAGGAAAATTGGTTAA
 GAAACCACTGTGAAACGAAT

SEQ ID NO. 8404

STRAIN H36B

AAAGTTTTAGCCTTTGATACTTCAAGCAAAGCACTATCA
 GTGGCTGTACTAAACAATATGGAATGTTTAGCGACTGTCACTATCAATAT
 CAAAAAGAATCATAGCATTAAATTTGATGCCAGCCATTGATTTTTTAATGC
 AATCAATTGATTTAGAACCTCAAGATTTGGACCGTATCGTAGTAGCAGAG
 GGTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGCTACAGCAAAAAT
 GCTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACG
 CTTTAACAAATGGATTTTCAGAAAATGATTTATTGGTACCCTTATAGAT
 GCACGACGTAACAATGTTTATGTTGGTTTCTATCAAAATGGAGATACTGT
 TAAACCAGACTGTCACTTCTCTTGAAGAAGTCTTACAAGAGGTGGGGA
 ATAAAGCCAATGTTTCATTTTGTGCGAGAGGTTGCAGCATTTGTTGACCAG
 ATTAAGAAAGTTTTACCACATGCTAAAATTACAGAACTTTACCTTGTGC
 AGTGGCAATTGGGCGCAAAGGACAAAAATGAAAAGCGTTAATGTAGATG
 CGTTTGTTCACGATACTTAAAACGTGTTGAAGCTGAGGAAAATTGGTTA
 AGAAACCACTGTGAAACGAATACAGAAGAATATATTAAGAGAGTT

SEQ ID NO. 8405

STRAIN 18RS21

AAAGTTTTAGCCTTTGATACTTCAAGCAAAGCACTATCA
 GTGGCTGTACTAAACAATATGGAATGTTTAGCGACTGTCACTATCAATAT
 CAAAAAGAATCATAGCATTAAATTTGATGCCAGCCATTGATTTTTTAATGC
 AATCAATTGATTTAGAACCTCAAGATTTGGACCGTATCGTAGTAGCAGAG
 GGTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGCTACAGCAAAAAT
 GCTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACG
 CTTTAACAAATGGATTTTCAGAAAATGATTTATTGGTACCCTTATAGAT
 GCACGACGTAATAATGTTTATGTTGGTTTCTATCAAAATGGTGATACTGT
 TAAACCAGACTGTCACTTCTCTTGAAGAAGTCTTACAAGAGGTGGGGA
 ATAAAGCCAATGTTTCATTTTGTGCGAGAGGtTGCAGCATTTTTTGGATCag
 ATTAAGAAAGCCTTACCACATGCTAAAATTACAGAACTTTACCTTGTGC
 AGTAGCAATTGGGCGCAAAGGACAAAAATGAAAAGCGTTAATGTAGATG
 CGTTTGTTCACGATACTTAAAACGTGTTGAAGCTGAGGAAAATTGGTTA
 AAAAACCACTGTGAAACGAATACAGAAGAATATATTAAGAGAGTT

Table 84: Comparative Sequences relating to SAG0267

SEQ ID NO. 8406

STRAIN M732

AAAGTTTTAGCCTTTGATACCTCAAGCAAAGCACTATCA
 GTGGCTGTACTAAACAATATGGAATGTTTAGCGACTGTCACTATCAATAT
 CAAAAAGAATCATAGCATTAAATTTGATGCCAGCCATTGATTTTTTAATGC
 AATCAATTGATTTAGAACCTCAAGATTTGGACCGTATCGTAGTAGCAGAG
 GGTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGCTACAGCAAAAAT
 GCTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACG
 CTTTAACAAATGGATTTTCAGAAAATGATTTATTGGTACCACTTATAGAT
 GCACGACGTAACAATGTTTATGTTGGTTTCTATCAAAATGGTGATACTGT
 TAAACCAGACTGTCACTTCTCTTGAAGAAGTCTTACAAGAGGTGGGGA
 ATAAAGCCAATGTTCAATTTTGTGCGAGAGGTTGCAGCATTTTTTGATCAG
 ATTAAGAAAGCCTTACCACATGCTAAAATTACAGAACTTTACCTTGTGC
 AGTAGCAATTGGGCGCAAAGGACAAAAATGAAAAGCGTTAATGTAGAnn
 CGTTTGTTCACGATACTTAAAACGTGTTGAAGCTGAGGAAAATTGGTTA
 AAAAACCCTGTGAAACGAATACAGAAGAATATATTAAGAGAGTT

SEQ ID NO. 8407

STRAIN COH1

AAAGTTTTAGCCTTTGATACCTCAAGCAAAGCAC
 TATCAGTGGCTGTACTAAACAATATGGAATGTTTAGCGACTGTCACTATC
 AATATCAAAAAGAATCATAGCATTAAATTTGATGCCAGCCATTGATTTTTT
 AATGCAATCAATTGATTTAGAACCTCAAGATTTGGACCGTATCGTAGTAG
 CAGAGGGTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGCTACAGCA
 AAAATGCTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCT
 GTACGCTTTAACAAATGGATTTTCAGAAAATGATTTATTGGTACCACTTA
 TAGATGCACGACGTAACAATGTTTATGTTGGTTTCTATCAAAATGGTGAT
 ACTGTTAAACCAGACTGTCACTTCTCTTGAAGAAGTCTTACAAGAGGT
 GGGGAATAAAGCCAATGTTCAATTTTGTGCGAGAGGTTGCAGCATTTTTTG
 ATCAGATTAAAGAAAGCCTTACCACATGCTAAAATTACAGAACTTTACCT
 TGTGCAGTAGCAATTGGGCGCAAAGGACAAAAATGAAAAGCGTTAATGT
 AGATGCGTTTGTTCACGATACTTAAAACGTGTTGAAGCTGAGGAAAATT
 GGTAAAAAACCACTGTGAAACGAATACAGAAGAATATATTAAGAGAGTT

SEQ ID NO. 8408

STRAIN M781

AAAGTTTTAGCCTTTGATACCTCAAGCAAAGCACTA
 TCAGTGGCTGTACTAAACAATATGGAATGTTTAGCGACTGTCACTATCAA
 TATCAAAAAGAATCATAGCATTAAATTTGATGCCAGCCATTGATTTTTTAA
 TGCAATCAATTGATTTAGAACCTCAAGATTTGGACCGTATCGTAGTATCA
 GAGGGTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGCTACAGCAAA
 AATGCTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGT
 ACGCTTTAACAAATGGATTTTCAGAAAATGATTTATTGGTACCACTTATA
 GATGCACGACGTAACAATGTTTATGTTGGTTTCTATCAAAATGGTGATAC
 TGTTAAACCAGACTGTCACTTCTCTTGAAGAAGTCTTACAAGAGGTGG
 GGAATAAAGCCAATGTTCAATTTTGTGCGAGAGGTTGCAGCATTTTTTGAT
 CAGATTAAAGAAAGCCTTACCACATGCTAAAATTACAGAACTTTACCTTG
 TGCAGTAGCAATTGGGCGCAAAGGACAAAAATGAAAAGCGTTAATGTAG
 ATGCGTTTGTTCACGATACTTAAAACGTGTTGAAGCTGAGGAAAATTGG
 TAAAAAACCACTGTGAAACGAATACAGAAGAATATATTAAGAGAGTT

SEQ ID NO. 8409

STRAIN CJB110

AAAGTTTTAGCCTTTGATACCTCAAGCAAAGCACTATCA
 GTGGCTGTaCTAAACAATATGGAATGTTTAGCGACTGTCACTATCAATAT
 CAAAAAGAATCATAGCATTAAATTTGATGCCAGCCATTGATTTTTTAATGC
 AATCAATTGATTTAGAACCTCAAGATTTGGACCGTATCGTAGTGGCAGAG
 GGTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGCTACAGCAAAAAT
 GCTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACG
 CTTTAACAAATGGATTTTCAGAAAATGATTTGTTGGTACCACTTATAGAT
 GCACGACGTAACAATGTTTATGTTGGTTTCTATCAAAATGGTGATACTGT
 TAAACCAGACTGTCACTTCTCTTGAAGAAGTCTTACAAGAGGTGGGGA
 ATAAAGCCAATGTTCAATTTTGTGCGAGAGGTTGCAGCATTTTTtgATCAG
 ATTAAGAAAGCCTTACCACATGCTAAAATTACAGAACTTTACCTTGTGC
 AGTGGCAATTGGGCGCAAAGGACAAAAATGGAAAGCGTTAATGTAgATG
 CGTTTGTTCACGATACTTAAAACGAGTTGAAGCTGAGGAAAATTGGTTA
 AAAAACCCTGTGAAACGAATACAGAAGAATATATTAAGAGAGTT

SEQ ID NO. 8410

STRAIN 1169NT

AAAGTTTTAGCCTTTGATACCTCAAGCAAAGCACTATCA
 GTGGCTGTACTAAACAATATGGAATGTTTAGCGACTGTCACTATCAATAT
 CAAAAAGAATCATAGCATTAAATTTGATGCCAGCCaTTGATTTTTTAATGC
 AATCAATTGATTTAGAACCTCAAGATTTGGACCGTATCGTAGTAGCAGAG
 GGTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGCTACAGCAAAAAT
 GCTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACG
 CTTTAACAAATGGATTTTCAGAAAATGATTTATTGGTACCACTTATAGAT
 GCACGACGTAACAATGTTTATGTTGGTTTCTATCAAAATGGTGATACTGT
 TAAACCAGACTGTCACTTCTCTTGAAGAAGTCTTACAAGAGGTGGGGA
 ATAAAGCCAATGTTCAATTTTGTGCGAGAGGTTGCAGCATTTTTtgATCAG
 ATTAAGAAAGCCTTACCACATGCTAAAATTACAGAACTTTACCTTGTGC
 AGTGGCAATTGGGCGCAAAGGACAAAAATGGAAAGCGTTAATGTAgATG
 CGTTTGTTCACGATACTTAAAACGAGTTGAAGCTGAGGAAAATTGGTTA
 AAAAACCCTGTGAAACGAATACAGAAGAATATATTAAGAGAGTT

Table 84: Comparative Sequences relating to SAG0267

AGTGGCAATTGGGCGCAAAGGACAAAAATGGAAAGCGTTAATGTAGATG
CGTTTGTTCACGATACTTAAACGTGTTGAAGCTGAGGAAAATTGGTTA
AAAAACCACTGTGAAACGAATACAGAAGAATATATTAAGAGAGTT

SEQ ID NO. 8411

STRAIN JM9130013

AAAGTTTTAGCCTTTGATACCTCAAGCAAAGCACTATCA
GTGGCTGTACTAAACAATATGGAATGTTTAGCGACTGTCACTATCAATAT
CAAAAAGAATCATAGCATTAAATTTGATGCCAGCCATTGATTTTTTAATGC
AATCAATTGATTTAGAACCTCAAGATTTGGACCGTATCGTAGTAGCAGAG
GGTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGCTACAGCAAAAAT
gCTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACG
CTTTAACAAATGGATTTTCAGAAAATGATTTATTGGTACCCTTATAGAT
GCACGACGTAACAATGTTTATGTTGGTTTCTATCAAAATGGAGATACTGT
TAAACCAGACTGTCACACTTCTCTTGAAGAAGTCTTACAAGAGGTGGGGA
ATAAAGCCAATGTTTCAATTTGTGCGAGAGGTTGCAGCATTGTTGACCAG
ATTAAGAAAGTTTACCACATGCTAAAATTACAGAACTTTACCTTGTGC
AGTGGCAATTGGGCGCAAAGGACAAAAATGAAAGCGTTAATGTAGATG
CGTTTGTTCACGATACTTAAACGTGTTGAAGCTGAGGAAAATTGGTTA
AGAAACCACTGTGAAACGAATACAGAAGAATATATTAAGAGAGTT

PRETTY of: /biotmp/msa521675.2{*} March 10, 2003 08:34 ..

	1		50
msa521675.2{69_A909}	-----AAAG	TTTTAGCCTT	TGATACTTCA AGCAAAGCAC TATCAGTGGC
msa521675.2{69_H36B}	-----AAAG	TTTTAGCCTT	TGATACTTCA AGCAAAGCAC TATCAGTGGC
msa521675.2{69_JM9130013}	-----AAAG	TTTTAGCCTT	TGATACTTCA AGCAAAGCAC TATCAGTGGC
msa521675.2{69_1169NT}	-----AAAG	TTTTAGCCTT	TGATACTTCA AGCAAAGCAC TATCAGTGGC
msa521675.2{69_090}	-----AAAG	TTTTAGCCTT	TGATACTTCA AGCAAAGCAC TATCAGTGGC
msa521675.2{69_CJB110}	-----AAAG	TTTTAGCCTT	TGATACTTCA AGCAAAGCAC TATCAGTGGC
msa521675.2{69_18RS21}	-----AAAG	TTTTAGCCTT	TGATACTTCA AGCAAAGCAC TATCAGTGGC
msa521675.2{69_2603}	atgatgAAAG	TTTTAGCCTT	TGATACTTCA AGCAAAGCAC TATCAGTGGC
msa521675.2{69_COH1}	-----AAAG	TTTTAGCCTT	TGATACTTCA AGCAAAGCAC TATCAGTGGC
msa521675.2{69_M732}	-----AAAG	TTTTAGCCTT	TGATACTTCA AGCAAAGCAC TATCAGTGGC
msa521675.2{69_M781}	-----AAAG	TTTTAGCCTT	TGATACTTCA AGCAAAGCAC TATCAGTGGC
Consensus	*****	*****	*****

	51		100
msa521675.2{69_A909}	TGTACTAAAC	AATATGGAAT	GTTTAGCGAC TGTCACATC AATATCAAAA
msa521675.2{69_H36B}	TGTACTAAAC	AATATGGAAT	GTTTAGCGAC TGTCACATC AATATCAAAA
msa521675.2{69_JM9130013}	TGTACTAAAC	AATATGGAAT	GTTTAGCGAC TGTCACATC AATATCAAAA
msa521675.2{69_1169NT}	TGTACTAAAC	AATATGGAAT	GTTTAGCGAC TGTCACATC AATATCAAAA
msa521675.2{69_090}	TGTACTAAAC	AATATGGAAT	GTTTAGCGAC TGTCACATC AATATCAAAA
msa521675.2{69_CJB110}	TGTACTAAAC	AATATGGAAT	GTTTAGCGAC TGTCACATC AATATCAAAA
msa521675.2{69_18RS21}	TGTACTAAAC	AATATGGAAT	GTTTAGCGAC TGTCACATC AATATCAAAA
msa521675.2{69_2603}	TGTACTAAAC	AATATGGAAT	GTTTAGCGAC TGTCACATC AATATCAAAA
msa521675.2{69_COH1}	TGTACTAAAC	AATATGGAAT	GTTTAGCGAC TGTCACATC AATATCAAAA
msa521675.2{69_M732}	TGTACTAAAC	AATATGGAAT	GTTTAGCGAC TGTCACATC AATATCAAAA
msa521675.2{69_M781}	TGTACTAAAC	AATATGGAAT	GTTTAGCGAC TGTCACATC AATATCAAAA
Consensus	*****	*****	*****

	101		150
msa521675.2{69_A909}	AGAATCATAG	CATTAATTTG	ATGCCAGCCA TTGATTTTTT AATGCAATCA
msa521675.2{69_H36B}	AGAATCATAG	CATTAATTTG	ATGCCAGCCA TTGATTTTTT AATGCAATCA
msa521675.2{69_JM9130013}	AGAATCATAG	CATTAATTTG	ATGCCAGCCA TTGATTTTTT AATGCAATCA
msa521675.2{69_1169NT}	AGAATCATAG	CATTAATTTG	ATGCCAGCCA TTGATTTTTT AATGCAATCA
msa521675.2{69_090}	AGAATCATAG	CATTAATTTG	ATGCCAGCCA TTGATTTTTT AATGCAATCA
msa521675.2{69_CJB110}	AGAATCATAG	CATTAATTTG	ATGCCAGCCA TTGATTTTTT AATGCAATCA
msa521675.2{69_18RS21}	AGAATCATAG	CATTAATTTG	ATGCCAGCCA TTGATTTTTT AATGCAATCA
msa521675.2{69_2603}	AGAATCATAG	CATTAATTTG	ATGCCAGCCA TTGATTTTTT AATGCAATCA
msa521675.2{69_COH1}	AGAATCATAG	CATTAATTTG	ATGCCAGCCA TTGATTTTTT AATGCAATCA
msa521675.2{69_M732}	AGAATCATAG	CATTAATTTG	ATGCCAGCCA TTGATTTTTT AATGCAATCA
msa521675.2{69_M781}	AGAATCATAG	CATTAATTTG	ATGCCAGCCA TTGATTTTTT AATGCAATCA
Consensus	*****	*****	*****

	151		200
msa521675.2{69_A909}	ATTGATTTAG	AACCTCAAGA	TTTGGACCGT ATCGTAGTag CAGAGGGTCC
msa521675.2{69_H36B}	ATTGATTTAG	AACCTCAAGA	TTTGGACCGT ATCGTAGTag CAGAGGGTCC
msa521675.2{69_JM9130013}	ATTGATTTAG	AACCTCAAGA	TTTGGACCGT ATCGTAGTag CAGAGGGTCC
msa521675.2{69_1169NT}	ATTGATTTAG	AACCTCAAGA	TTTGGACCGT ATCGTAGTag CAGAGGGTCC
msa521675.2{69_090}	ATTGATTTAG	AACCTCAAGA	TTTGGACCGT ATCGTAGTgg CAGAGGGTCC
msa521675.2{69_CJB110}	ATTGATTTAG	AACCTCAAGA	TTTGGACCGT ATCGTAGTgg CAGAGGGTCC
msa521675.2{69_18RS21}	ATTGATTTAG	AACCTCAAGA	TTTGGACCGT ATCGTAGTag CAGAGGGTCC
msa521675.2{69_2603}	ATTGATTTAG	AACCTCAAGA	TTTGGACCGT ATCGTAGTag CAGAGGGTCC
msa521675.2{69_COH1}	ATTGATTTAG	AACCTCAAGA	TTTGGACCGT ATCGTAGTag CAGAGGGTCC
msa521675.2{69_M732}	ATTGATTTAG	AACCTCAAGA	TTTGGACCGT ATCGTAGTag CAGAGGGTCC
msa521675.2{69_M781}	ATTGATTTAG	AACCTCAAGA	TTTGGACCGT ATCGTAGTat CAGAGGGTCC
Consensus	*****	*****	*****

	201		250
msa521675.2{69_A909}	AGGATCTTAT	ACGGGCTTAC	GTGTAGCTGT TGCTACAGCA AAAATGCTAG
msa521675.2{69_H36B}	AGGATCTTAT	ACGGGCTTAC	GTGTAGCTGT TGCTACAGCA AAAATGCTAG

Table 84: Comparative Sequences relating to SAG0267

msa521675.2{69_JM9130013}	AGGATCTTAT	ACGGGCTTAC	GTGTAGCTGT	TGCTACAGCA	AAAATGCTAG
msa521675.2{69_1169NT}	AGGATCTTAT	ACGGGCTTAC	GTGTAGCTGT	TGCTACAGCA	AAAATGCTAG
msa521675.2{69_090}	AGGATCTTAT	ACGGGCTTAC	GTGTAGCTGT	TGCTACAGCA	AAAATGCTAG
msa521675.2{69_CJB110}	AGGATCTTAT	ACGGGCTTAC	GTGTAGCTGT	TGCTACAGCA	AAAATGCTAG
msa521675.2{69_18RS21}	AGGATCTTAT	ACGGGCTTAC	GTGTAGCTGT	TGCTACAGCA	AAAATGCTAG
msa521675.2{69_2603}	AGGATCTTAT	ACGGGCTTAC	GTGTAGCTGT	TGCTACAGCA	AAAATGCTAG
msa521675.2{69_COH1}	AGGATCTTAT	ACGGGCTTAC	GTGTAGCTGT	TGCTACAGCA	AAAATGCTAG
msa521675.2{69_M732}	AGGATCTTAT	ACGGGCTTAC	GTGTAGCTGT	TGCTACAGCA	AAAATGCTAG
msa521675.2{69_M781}	AGGATCTTAT	ACGGGCTTAC	GTGTAGCTGT	TGCTACAGCA	AAAATGCTAG
Consensus	*****	*****	*****	*****	*****
251					
msa521675.2{69_A909}	CTTATACGCT	TAAGATTGAC	TTAGTTGGAG	TATCTAGCCT	GTACGCTTTA
msa521675.2{69_H36B}	CTTATACGCT	TAAGATTGAC	TTAGTTGGAG	TATCTAGCCT	GTACGCTTTA
msa521675.2{69_JM9130013}	CTTATACGCT	TAAGATTGAC	TTAGTTGGAG	TATCTAGCCT	GTACGCTTTA
msa521675.2{69_1169NT}	CTTATACGCT	TAAGATTGAC	TTAGTTGGAG	TATCTAGCCT	GTACGCTTTA
msa521675.2{69_090}	CTTATACGCT	TAAGATTGAC	TTAGTTGGAG	TATCTAGCCT	GTACGCTTTA
msa521675.2{69_CJB110}	CTTATACGCT	TAAGATTGAC	TTAGTTGGAG	TATCTAGCCT	GTACGCTTTA
msa521675.2{69_18RS21}	CTTATACGCT	TAAGATTGAC	TTAGTTGGAG	TATCTAGCCT	GTACGCTTTA
msa521675.2{69_2603}	CTTATACGCT	TAAGATTGAC	TTAGTTGGAG	TATCTAGCCT	GTACGCTTTA
msa521675.2{69_COH1}	CTTATACGCT	TAAGATTGAC	TTAGTTGGAG	TATCTAGCCT	GTACGCTTTA
msa521675.2{69_M732}	CTTATACGCT	TAAGATTGAC	TTAGTTGGAG	TATCTAGCCT	GTACGCTTTA
msa521675.2{69_M781}	CTTATACGCT	TAAGATTGAC	TTAGTTGGAG	TATCTAGCCT	GTACGCTTTA
Consensus	*****	*****	*****	*****	*****
301					
msa521675.2{69_A909}	ACAAATGGAT	TTTCAGAAAA	TGATTTaTTG	GTACCACTTA	TAGATGCACG
msa521675.2{69_H36B}	ACAAATGGAT	TTTCAGAAAA	TGATTTaTTG	GTACCACTTA	TAGATGCACG
msa521675.2{69_JM9130013}	ACAAATGGAT	TTTCAGAAAA	TGATTTaTTG	GTACCACTTA	TAGATGCACG
msa521675.2{69_1169NT}	ACAAATGGAT	TTTCAGAAAA	TGATTTaTTG	GTACCACTTA	TAGATGCACG
msa521675.2{69_090}	ACAAATGGAT	TTTCAGAAAA	TGATTTgTTG	GTACCACTTA	TAGATGCACG
msa521675.2{69_CJB110}	ACAAATGGAT	TTTCAGAAAA	TGATTTgTTG	GTACCACTTA	TAGATGCACG
msa521675.2{69_18RS21}	ACAAATGGAT	TTTCAGAAAA	TGATTTaTTG	GTACCACTTA	TAGATGCACG
msa521675.2{69_2603}	ACAAATGGAT	TTTCAGAAAA	TGATTTaTTG	GTACCACTTA	TAGATGCACG
msa521675.2{69_COH1}	ACAAATGGAT	TTTCAGAAAA	TGATTTaTTG	GTACCACTTA	TAGATGCACG
msa521675.2{69_M732}	ACAAATGGAT	TTTCAGAAAA	TGATTTaTTG	GTACCACTTA	TAGATGCACG
msa521675.2{69_M781}	ACAAATGGAT	TTTCAGAAAA	TGATTTaTTG	GTACCACTTA	TAGATGCACG
Consensus	*****	*****	*****-***	*****	*****
351					
msa521675.2{69_A909}	ACGTAAcAAT	GTTTATGTTG	GTTTCTATCA	AAATGGaGAT	ACTGTTAAAC
msa521675.2{69_H36B}	ACGTAAcAAT	GTTTATGTTG	GTTTCTATCA	AAATGGaGAT	ACTGTTAAAC
msa521675.2{69_JM9130013}	ACGTAAcAAT	GTTTATGTTG	GTTTCTATCA	AAATGGaGAT	ACTGTTAAAC
msa521675.2{69_1169NT}	ACGTAAcAAT	GTTTATGTTG	GTTTCTATCA	AAATGGtGAT	ACTGTTAAAC
msa521675.2{69_090}	ACGTAAcAAT	GTTTATGTTG	GTTTCTATCA	AAATGGtGAT	ACTGTTAAAC
msa521675.2{69_CJB110}	ACGTAAcAAT	GTTTATGTTG	GTTTCTATCA	AAATGGtGAT	ACTGTTAAAC
msa521675.2{69_18RS21}	ACGTAAcAAT	GTTTATGTTG	GTTTCTATCA	AAATGGtGAT	ACTGTTAAAC
msa521675.2{69_2603}	ACGTAAcAAT	GTTTATGTTG	GTTTCTATCA	AAATGGtGAT	ACTGTTAAAC
msa521675.2{69_COH1}	ACGTAAcAAT	GTTTATGTTG	GTTTCTATCA	AAATGGtGAT	ACTGTTAAAC
msa521675.2{69_M732}	ACGTAAcAAT	GTTTATGTTG	GTTTCTATCA	AAATGGtGAT	ACTGTTAAAC
msa521675.2{69_M781}	ACGTAAcAAT	GTTTATGTTG	GTTTCTATCA	AAATGGtGAT	ACTGTTAAAC
Consensus	*****-***	*****	*****	*****-***	*****
401					
msa521675.2{69_A909}	CAGACTGTCA	CACCTCTCTT	GAAGAAGTCT	TACAAGAGGT	GGGGAATAAA
msa521675.2{69_H36B}	CAGACTGTCA	CACCTCTCTT	GAAGAAGTCT	TACAAGAGGT	GGGGAATAAA
msa521675.2{69_JM9130013}	CAGACTGTCA	CACCTCTCTT	GAAGAAGTCT	TACAAGAGGT	GGGGAATAAA
msa521675.2{69_1169NT}	CAGACTGTCA	CACCTCTCTT	GAAGAAGTCT	TACAAGAGGT	GGGGAATAAA
msa521675.2{69_090}	CAGACTGTCA	CACCTCTCTT	GAAGAAGTCT	TACAAGAGGT	GGGGAATAAA
msa521675.2{69_CJB110}	CAGACTGTCA	CACCTCTCTT	GAAGAAGTCT	TACAAGAGGT	GGGGAATAAA
msa521675.2{69_18RS21}	CAGACTGTCA	CACCTCTCTT	GAAGAAGTCT	TACAAGAGGT	GGGGAATAAA
msa521675.2{69_2603}	CAGACTGTCA	CACCTCTCTT	GAAGAAGTCT	TACAAGAGGT	GGGGAATAAA
msa521675.2{69_COH1}	CAGACTGTCA	CACCTCTCTT	GAAGAAGTCT	TACAAGAGGT	GGGGAATAAA
msa521675.2{69_M732}	CAGACTGTCA	CACCTCTCTT	GAAGAAGTCT	TACAAGAGGT	GGGGAATAAA
msa521675.2{69_M781}	CAGACTGTCA	CACCTCTCTT	GAAGAAGTCT	TACAAGAGGT	GGGGAATAAA
Consensus	*****	*****	*****	*****	*****
451					
msa521675.2{69_A909}	GCCAATGTTT	ATTTTGTCCG	AGAGGTTGCA	GCATTTgTTG	AcCAGATTAA
msa521675.2{69_H36B}	GCCAATGTTT	ATTTTGTCCG	AGAGGTTGCA	GCATTTgTTG	AcCAGATTAA
msa521675.2{69_JM9130013}	GCCAATGTTT	ATTTTGTCCG	AGAGGTTGCA	GCATTTgTTG	AcCAGATTAA
msa521675.2{69_1169NT}	GCCAATGTTT	ATTTTGTCCG	AGAGGTTGCA	GCATTTgTTG	AcCAGATTAA
msa521675.2{69_090}	GCCAATGTTT	ATTTTGTCCG	AGAGGTTGCA	GCATTTtTTG	AtCAGATTAA
msa521675.2{69_CJB110}	GCCAATGTTT	ATTTTGTCCG	AGAGGTTGCA	GCATTTtTTG	AtCAGATTAA
msa521675.2{69_18RS21}	GCCAATGTTT	ATTTTGTCCG	AGAGGTTGCA	GCATTTtTTG	AtCAGATTAA
msa521675.2{69_2603}	GCCAATGTTT	ATTTTGTCCG	AGAGGTTGCA	GCATTTtTTG	AtCAGATTAA
msa521675.2{69_COH1}	GCCAATGTTT	ATTTTGTCCG	AGAGGTTGCA	GCATTTtTTG	AtCAGATTAA
msa521675.2{69_M732}	GCCAATGTTT	ATTTTGTCCG	AGAGGTTGCA	GCATTTtTTG	AtCAGATTAA
msa521675.2{69_M781}	GCCAATGTTT	ATTTTGTCCG	AGAGGTTGCA	GCATTTtTTG	AtCAGATTAA
Consensus	*****	*****	*****	*****-***	*-*****
501					
msa521675.2{69_A909}	GAAAGtTTTA	CCACATGCTA	AAATTACAGA	AACTTTACCT	TGTGCAGTgG
550					

Table 84: Comparative Sequences relating to SAG0267

msa521675.2{69_H36B}	GAAAGcttTTA	CCACATGCTA	AAATTACAGA	AACTTTACCT	TGTGCAGTgG
msa521675.2{69_JM9130013}	GAAAGcttTTA	CCACATGCTA	AAATTACAGA	AACTTTACCT	TGTGCAGTgG
msa521675.2{69_1169NT}	GAAAGcttTTA	CCACATGCTA	AAATTACAGA	AACTTTACCT	TGTGCAGTgG
msa521675.2{69_090}	GAAAGccTTA	CCACATGCTA	AAATTACAGA	AACTTTACCT	TGTGCAGTgG
msa521675.2{69_CJB110}	GAAAGccTTA	CCACATGCTA	AAATTACAGA	AACTTTACCT	TGTGCAGTgG
msa521675.2{69_18RS21}	GAAAGccTTA	CCACATGCTA	AAATTACAGA	AACTTTACCT	TGTGCAGTaG
msa521675.2{69_2603}	GAAAGccTTA	CCACATGCTA	AAATTACAGA	AACTTTACCT	TGTGCAGTaG
msa521675.2{69_COH1}	GAAAGccTTA	CCACATGCTA	AAATTACAGA	AACTTTACCT	TGTGCAGTaG
msa521675.2{69_M732}	GAAAGccTTA	CCACATGCTA	AAATTACAGA	AACTTTACCT	TGTGCAGTaG
msa521675.2{69_M781}	GAAAGccTTA	CCACATGCTA	AAATTACAGA	AACTTTACCT	TGTGCAGTaG
Consensus	*****_--**	*****	*****	*****	*****_--*
551					
msa521675.2{69_A909}	CAATTGGGCG	CAAAGGACAA	AAAATGaAAA	GCGTTAATGT	AGAtgCGTTT
msa521675.2{69_H36B}	CAATTGGGCG	CAAAGGACAA	AAAATGaAAA	GCGTTAATGT	AGAtgCGTTT
msa521675.2{69_JM9130013}	CAATTGGGCG	CAAAGGACAA	AAAATGaAAA	GCGTTAATGT	AGAtgCGTTT
msa521675.2{69_1169NT}	CAATTGGGCG	CAAAGGACAA	AAAATGgAAA	GCGTTAATGT	AGAtgCGTTT
msa521675.2{69_090}	CAATTGGGCG	CAAAGGACAA	AAAATGgAAA	GCGTTAATGT	AGAtgCGTTT
msa521675.2{69_CJB110}	CAATTGGGCG	CAAAGGACAA	AAAATGgAAA	GCGTTAATGT	AGAtgCGTTT
msa521675.2{69_18RS21}	CAATTGGGCG	CAAAGGACAA	AAAATGaAAA	GCGTTAATGT	AGAtgCGTTT
msa521675.2{69_2603}	CAATTGGGCG	CAAAGGACAA	AAAATGaAAA	GCGTTAATGT	AGAtgCGTTT
msa521675.2{69_COH1}	CAATTGGGCG	CAAAGGACAA	AAAATGaAAA	GCGTTAATGT	AGAtgCGTTT
msa521675.2{69_M732}	CAATTGGGCG	CAAAGGACAA	AAAATGaAAA	GCGTTAATGT	AGAnnCGTTT
msa521675.2{69_M781}	CAATTGGGCG	CAAAGGACAA	AAAATGaAAA	GCGTTAATGT	AGAtgCGTTT
Consensus	*****	*****	*****_--**	*****	***_--*****
601					
msa521675.2{69_A909}	GTTCCACGAT	ACTTAAAACG	tGTTGAAGCT	GAGGAAAATT	GGTTAAgAAA
msa521675.2{69_H36B}	GTTCCACGAT	ACTTAAAACG	tGTTGAAGCT	GAGGAAAATT	GGTTAAgAAA
msa521675.2{69_JM9130013}	GTTCCACGAT	ACTTAAAACG	tGTTGAAGCT	GAGGAAAATT	GGTTAAgAAA
msa521675.2{69_1169NT}	GTTCCACGAT	ACTTAAAACG	tGTTGAAGCT	GAGGAAAATT	GGTTAAaAAA
msa521675.2{69_090}	GTTCCACGAT	ACTTAAAACG	aGTTGAAGCT	GAGGAAAATT	GGTTAAaAAA
msa521675.2{69_CJB110}	GTTCCACGAT	ACTTAAAACG	aGTTGAAGCT	GAGGAAAATT	GGTTAAaAAA
msa521675.2{69_18RS21}	GTTCCACGAT	ACTTAAAACG	tGTTGAAGCT	GAGGAAAATT	GGTTAAaAAA
msa521675.2{69_2603}	GTTCCACGAT	ACTTAAAACG	tGTTGAAGCT	GAGGAAAATT	GGTTAAaAAA
msa521675.2{69_COH1}	GTTCCACGAT	ACTTAAAACG	tGTTGAAGCT	GAGGAAAATT	GGTTAAaAAA
msa521675.2{69_M732}	GTTCCACGAT	ACTTAAAACG	tGTTGAAGCT	GAGGAAAATT	GGTTAAaAAA
msa521675.2{69_M781}	GTTCCACGAT	ACTTAAAACG	tGTTGAAGCT	GAGGAAAATT	GGTTAAaAAA
Consensus	*****	*****	_--*****	*****	*****_--**
651					
msa521675.2{69_A909}	CCACTGTGAA	ACGAAT----	-----	-----	-----
msa521675.2{69_H36B}	CCACTGTGAA	ACGAATACAG	AAGAATATAT	TAAGAGAGTT	-----
msa521675.2{69_JM9130013}	CCACTGTGAA	ACGAATACAG	AAGAATATAT	TAAGAGAGTT	-----
msa521675.2{69_1169NT}	CCACTGTGAA	ACGAATACAG	AAGAATATAT	TAAGAGAGTT	-----
msa521675.2{69_090}	CCACTGTGAA	ACGAAT----	-----	-----	-----
msa521675.2{69_CJB110}	CCACTGTGAA	ACGAATACAG	AAGAATATAT	TAAGAGAGTT	-----
msa521675.2{69_18RS21}	CCACTGTGAA	ACGAATACAG	AAGAATATAT	TAAGAGAGTT	-----
msa521675.2{69_2603}	CCACTGTGAA	ACGAATACAG	AAGAATATAT	TAAGAGAGTT	-----
msa521675.2{69_COH1}	CCACTGTGAA	ACGAATACAG	AAGAATATAT	TAAGAGAGTT	-----
msa521675.2{69_M732}	CCACTGTGAA	ACGAATACAG	AAGAATATAT	TAAGAGAGTT	-----
msa521675.2{69_M781}	CCACTGTGAA	ACGAATACAG	AAGAATATAT	TAAGAGAGTT	-----
Consensus	*****	*****	*****	*****	*****

SEQ ID NO. 8412

STRAIN 2603 frame: 1

MMKVLAFDTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDR
 IVVAEGPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNN
 VYVGFYQNGDTVKPDCHTSLEEVLQEVGNKANVHFVGEVAAFFDQIKKALPHAKITETLP
 CAVAIGRKGQMKSVNVDAFVPRYLKRVEAEENWLNHCETNTEEYIKRV

SEQ ID NO. 8413

STRAIN 090 frame: 1

KVLAFDTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
 VAEGPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGFYQNGDTVKPDCHTSLEEVLQEVGNKANVHFVGEVAAFFDQIKKALPHAKITETLPCA
 VAIGRKGQKMSVNVDAFVPRYLKRVEAEENWLNHCETN

SEQ ID NO. 8414

STRAIN A909 frame: 1

KVLAFDTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
 VAEGPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGFYQNGDTVKPDCHTSLEEVLQEVGNKANVHFVGEVAAFFDQIKKALPHAKITETLPCA
 VAIGRKGQKMSVNVDAFVPRYLKRVEAEENWLNHCETN

SEQ ID NO. 8415

STRAIN H36B frame: 1

KVLAFDTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
 VAEGPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGFYQNGDTVKPDCHTSLEEVLQEVGNKANVHFVGEVAAFFDQIKKALPHAKITETLPCA
 VAIGRKGQKMSVNVDAFVPRYLKRVEAEENWLNHCETNTEEYIKRV

SEQ ID NO. 8416

Table 84: Comparative Sequences relating to SAG0267

STRAIN 18RS21 frame: 1
 KVLAFDTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
 VAEGPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGFYQNGDTPKPDCHTSLEEVLQEVGNKANVHFVGEVAAFFDQIKKALPHAKITETLPCA
 VAIGRKGQMKSVNVDAFVPRYLKRVEAEENWLKNHCETNTEEYIKRV

SEQ ID NO. 8417

STRAIN M732 frame: 1
 KVLAFDTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
 VAEGPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGFYQNGDTPKPDCHTSLEEVLQEVGNKANVHFVGEVAAFFDQIKKALPHAKITETLPCA
 VAIGRKGQMKSVNVXXFVPRYLKRVEAEENWLKNHCETNTEEYIKRV

SEQ ID NO. 8418

STRAIN COH1 frame: 1
 KVLAFDTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
 VAEGPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGFYQNGDTPKPDCHTSLEEVLQEVGNKANVHFVGEVAAFFDQIKKALPHAKITETLPCA
 VAIGRKGQMKSVNVDAFVPRYLKRVEAEENWLKNHCETNTEEYIKRV

SEQ ID NO. 8419

STRAIN M781 frame: 1
 KVLAFDTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
 VSEPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGFYQNGDTPKPDCHTSLEEVLQEVGNKANVHFVGEVAAFFDQIKKALPHAKITETLPCA
 VAIGRKGQMKSVNVDAFVPRYLKRVEAEENWLKNHCETNTEEYIKRV

SEQ ID NO. 8420

STRAIN CJB110 frame: 1
 KVLAFDTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
 VAEGPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGFYQNGDTPKPDCHTSLEEVLQEVGNKANVHFVGEVAAFFDQIKKALPHAKITETLPCA
 VAIGRKGQKMSVNVDAFVPRYLKRVEAEENWLKNHCETNTEEYIKRV

SEQ ID NO. 8421

STRAIN 1169NT frame: 1
 KVLAFDTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
 VAEGPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGFYQNGDTPKPDCHTSLEEVLQEVGNKANVHFVGEVAAFFDQIKKALPHAKITETLPCA
 VAIGRKGQKMSVNVDAFVPRYLKRVEAEENWLKNHCETNTEEYIKRV

SEQ ID NO. 8422

STRAIN JM9130013 frame: 1
 KVLAFDTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
 VAEGPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGFYQNGDTPKPDCHTSLEEVLQEVGNKANVHFVGEVAAFFDQIKKALPHAKITETLPCA
 VAIGRKGQKMSVNVDAFVPRYLKRVEAEENWLKNHCETNTEEYIKRV

PRETTY of: /biotmp/msa521982.2{*} March 10, 2003 08:40 ..

	1		50
msa521982.2{69_A909}	--KVLAFDTS	SKALSVAVLN NMECLATVTI	NIKKNHSINL MPAIDFLMQS
msa521982.2{69_H36B}	--KVLAFDTS	SKALSVAVLN NMECLATVTI	NIKKNHSINL MPAIDFLMQS
msa521982.2{69_JM9130013}	--KVLAFDTS	SKALSVAVLN NMECLATVTI	NIKKNHSINL MPAIDFLMQS
msa521982.2{69_090}	--KVLAFDTS	SKALSVAVLN NMECLATVTI	NIKKNHSINL MPAIDFLMQS
msa521982.2{69_CJB110}	--KVLAFDTS	SKALSVAVLN NMECLATVTI	NIKKNHSINL MPAIDFLMQS
msa521982.2{69_18RS21}	--KVLAFDTS	SKALSVAVLN NMECLATVTI	NIKKNHSINL MPAIDFLMQS
msa521982.2{69_2603}	mmKVLAFDTS	SKALSVAVLN NMECLATVTI	NIKKNHSINL MPAIDFLMQS
msa521982.2{69_COH1}	--KVLAFDTS	SKALSVAVLN NMECLATVTI	NIKKNHSINL MPAIDFLMQS
msa521982.2{69_M781}	--KVLAFDTS	SKALSVAVLN NMECLATVTI	NIKKNHSINL MPAIDFLMQS
msa521982.2{69_1169NT}	--KVLAFDTS	SKALSVAVLN NMECLATVTI	NIKKNHSINL MPAIDFLMQS
msa521982.2{69_M732}	--KVLAFDTS	SKALSVAVLN NMECLATVTI	NIKKNHSINL MPAIDFLMQS
Consensus	*****	*****	*****
	51		100
msa521982.2{69_A909}	IDLEPQDLDR	IVVaEGPGSY TGLRVAVATA	KMLAYTLKID LVGVSSLYAL
msa521982.2{69_H36B}	IDLEPQDLDR	IVVaEGPGSY TGLRVAVATA	KMLAYTLKID LVGVSSLYAL
msa521982.2{69_JM9130013}	IDLEPQDLDR	IVVaEGPGSY TGLRVAVATA	KMLAYTLKID LVGVSSLYAL
msa521982.2{69_090}	IDLEPQDLDR	IVVaEGPGSY TGLRVAVATA	KMLAYTLKID LVGVSSLYAL
msa521982.2{69_CJB110}	IDLEPQDLDR	IVVaEGPGSY TGLRVAVATA	KMLAYTLKID LVGVSSLYAL
msa521982.2{69_18RS21}	IDLEPQDLDR	IVVaEGPGSY TGLRVAVATA	KMLAYTLKID LVGVSSLYAL
msa521982.2{69_2603}	IDLEPQDLDR	IVVaEGPGSY TGLRVAVATA	KMLAYTLKID LVGVSSLYAL
msa521982.2{69_COH1}	IDLEPQDLDR	IVVaEGPGSY TGLRVAVATA	KMLAYTLKID LVGVSSLYAL
msa521982.2{69_M781}	IDLEPQDLDR	IVVaEGPGSY TGLRVAVATA	KMLAYTLKID LVGVSSLYAL
msa521982.2{69_1169NT}	IDLEPQDLDR	IVVaEGPGSY TGLRVAVATA	KMLAYTLKID LVGVSSLYAL
msa521982.2{69_M732}	IDLEPQDLDR	IVVaEGPGSY TGLRVAVATA	KMLAYTLKID LVGVSSLYAL
Consensus	*****	***_*****	*****
	101		150
msa521982.2{69_A909}	TNGFSENDLL	VPLIDARRNN VYVGFYQNGD	TVKPDCHTSL EEVLQEVGNK
msa521982.2{69_H36B}	TNGFSENDLL	VPLIDARRNN VYVGFYQNGD	TVKPDCHTSL EEVLQEVGNK

Table 84: Comparative Sequences relating to SAG0267

msa521982.2{69_JM9130013}	TNGFSENDLL	VPLIDARRNN	VYVGfYQNGD	TVKPDCHTSL	EEVLQEVGNK
msa521982.2{69_090}	TNGFSENDLL	VPLIDARRNN	VYVGfYQNGD	TVKPDCHTSL	EEVLQEVGNK
msa521982.2{69_CJB110}	TNGFSENDLL	VPLIDARRNN	VYVGfYQNGD	TVKPDCHTSL	EEVLQEVGNK
msa521982.2{69_18RS21}	TNGFSENDLL	VPLIDARRNN	VYVGfYQNGD	TVKPDCHTSL	EEVLQEVGNK
msa521982.2{69_2603}	TNGFSENDLL	VPLIDARRNN	VYVGfYQNGD	TVKPDCHTSL	EEVLQEVGNK
msa521982.2{69_COH1}	TNGFSENDLL	VPLIDARRNN	VYVGfYQNGD	TVKPDCHTSL	EEVLQEVGNK
msa521982.2{69_M781}	TNGFSENDLL	VPLIDARRNN	VYVGfYQNGD	TVKPDCHTSL	EEVLQEVGNK
msa521982.2{69_1169NT}	TNGFSENDLL	VPLIDARRNN	VYVGfYQNGD	TVKPDCHTSL	EEVLQEVGNK
msa521982.2{69_M732}	TNGFSENDLL	VPLIDARRNN	VYVGfYQNGD	TVKPDCHTSL	EEVLQEVGNK
Consensus	*****	*****	*****	*****	*****
151					
msa521982.2{69_A909}	ANVHFVGEVA	AFvDQIKKvL	PHAKITETLP	CAVAIGRKGQ	KMkSVNVdaF
msa521982.2{69_H36B}	ANVHFVGEVA	AFvDQIKKvL	PHAKITETLP	CAVAIGRKGQ	KMkSVNVdaF
msa521982.2{69_JM9130013}	ANVHFVGEVA	AFvDQIKKvL	PHAKITETLP	CAVAIGRKGQ	KMkSVNVdaF
msa521982.2{69_090}	ANVHFVGEVA	AFfdQIKKaL	PHAKITETLP	CAVAIGRKGQ	KMeSVNVdaF
msa521982.2{69_CJB110}	ANVHFVGEVA	AFfdQIKKaL	PHAKITETLP	CAVAIGRKGQ	KMeSVNVdaF
msa521982.2{69_18RS21}	ANVHFVGEVA	AFfdQIKKaL	PHAKITETLP	CAVAIGRKGQ	KMkSVNVdaF
msa521982.2{69_2603}	ANVHFVGEVA	AFfdQIKKaL	PHAKITETLP	CAVAIGRKGQ	KMkSVNVdaF
msa521982.2{69_COH1}	ANVHFVGEVA	AFfdQIKKaL	PHAKITETLP	CAVAIGRKGQ	KMkSVNVdaF
msa521982.2{69_M781}	ANVHFVGEVA	AFfdQIKKaL	PHAKITETLP	CAVAIGRKGQ	KMkSVNVdaF
msa521982.2{69_1169NT}	ANVHFVGEVA	AFvDQIKKaL	PHAKITETLP	CAVAIGRKGQ	KMeSVNVdaF
msa521982.2{69_M732}	ANVHFVGEVA	AFfdQIKKaL	PHAKITETLP	CAVAIGRKGQ	KMkSVNVxxF
Consensus	*****	**_*****_*	*****	*****	**-*****-*
201					
msa521982.2{69_A909}	VPRYLKRVEA	EENWLrNHCE	TN-----	230	
msa521982.2{69_H36B}	VPRYLKRVEA	EENWLrNHCE	TNTEEYIKRV		
msa521982.2{69_JM9130013}	VPRYLKRVEA	EENWLrNHCE	TNTEEYIKRV		
msa521982.2{69_090}	VPRYLKRVEA	EENWLkNHCE	TN-----		
msa521982.2{69_CJB110}	VPRYLKRVEA	EENWLkNHCE	TNTEEYIKRV		
msa521982.2{69_18RS21}	VPRYLKRVEA	EENWLkNHCE	TNTEEYIKRV		
msa521982.2{69_2603}	VPRYLKRVEA	EENWLkNHCE	TNTEEYIKRV		
msa521982.2{69_COH1}	VPRYLKRVEA	EENWLkNHCE	TNTEEYIKRV		
msa521982.2{69_M781}	VPRYLKRVEA	EENWLkNHCE	TNTEEYIKRV		
msa521982.2{69_1169NT}	VPRYLKRVEA	EENWLkNHCE	TNTEEYIKRV		
msa521982.2{69_M732}	VPRYLKRVEA	EENWLkNHCE	TNTEEYIKRV		
Consensus	*****	*****_****	*****		

Table 85: Comparative Sequences relating to SAG1361

SEQ ID NO. 8501

STRAIN 2603

atgagtaaacgacaaaatttaggaattagtaaaaaaggagcaattatatcaggggctctca
gtggcactaattttagtaaataggtggctttttatgggtacaatctcaacctaatagagt
gcagtaaaaaactaactacaaagtttttaattgtagagaaggaagtggttcgtcctcaact
cttttgacaggaaaagctaaggctaatacaagaacagtatgtgtattttgatgctaataaa
ggtaatcgagcaactgtcacagttaaagtgggtgataaaatcacagctggtcagcagtta
gttcaatatgatacaacaactgcacaagcagcctacgacactgctaatacgtcaattaaat
aaagtagcgcgtcagatttaataatctaagacaacaggaagtctccagctatggaatca
agtgatcaatcttcttcatcatcacaaggacaagggactcaatcgactagtgggtgcgacg
aatcgtctacagcaaaaattatcaaagtcaagctaattgcttcatacaaccaacaacttcaa
gatttgaatgatgcttatgacagatgcacaggcagaagtaataaaagcacaaaaagcattg
aatgatactgttattacaagtgcgtatcagggacagttgttgaagttaatagtgatatt
gatccagcttcaaaaactagtcaagtacttgtccatgtagcaactgaaggtaaaactccaa
gtacaaggaacgatgagtgagtgatgatttggctaattgttaaaaaagaccaggctgttaa
ataaaatctaaggtctatcctgacaaggaatgggaaggtaaaatttcatatatctcaaat
tatccagaagcagaagcaacaacaatgactctaataacggctctagtgtgttaaattat
aatataaagtagatattactagccctctcgatgcattaaaacaagggtttaccgtatca
gttgaagtagttaatggagataagcaccttattgtccctacaagttctgtgataaaca
gataataaacactttgtttgggtatacaatgatttctaatacgtaaaatttccaaagttgaa
gtcaaaattggtaagctgatgctaagacacaagaaattttatcaggtttgaaagcagga
caaatcgtgggttactaatccaagtaaaaccttcaaggatgggcaaaaatttgataatatt
gaatcaatcgatcttaactctaataagaaatcagaggtgaaa

SEQ ID NO. 8502

STRAIN 090

TTTTTATGGGTACAATCTCAACCTAATAAGAGTGCAGTAAAACTAACTA
CAAAGTTTTTAATGTTAGAGAAGGAAGTGTTCGTCTCAACTCTTTTGA
CAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTTGATGCTAAT
AAAGGTAATCGAGCAACTGTCAAGTTAAAGTGGGTGATAAAATCACAGC
TGGTCAGCAGTTAGTTCAATATGATACAACTGCACAAGCAGCCTACG
ACACTGCTAATCGTCAATTAAATAAAGTAGCGCGTCAGATTAAATAATCTA
AAGACAACAGGAAGTCTTCAGCTATGGAATTAAGTGATCAATCTTCTTC
ATCATCACAGGACAAGGGACTCAATCGACTAGTGGTGCGACGAATCGTC
TACAGCAAAATTATCAAAAGTCAAGCTAATGCTTCATACAAACCAACTT
CAAGATTTGAATGATGCTTATGCAGATGCACAGGCAGAAAGTAAATAAAGC
ACAAAAGCATTGAATGATACTGTTATTACAAGTGACGTATCAGGGACAG
TTGTTGAAGTTAATAGTGATATTGATCCAGCTTCAAAAACCTAGTCAAGTA
CTTGTCATGTAGCAACTGAAGGTAAACTCCAAGTACAAGGAACGATGAG
TGAGTATGATTTGGCTAATGTTAAAAAAGACCAGGCTGTTAAAAATAAAT
CTAAGGTCTATCCTGACAAGGAATGGGAAGGTAAAAATTTTATATATCTCA
AATTATCCAGAAGCAGAAGCAAACAACATGACTCTAATAACGGCTCTAG
TGCTGTAAATTATAAATATAAAGTAGATATTACTAGCCCTCTCGATGCAT
TAAACAAGGTTTTACCGTATCAGTTGAAGTAGTTAATGGAGATAAGCAC
CTTATTGTCCCTACAAGTTCTGTGATAAAACAAAGATAATAAACACTTTGT
TTGGGTATACAATGATTCTAATCGTAAAATTTCCAAAGTTGAAGTCAAAA
TTGGTAAAGCTGATGCTAAGACACAAGAAATTTTATCAGGTTTGAAAGCA
GGACAAATCGTGGTTACTAATCCAAGTAAAACCTTCAAGGATGGGCAAAA
AATTGATAATATTGAATCAATCGATCTTAACCTAATAAGAAATCAGAGG

SEQ ID NO. 8503

STRAIN A909

TTTTTATGGGTACAATCTCAACCTAATAAGAGTGCAGTAAAACTAA
CTACAAAGTTTTTAATGTTAGAGAAGGAAGTGTTCGTCTCAACTCTTT
TGACAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTTGATGCT
AATAAAGGTAATCGAGCAACTGTTACAGTTAAAGTGGGTGATAAAATCAC
AGCTGGTCAGCAGTTAGTTCAATATGATACAACTGCACAAGCAGCCT
ACGACACTGCTAATCGTCAATTAAATAAAGTAGCGCGTCAGATTAAATAAT
CTAAAGACAACAGGAAGTCTTCAGCTATGGAATCAAGTGATCAATCTTC
ATCATCATCACAGGACAAGGGGCTCAATCGACTAGTGGTGCGACGAATC
GTCTACAGCAAAATTATCAAAGTCAAGCTAATGCTTCATACAAACCAAA
CTTCAAGATTTGAATGATGCTTATGCAGATGCACAGGCAGAAAGTAAATAA
AGCACAAAAGCATTGAATGATACTGTTATTACAAGTGACGTATCAGGGA
CAGTTGTTGAAGTTAATAGTGATATTGATCCAGCTTCAAAAACCTAGTCAA
GTACTTGTCCATGTAGCAACTGAGGGTAAACTCCAAGTACAAGGAACGAT
GAGTGAGTATGATTTGGCTAATGTTAAAAAAGACCAGTCTGTTAAAAATAA
AATCTAAGGTCTATCCTGACAAGGAATGGGAAGGTAAAAATTTTATATATC
TCAAATTATCCAGAAGCAGAAGCAAACAACATGACTCTAATAACGGCTC
TAGTGCTGTAAATTATAAATATAAAGTAGATATTACTAGCCCTCTCGATG
CATTAAACAAGGTTTTACTGTATCAGTTGAAGTAGTTAATGGAGATAAG
CACCTTATTGTTCTTACAAGTTCTGTGACAAAACAAAGATAATAAACACTT
TGTTTGGGTATACAATGATTCTAATCGTAAAATTTCCAAAGTTGAAGTCA
AAATTGGTAAAGCTGATGCTAAGACACAAGAAATTTTATCAGGTTTGAAA
GCAGGACAAATCGTGGTTACTAATCCAAGCAAACTTTCAAGGATGGGCA
AAAAATTGATAATATTGAATCAATAGATCTTAAGTCTAATAAGAAATCAG
AGGTGAAA

SEQ ID NO. 8504

STRAIN H36B

TTTTTATGGGTACAATCTCAACCTAATAAGAGTGCAGTAAAACTAATTA
CAAAGTTTTTAATGTTAGAGAAGGAAGTGTTCGTCTCAACTCTTTTGA
CAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTTGATGCTAAT
AAGGTAATCGAGCAACTGTTACAGTTAAAGTGGGTGATAAAATCACAGC

Table 85: Comparative Sequences relating to SAG1361

TGGTCAGCAGTTAGTTCAATATGATACAACAACCTGCACAAGCAGCCTACG
 AACTGCTAATCGTCAATTAAATAAAGTAGCGCGTCAGATTAATAATCTA
 AAGACAACAGGAAGTCTTCCAGCTATGGAATCAAGTGATCAATCTTCATC
 ATCATCACAAGGACAAGGGACTCAATCGACTAGTGGTGCGACGAATCGTC
 TACAGCAAAATTATCAAAGTCAAGCTAATGCTTCATACAACCAACAACCTT
 CAAGATTTGAATGATGCTTATGCAGATGCACAGGCAGAAGTAAATAAAGC
 ACAAAAAGCATTGAATGATACTGTTATTACAAGTGACGTATCAGGGACAG
 TTGTTGAAGTTAATAGTGATATTGATCCAGCTTCAAAAACTAGTCAAGTA
 CTTGTCCATGTAGCAACTGAAGGTAAACTCCAAGTACAAGGAACGATGAG
 TGAGTATGATTTGGCTAATGTAAAAAAGACCAGGCTGTTAAAAATAAAAT
 CTAAGGTCTATCCTGACAAGGAATGGGAAGGTAAAAATTTTATATATCTCA
 AATTATCCAGAAGCAGAAGCAAACAACAATGACTCTAATAACGGCTCTAG
 TGCTGTAAATTATAAATATAAAGTAGATATTACTAGCCCTCTCGATGCAT
 TAAAAACAAGGTTTTTACTGTATCAGTTGAAGTAGTTAATGGAGATAAGCAC
 CTTATTGTTCCCTACAAGTTCTGTGACAAACAAGATAATAAACACTTTGT
 TTGGGTATACAATGATTCTAATCGTAAAAATTTCCAAAGTTGAAGTCAAAA
 TTGGTAAAGCTGATGCTAAGACACAAGAAATTTTATCAGGTTTGAAAGCA
 GGACAAATCGTAGTTACTAATCCAAGTAAAGCTTTCAAGGATGGGCAAAA
 AATTGATAATATTGAATCAATCGATCTTAAGTCTAATAAGAAATCAGAGG
 TG

SEQ ID NO. 8505

STRAIN 18RS21

TTTTTATGGGTACAATCTCAACCTAATAAGAGTGCAGTAAAACTAACTA
 CAAAGTTTTTAATGTTAGAGAAGGAAGTGTTCGTCTCAACTCTTTTGA
 CAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTTGATGCTAAT
 AAAGGTAATCGAGCAACTGTCAAGTTAAAGTGGGTGATAAAATCACAGC
 TGGTCAGCAGTTAGTTCAATATGATACAACAACCTGCACAAGCAGCCTACG
 AACTGCTAATCGTCAATTAAATAAAGTAGCGCGTCAGATTAATAATCTA
 AAGACAACAGGAAGTCTTCCAGCTATGGAATCAAGTGATCAATCTTCTTC
 ATCATCACAAGGACAAGGGACTCAATCGACTAGTGGTGCGACGAATCGTC
 TACAGCAAAATTATCAAAGTCAAGCTAATGCTTCATACAACCAACAACCTT
 CAAGATTTGAATGATGCTTATGCAGATGCACAGGCAGAAGTAAATAAAGC
 ACAAAAAGCATTGAATGATACTGTTATTACAAGTGACGTATCAGGGACAG
 TTGTTGAAGTTAATAGTGATATTGATCCAGCTTCAAAAACTAGTCAAGTA
 CTTGTCCATGTAGCAACTGAAGGTAAACTCCAAGTACAAGGAACGATGAG
 TGAGTATGATTTGGCTAATGTAAAAAAGACCAGGCTGTTAAAAATAAAAT
 CTAAGGTCTATCCTGACAAGGAATGGGAAGGTAAAAATTTTATATATCTCA
 AATTATCCAGAAGCAGAAGCAAACAACAATGACTCTAATAACGGCTCTAG
 TGCTGTAAATTATAAATATAAAGTAGATATTACTAGCCCTCTCGATGCAT
 TAAAAACAAGGTTTTTACCGTATCAGTTGAAGTAGTTAATGGAGATAAGCAC
 CTTATTGTCCCTACAAGTTCTGTGATAAACAAGATAATAAACACTTTGT
 TTGGGTATACAATGATTCTAATCGTAAAAATTTCCAAAGTTGAAGTCAAAA
 TTGGTAAAGCTGATGCTAAGACACAAGAAATTTTATCAGGTTTGAAAGCA
 GGACAAATCGTGGTTACTAATCCAAGTAAACCTTTCAAGGATGGGCAAAA
 AATTGATAATATTGAATCAATCGATCTTAAGTCTAATAAGAAATCAGAG

SEQ ID NO. 8506

STRAIN M732

TTTTTATGGGTACAATCTCAACCTAATAAGAGTGCAGTAAAACTAATTA
 CAAAGTTTTTAATGTTAGAGAAGGAAGTGTTCGTCTCAACTCTTTTGA
 CAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTTGATGCTAAT
 AAAGGTAATCGAGCAACTGTTACAGTTAAAGTGGGTGATAAAATCACAGC
 TGGTCAGCAGTTAGTTCAATATGATACAACAACCTGCACAAGCAGCCTACG
 AACTGCTAATCGTCAATTAAATAAAGTAGCGCGTCAGATTAATAATCTA
 AAGACAACAGGGAGTTTTTCCAGCTATGGAATCAAGTGATCAATCTTCATC
 ATCATCACAAGGACAAGGGACTCAATCGACTAGTGGTGCGACGAATCGTC
 TACAGCAAAATTATCAAAGTCAAGCTAATGCTTCATACAACCAACAACCTT
 CAAGATTTGAATGATGCTTATGCAGATGCACAGGCAGAAGTAAATAAAGC
 ACAAAAAGCATTGAATGATACTGTTATTACAAGTGACGTATCAGGGACAG
 TTGTTGAAGTTAATAGTGATATTGATCCAGCTTCAAAAACTAGTCAAGTA
 CTTGTCCATGTAGCAACTGAAGGTAAACTCCAAGTACAAGGAACGATGAG
 TGAGTATGATTTGGCTAATGTAAAAAAGATCAGGCTGTTAAAAATAAAAT
 CTAAGGTCTATCCTGACAAGGAATGGGAAGGTAAAAATTTTATATATCTCA
 AATTATCCAGAAGCAGAAGCAAACAACAATGACTCTAATAACGGCTCTAG
 TGCTGTAAATTATAAATATAAAGTAGATATTACTAGCCCTCTCGATGCAT
 TAAAAACAAGGTTTTTACCGTATCAGTTGAAGTAGTTAATGGAGATAAGCAC
 CTTATTGTCCCTACAAGTTCTGTGATAAACAAGATAATAAACACTTTGT
 TTGGGTATACAATGATTCTAATCGTAAAAATTTCCAAAGTTGAAGTCAAAA
 TTGGTAAAGCTGATGCTAAGACACAAGAAATTTTATCAGGTTTGAAAGCA
 GGACAAATCGTGGTTACTAATCCAAGCAAAACCTTTCAAGGATGGGCAAAA
 AATTGATAATATTGAATCAATCGATCTTAAGTCTAATAAGAAATCAGAGG
 TGAA

SEQ ID NO. 8507

STRAIN COH1

TTTTTATGGGTACAATCTCAACCTAATAAGAGTGCAGTAAAAAC
 TAATTACAAAGTTTTTAATGTTAGAGAAGGAAGTGTTCGTCTCAACTC
 TTTTGACAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTTGA
 GCTAATAAAGGTAATCGAGCAACTGTTACAGTTAAAGTGGGTGATAAAAT
 CACAGCTGGTCAGCAGTTAGTTCAATATGATACAACAACCTGCACAAGCAG
 CCTACGACACTGCTAATCGTCAATTAAATAAAGTAGCGCGTCAGATTAAT
 AATCTAAAGACAACAGGGAGTTTTTCCAGCTATGGAATCAAGTGATCAATC

Table 85: Comparative Sequences relating to SAG1361

TTCATCATCATCACAAGGACAAGGGACTCAATCGACTAGTGGTGCGACGA
 ATCGTCTACAGCAAAATTATCAAAGTCAAGCTAATGCTTCATACAACCAA
 CAACTTCAAGATTTGAATGATGCTTATGCAGATGCACAGGCAGAAGTAAA
 TAAAGCACAAAAAGCATTGAATGATACTGTTATTACAAGTGACGTATCAG
 GGACAGTTGTTGAAGTTAATAGTGATATTGATCCAGCTTCAAAAAGTAGT
 CAAGTACTTGTCCATGTAGCAACTGAAGGTAACTCCAAGTACAAGGAAC
 GATGAGTGAGTATGATTTGGCTAATGTTAAAAAGATCAGGCTGTTAAAA
 TAAAAATCTAAGGTCTATCCTGACAAGGAATGGGAAGGTAAAAATTTATAT
 ATCTCAAATTATCCAGAAGCAGAAGCAAACAACATGACTCTAATAACGG
 CTCTAGTGCTGTAAATTATAAATATAAAGTAGATATTACTAGCCCTCTCG
 ATGCATTAAAAACAAGGTTTTACCGTATCAGTTGAAGTAGTTAATGGAGAT
 AAGCACCTTATTGTCCCTACAAGTTCTGTGATAAAACAAGATAATAACA
 CTTTGTGTTGGGTATACAATGATTCTAATCGTAAAAATTTCCAAAGTTGAAG
 TCAAAATTTGGTAAAGCTGATGCTAAGACACAAGAAATTTTATCAGGTTTG
 AAAGCAGGACAAATCGTGGTTACTAATCCAAGCAAACTTTCAAGGATGG
 GCAAAAATTGATAATATTGAATCAATCGATCTTAAGTCTAATAAGAAAT
 CAGAGGTGAA

SEQ ID NO. 8507

STRAIN M781

TTTTTATGGGTACAATCTCAACCTAATAAGAGTGCAGTAAAACTAATTA
 CAAAGTTTTTAATGTTAGAGAAGGAAGTGTTCGTCTCAACTCTTTTGA
 CAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTTGTATGCTAAT
 AAAGGTAATCGAGCAACTGTTACAGTTAAAGTGGGTGATAAAATCACAGC
 TGGTCAGCAGTTAGTTCAATATGATACAACAACCTGCACAAGCAGCCTACG
 AACTGCTAATCGTCAATTAAATAAAGTAGCGCGTCAGATTAATAATCTA
 AAGACAACAGGGAGTTTTCCAGCTATGGAATCAAGTGATCAATCTTCATC
 ATCATCACAAGGACAAGGGACTCAATCGACTAGTGGTGCGACGAATCGTC
 TACAGCAAAATTATCAAAGTCAAGCTAATGCTTCATACAACCAACAACCTT
 CAAGATTTGAATGATGCTTATGCAGATGCACAGGCAGAAGTAAATAAAGC
 ACAAAAAGCATTGAATGATACTGTTATTACAAGTGACGTATCAGGGACAG
 TTGTTGAAGTTAATAGTGATATTGATCCAGCTTCAAAAAGTAGTCAAGTA
 CTTGTCCATGTAGCAACTGAAGGTAACTCCAAGTACAAGGAACGATGAG
 TGAGTATGATTTGGCTAATGTTAAAAAGATCAGGCTGTAAAAATAAAAT
 CTAAGGTCTATCCTGACAAGGAATGGGAAGGTAAAAATTTATATATCTCA
 AATTATCCAGAAGCAGAAGCAAACAACAATGACTCTAATAACGGCTCTAG
 TGCTGTAAATTATAAATATAAAGTAGATATTACTAGCCCTCTCGATGCAT
 TAAAACAAGGTTTTACCGTATCAGTTGAAGTAGTTAATGGAGATAAGCAC
 CTTATTGTCCCTACAAGTTCTGTGATAAAACAAGATAATAAACACTTTGT
 TTGGGTATACAATGATTCTAATCGTAAAAATTTCCAAAGTTGAAGTCAAAA
 TTGGTAAAGCTGATGCTAAGACACAAGAAATTTTATCAGGTTTGAAAGCA
 GGACAAATCGTGGTTACTAATCCAAGCAAACTTTCAAGGATGGGCAAAA
 AATTGATAATATTGAATCAATCGATCTTAAGTCTAATAAGAAATCAGAGG
 TGAA

SEQ ID NO. 8508

STRAIN CJB110

TTTTTATGGGTACAATCTCAACCTAATAAGAGTGCAGTAAAACTAACTA
 CAAAGTTTTTAATGTTAGAGAAGGAAGTGTTCGTCTCAACTCTTTTGA
 CAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTTGTATGCTAAT
 AAAGGTAATCGAGCAACTGTACAGTTAAAGTGGGTGATAAAATCACAGC
 TGGTCAGCAGTTAGTTCAATATGATACAACAACCTGCACAAGCAGCCTACG
 AACTGCTAATCGTCAATTAAATAAAGTAGCGCGTCAGATTAATAATCTA
 AAGACAACAGGAAGTCTTCCAGCTATGGAATTAAGTGATCAATCTTCTTC
 ATCATCACAAGGACAAGGGACTCAATCGACTAGTGGTGCGACGAATCGTC
 TACAGCAAAATTATCAAAGTCAAGCTAATGCTTCATACAACCAACAACCTT
 CAAGATTTGAATGATGCTTATGCAGATGCACAGGCAGAAGTAAATAAAGC
 ACAAAAAGCATTGAATGATACTGTTATTACAAGTGACGTATCAGGGACAG
 TTGTTGAAGTTAATAGTGATATTGATCCAGCTTCAAAAAGTAGTCAAGTA
 CTTGTCCATGTAGCAACTGAAGGTAACTCCAAGTACAAGGAACGATGAG
 TGAGTATGATTTGGCTAATGTTAAAAAGACCAGGCTGTAAAAATAAAAT
 CTAAGGTCTATCCTGACAAGGAATGGGAAGGTAAAAATTTATATATCTCA
 AATTATCCAGAAGCAGAAGCAAACAACAATGACTCTAATAACGGCTCTAG
 TGCTGTAAATTATAAATATAAAGTAGATATTACTAGCCCTCTCGATGCAT
 TAAAACAAGGTTTTACCGTATCAGTTGAAGTAGTTAATGGAGATAAGCAC
 CTTATTGTCCCTACAAGTTCTGTGATAAAACAAGATAATAAACACTTTGT
 TTGGGTATACAATGATTCTAATCGTAAAAATTTCCAAAGTTGAAGTCAAAA
 TTGGTAAAGCTGATGCTAAGACACAAGAAATTTTATCAGGTTTGAAAGCA
 GGACAAATCGTGGTTACTAATCCAAGTAAACCTTCAAGGATGGGCAAAA
 AATTGATAATATTGAATCAATCGATCTTAAGTCTAATAAGAAATCAGAGG
 TGA

SEQ ID NO. 8509

STRAIN 1169NT

TTTTTATGGGTACAATCTCAACCTAATAAGAGTGCAGTAAAACT
 AACTACAAAGTTTTTAATGTTAGAGAAGGAAGTGTTCGTCTCAACTCT
 TTTGACAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTTGTATG
 CTAATAAAGGTAATCGAGCAACTGTACAGTTAAAGTGGGTGATAAAATC
 ACAGCTGGTCAGCAGTTAGTTCAATATGATACAACAACCTGCACAAGCAGC
 CTACGACACTGCTAATCGTCAATTAAATAAAGTAGCGCGTCAGATTAATA
 ATCTAAAGACAACAGGAAGTCTTCCAGCTATGGAATCAAGTGATCAATCT
 TCTTCATCATCACAAGGACAAGGGACTCAATCGACTAGTGGTGCGACGAA
 TCGTCTACAGCAAAATTATCAAAGTCAAGCTAATGCTTCATACAACCAAC

Table 85: Comparative Sequences relating to SAG1361

AACTTCAAGATTTGAATGATGCTTATGCAGATGCACAGGCAGAAGTAAAT
 AAAGCACAAAAGCATTGAATGATACTGTTATTACAAGTGACGTATCAGG
 GACAGTTGTTGAAGTTAATAGTGATATTGATCCAGCTTCAAAAACAGTC
 AAGTACTTGTCCATGTAGCAACTGAAGGTAACTCCAAGTACAAGGAACG
 ATGAGTGAGTATGATTTGGCTAATGTTAAAAAGACCAGGCTGTTAAAT
 AAAATCTAAGGTCTATCCTGACAAGGAATGGGAAGGTAAAATTTTCATATA
 TCTCAAATTATCCAGAAGCAGAAGCAAACAACATGACTCTAATAACGGC
 TCTAGTGCTGTAAATTATAAATATAAAGTAGATATTACTAGCCCTCTCGA
 TGCATTAAAAACAAGGTTTTACCGTATCAGTTGAAGTAGTTAATGGAGATA
 AGCACCTTATTGTCCCTACAAGTTCTGTGATAAACAAGATAATAACAC
 TTTGTTTGGGTATACAATGATTCTAATCGTAAAAATTTCCAAAGTTGAAGT
 CAAAATTGGTAAAGCTGATGCTAAGACACAAGAAATTTTATCAGGTTTGA
 AAGCAGGACAAATCGTGGTTACTAATCCAAGTAAAACCTTCAAGGATGGG
 CAAAAATTGATAATATTGAATCAATCGATCTTAAGTCTAATAAGAAATC
 AGAGGTGAA

SEQ ID NO. 8510

STRAIN JM9130013

TTTTTATGGGTACAATCTCAACCTAATAAGAGTGCAGTAAAACTAACTA
 CAAAGTTTTTAATGTTAGAGAAGGAAGTGTTCGTCTCAACTCTTTTGA
 CAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTTGATGCTAAT
 AAAGGTAATCGAGCAACTGTTACAGTTAAAGTGGGTGATAAAATCACAGC
 TGGTCAGCAGTTAGTTCAATATGATACAACTGCACAAGCAGCCTACG
 ACCTGCTAATCGTCAATTAATAAAGTAGCGCTCAGATTAAATAATCTA
 AAGACAACAGGAAGTCTTCCAGCTATGGAATCAAGTGATCAATCTTCATC
 ATCATCACAAGGACAAGGGCTCAATCGACTAGTGGTGCGACGAATCGTC
 TACAGCAAAATTATCAAAGTCAAGCTAATGCTTCATACAACCAACAACTT
 CAAGATTTGAATGATGCTTATGCAGATGCACAGGCAGAAGTAAATAAAGC
 ACAAAAAGCATTGAATGATACTGTTATTACAAGTGACGTATCAGGGACAG
 TTGTTGAAGTTAATAGTGATATTGATCCAGCTTCAAAAAGTCAAGTA
 CTTGTCCATGTAGCAACTGAGGGTAACTCCAAGTACAAGGAACGATGAG
 TGAGTATGATTTGGCTAATGTTAAAAAGACCAGTCTGTTAAAAATAAAT
 CTAAGGTCTATCCTGACAAGGAATGGGAAGGTAAAATTTTCATATATCTCA
 AATTATCCAGAAGCAGAAGCAAACAACATGACTCTAATAACGGCTCTAG
 TGCTGTAAATTTATAAATATAAAGTAGATATTACTAGCCCTCTCGATGCAT
 TAAAACAAGGTTTTACTGTATCAGTTGAAGTAGTTAATGGAGATAAGCAC
 CTTATTGTTCTACAAGTTCTGTGACAAACAAGATAATAAACACTTTGT
 TTGGGTATACAATGATTCTAATCGTAAAAATTTCCAAAGTTGAAGTCAAAA
 TTGGTAAAGCTGATGCTAAGACACAAGAAATTTTATCAGGTTTGAAGCA
 GGACAAATCGTGGTTACTAATCCAAGCAAACTTTCAAGGATGGGCAAAA
 AATTGATAATATTGAATCAATAGATCTTAAGTCTAATAAGAAATCAGAGG
 TGAAT

PRETTY of: /biotmp/msa363690.2{*} March 31, 2003 07:01 ..

	1				50
msa363690.2{690_COH1}	-----	-----	-----	-----	-----
msa363690.2{690_M732}	-----	-----	-----	-----	-----
msa363690.2{690_M781}	-----	-----	-----	-----	-----
msa363690.2{690_090}	-----	-----	-----	-----	-----
msa363690.2{690_CJB110}	-----	-----	-----	-----	-----
msa363690.2{690_1169NT}	-----	-----	-----	-----	-----
msa363690.2{690_18RS21}	-----	-----	-----	-----	-----
msa363690.2{690_2603}	atgagtaa	gacaaaattt	aggaattagt	aaaaaaggag	caattatatac
msa363690.2{690_A909}	-----	-----	-----	-----	-----
msa363690.2{690_JM9130013}	-----	-----	-----	-----	-----
msa363690.2{690_H36B}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	51				100
msa363690.2{690_COH1}	-----	-----	-----	TTT	TTATGGGTAC
msa363690.2{690_M732}	-----	-----	-----	TTT	TTATGGGTAC
msa363690.2{690_M781}	-----	-----	-----	TTT	TTATGGGTAC
msa363690.2{690_090}	-----	-----	-----	TTT	TTATGGGTAC
msa363690.2{690_CJB110}	-----	-----	-----	TTT	TTATGGGTAC
msa363690.2{690_1169NT}	-----	-----	-----	TTT	TTATGGGTAC
msa363690.2{690_18RS21}	-----	-----	-----	TTT	TTATGGGTAC
msa363690.2{690_2603}	agggtctctca	gtggcactaa	ttgtagtaat	agggtggcTTT	TTATGGGTAC
msa363690.2{690_A909}	-----	-----	-----	TTT	TTATGGGTAC
msa363690.2{690_JM9130013}	-----	-----	-----	TTT	TTATGGGTAC
msa363690.2{690_H36B}	-----	-----	-----	TTT	TTATGGGTAC
Consensus	*****	*****	*****	*****	*****
	101				150
msa363690.2{690_COH1}	AATCTCAACC	TAATAAGAGT	GCAGTAAAAA	CTAAAtTACAA	AGTTTTTAAT
msa363690.2{690_M732}	AATCTCAACC	TAATAAGAGT	GCAGTAAAAA	CTAAAtTACAA	AGTTTTTAAT
msa363690.2{690_M781}	AATCTCAACC	TAATAAGAGT	GCAGTAAAAA	CTAAAtTACAA	AGTTTTTAAT
msa363690.2{690_090}	AATCTCAACC	TAATAAGAGT	GCAGTAAAAA	CTAAAtTACAA	AGTTTTTAAT
msa363690.2{690_CJB110}	AATCTCAACC	TAATAAGAGT	GCAGTAAAAA	CTAAAtTACAA	AGTTTTTAAT
msa363690.2{690_1169NT}	AATCTCAACC	TAATAAGAGT	GCAGTAAAAA	CTAAAtTACAA	AGTTTTTAAT
msa363690.2{690_18RS21}	AATCTCAACC	TAATAAGAGT	GCAGTAAAAA	CTAAAtTACAA	AGTTTTTAAT
msa363690.2{690_2603}	AATCTCAACC	TAATAAGAGT	GCAGTAAAAA	CTAAAtTACAA	AGTTTTTAAT

Table 85: Comparative Sequences relating to SAG1361

msa363690.2{690_A909}	AATCTCAACC	TAATAAGAGT	GCAGTAAAAA	CTAAcTACAA	AGTTTTTAAT
msa363690.2{690_JM9130013}	AATCTCAACC	TAATAAGAGT	GCAGTAAAAA	CTAAcTACAA	AGTTTTTAAT
msa363690.2{690_H36B}	AATCTCAACC	TAATAAGAGT	GCAGTAAAAA	CTAAcTACAA	AGTTTTTAAT
Consensus	*****	*****	*****	*****	*****
msa363690.2{690_COH1}	GTTAGAGAAG	GAAGTGTTC	GTCCTCAACT	CTTTTGACAG	GAAAAGCTAA
msa363690.2{690_M732}	GTTAGAGAAG	GAAGTGTTC	GTCCTCAACT	CTTTTGACAG	GAAAAGCTAA
msa363690.2{690_M781}	GTTAGAGAAG	GAAGTGTTC	GTCCTCAACT	CTTTTGACAG	GAAAAGCTAA
msa363690.2{690_090}	GTTAGAGAAG	GAAGTGTTC	GTCCTCAACT	CTTTTGACAG	GAAAAGCTAA
msa363690.2{690_CJB110}	GTTAGAGAAG	GAAGTGTTC	GTCCTCAACT	CTTTTGACAG	GAAAAGCTAA
msa363690.2{690_1169NT}	GTTAGAGAAG	GAAGTGTTC	GTCCTCAACT	CTTTTGACAG	GAAAAGCTAA
msa363690.2{690_18RS21}	GTTAGAGAAG	GAAGTGTTC	GTCCTCAACT	CTTTTGACAG	GAAAAGCTAA
msa363690.2{690_2603}	GTTAGAGAAG	GAAGTGTTC	GTCCTCAACT	CTTTTGACAG	GAAAAGCTAA
msa363690.2{690_A909}	GTTAGAGAAG	GAAGTGTTC	GTCCTCAACT	CTTTTGACAG	GAAAAGCTAA
msa363690.2{690_JM9130013}	GTTAGAGAAG	GAAGTGTTC	GTCCTCAACT	CTTTTGACAG	GAAAAGCTAA
msa363690.2{690_H36B}	GTTAGAGAAG	GAAGTGTTC	GTCCTCAACT	CTTTTGACAG	GAAAAGCTAA
Consensus	*****	*****	*****	*****	*****
msa363690.2{690_COH1}	GGCTAATCAA	GAACAGTATG	TGTATTTTGA	TGCTAATAAa	GGTAATCGAG
msa363690.2{690_M732}	GGCTAATCAA	GAACAGTATG	TGTATTTTGA	TGCTAATAAa	GGTAATCGAG
msa363690.2{690_M781}	GGCTAATCAA	GAACAGTATG	TGTATTTTGA	TGCTAATAAa	GGTAATCGAG
msa363690.2{690_090}	GGCTAATCAA	GAACAGTATG	TGTATTTTGA	TGCTAATAAa	GGTAATCGAG
msa363690.2{690_CJB110}	GGCTAATCAA	GAACAGTATG	TGTATTTTGA	TGCTAATAAa	GGTAATCGAG
msa363690.2{690_1169NT}	GGCTAATCAA	GAACAGTATG	TGTATTTTGA	TGCTAATAAa	GGTAATCGAG
msa363690.2{690_18RS21}	GGCTAATCAA	GAACAGTATG	TGTATTTTGA	TGCTAATAAa	GGTAATCGAG
msa363690.2{690_2603}	GGCTAATCAA	GAACAGTATG	TGTATTTTGA	TGCTAATAAa	GGTAATCGAG
msa363690.2{690_A909}	GGCTAATCAA	GAACAGTATG	TGTATTTTGA	TGCTAATAAa	GGTAATCGAG
msa363690.2{690_JM9130013}	GGCTAATCAA	GAACAGTATG	TGTATTTTGA	TGCTAATAAa	GGTAATCGAG
msa363690.2{690_H36B}	GGCTAATCAA	GAACAGTATG	TGTATTTTGA	TGCTAATAAg	GGTAATCGAG
Consensus	*****	*****	*****	*****	*****
msa363690.2{690_COH1}	CAACTGTtAC	AGTTAAAGTG	GGTGATAAAA	TCACAGCTGG	TCAGCAGTTA
msa363690.2{690_M732}	CAACTGTtAC	AGTTAAAGTG	GGTGATAAAA	TCACAGCTGG	TCAGCAGTTA
msa363690.2{690_M781}	CAACTGTtAC	AGTTAAAGTG	GGTGATAAAA	TCACAGCTGG	TCAGCAGTTA
msa363690.2{690_090}	CAACTGTtAC	AGTTAAAGTG	GGTGATAAAA	TCACAGCTGG	TCAGCAGTTA
msa363690.2{690_CJB110}	CAACTGTtAC	AGTTAAAGTG	GGTGATAAAA	TCACAGCTGG	TCAGCAGTTA
msa363690.2{690_1169NT}	CAACTGTtAC	AGTTAAAGTG	GGTGATAAAA	TCACAGCTGG	TCAGCAGTTA
msa363690.2{690_18RS21}	CAACTGTtAC	AGTTAAAGTG	GGTGATAAAA	TCACAGCTGG	TCAGCAGTTA
msa363690.2{690_2603}	CAACTGTtAC	AGTTAAAGTG	GGTGATAAAA	TCACAGCTGG	TCAGCAGTTA
msa363690.2{690_A909}	CAACTGTtAC	AGTTAAAGTG	GGTGATAAAA	TCACAGCTGG	TCAGCAGTTA
msa363690.2{690_JM9130013}	CAACTGTtAC	AGTTAAAGTG	GGTGATAAAA	TCACAGCTGG	TCAGCAGTTA
msa363690.2{690_H36B}	CAACTGTtAC	AGTTAAAGTG	GGTGATAAAA	TCACAGCTGG	TCAGCAGTTA
Consensus	*****	*****	*****	*****	*****
msa363690.2{690_COH1}	GTTCAATATG	ATACAACAAC	TGCACAAGCA	GCCTACGACA	CTGCTAATCG
msa363690.2{690_M732}	GTTCAATATG	ATACAACAAC	TGCACAAGCA	GCCTACGACA	CTGCTAATCG
msa363690.2{690_M781}	GTTCAATATG	ATACAACAAC	TGCACAAGCA	GCCTACGACA	CTGCTAATCG
msa363690.2{690_090}	GTTCAATATG	ATACAACAAC	TGCACAAGCA	GCCTACGACA	CTGCTAATCG
msa363690.2{690_CJB110}	GTTCAATATG	ATACAACAAC	TGCACAAGCA	GCCTACGACA	CTGCTAATCG
msa363690.2{690_1169NT}	GTTCAATATG	ATACAACAAC	TGCACAAGCA	GCCTACGACA	CTGCTAATCG
msa363690.2{690_18RS21}	GTTCAATATG	ATACAACAAC	TGCACAAGCA	GCCTACGACA	CTGCTAATCG
msa363690.2{690_2603}	GTTCAATATG	ATACAACAAC	TGCACAAGCA	GCCTACGACA	CTGCTAATCG
msa363690.2{690_A909}	GTTCAATATG	ATACAACAAC	TGCACAAGCA	GCCTACGACA	CTGCTAATCG
msa363690.2{690_JM9130013}	GTTCAATATG	ATACAACAAC	TGCACAAGCA	GCCTACGACA	CTGCTAATCG
msa363690.2{690_H36B}	GTTCAATATG	ATACAACAAC	TGCACAAGCA	GCCTACGACA	CTGCTAATCG
Consensus	*****	*****	*****	*****	*****
msa363690.2{690_COH1}	TCAATTAAAT	AAAGTAGCGC	GTCAGATTAA	TAATCTAAAG	ACAACAGGgA
msa363690.2{690_M732}	TCAATTAAAT	AAAGTAGCGC	GTCAGATTAA	TAATCTAAAG	ACAACAGGgA
msa363690.2{690_M781}	TCAATTAAAT	AAAGTAGCGC	GTCAGATTAA	TAATCTAAAG	ACAACAGGgA
msa363690.2{690_090}	TCAATTAAAT	AAAGTAGCGC	GTCAGATTAA	TAATCTAAAG	ACAACAGGgA
msa363690.2{690_CJB110}	TCAATTAAAT	AAAGTAGCGC	GTCAGATTAA	TAATCTAAAG	ACAACAGGgA
msa363690.2{690_1169NT}	TCAATTAAAT	AAAGTAGCGC	GTCAGATTAA	TAATCTAAAG	ACAACAGGgA
msa363690.2{690_18RS21}	TCAATTAAAT	AAAGTAGCGC	GTCAGATTAA	TAATCTAAAG	ACAACAGGgA
msa363690.2{690_2603}	TCAATTAAAT	AAAGTAGCGC	GTCAGATTAA	TAATCTAAAG	ACAACAGGgA
msa363690.2{690_A909}	TCAATTAAAT	AAAGTAGCGC	GTCAGATTAA	TAATCTAAAG	ACAACAGGgA
msa363690.2{690_JM9130013}	TCAATTAAAT	AAAGTAGCGC	GTCAGATTAA	TAATCTAAAG	ACAACAGGgA
msa363690.2{690_H36B}	TCAATTAAAT	AAAGTAGCGC	GTCAGATTAA	TAATCTAAAG	ACAACAGGgA
Consensus	*****	*****	*****	*****	*****
msa363690.2{690_COH1}	GTtTTCCAGC	TATGGAATcA	AGTGATCAAT	CTTcATCATC	ATCACAAGGA
msa363690.2{690_M732}	GTtTTCCAGC	TATGGAATcA	AGTGATCAAT	CTTcATCATC	ATCACAAGGA
msa363690.2{690_M781}	GTtTTCCAGC	TATGGAATcA	AGTGATCAAT	CTTcATCATC	ATCACAAGGA
msa363690.2{690_090}	GTtTTCCAGC	TATGGAATtA	AGTGATCAAT	CTTcATCATC	ATCACAAGGA
msa363690.2{690_CJB110}	GTtTTCCAGC	TATGGAATtA	AGTGATCAAT	CTTcATCATC	ATCACAAGGA
msa363690.2{690_1169NT}	GTtTTCCAGC	TATGGAATcA	AGTGATCAAT	CTTcATCATC	ATCACAAGGA
msa363690.2{690_18RS21}	GTtTTCCAGC	TATGGAATcA	AGTGATCAAT	CTTcATCATC	ATCACAAGGA

Table 85: Comparative Sequences relating to SAG1361

msa363690.2{690_2603}	GTcTTCCAGC	TATGGAATcA	AGTGATCAAT	CTTCcTCATC	ATCACAAGGA
msa363690.2{690_A909}	GTcTTCCAGC	TATGGAATcA	AGTGATCAAT	CTTCaTCATC	ATCACAAGGA
msa363690.2{690_JM9130013}	GTcTTCCAGC	TATGGAATcA	AGTGATCAAT	CTTCaTCATC	ATCACAAGGA
msa363690.2{690_H36B}	GTcTTCCAGC	TATGGAATcA	AGTGATCAAT	CTTCaTCATC	ATCACAAGGA
Consensus	**-----*	*****_*	*****	****_*****	*****
451					
msa363690.2{690_COH1}	CAAGGGaCTC	AATCGACTAG	TGGTGCGACG	AATCGTCTAC	AGCAAAATTA
msa363690.2{690_M732}	CAAGGGaCTC	AATCGACTAG	TGGTGCGACG	AATCGTCTAC	AGCAAAATTA
msa363690.2{690_M781}	CAAGGGaCTC	AATCGACTAG	TGGTGCGACG	AATCGTCTAC	AGCAAAATTA
msa363690.2{690_090}	CAAGGGaCTC	AATCGACTAG	TGGTGCGACG	AATCGTCTAC	AGCAAAATTA
msa363690.2{690_CJB110}	CAAGGGaCTC	AATCGACTAG	TGGTGCGACG	AATCGTCTAC	AGCAAAATTA
msa363690.2{690_1169NT}	CAAGGGaCTC	AATCGACTAG	TGGTGCGACG	AATCGTCTAC	AGCAAAATTA
msa363690.2{690_18RS21}	CAAGGGaCTC	AATCGACTAG	TGGTGCGACG	AATCGTCTAC	AGCAAAATTA
msa363690.2{690_2603}	CAAGGGaCTC	AATCGACTAG	TGGTGCGACG	AATCGTCTAC	AGCAAAATTA
msa363690.2{690_A909}	CAAGGGgCTC	AATCGACTAG	TGGTGCGACG	AATCGTCTAC	AGCAAAATTA
msa363690.2{690_JM9130013}	CAAGGGgCTC	AATCGACTAG	TGGTGCGACG	AATCGTCTAC	AGCAAAATTA
msa363690.2{690_H36B}	CAAGGGaCTC	AATCGACTAG	TGGTGCGACG	AATCGTCTAC	AGCAAAATTA
Consensus	*****_***	*****	*****	*****	*****
501					
msa363690.2{690_COH1}	TCAAAGTCAA	GCTAATGCTT	CATACAACCA	ACAACCTCAA	GATTTGAATG
msa363690.2{690_M732}	TCAAAGTCAA	GCTAATGCTT	CATACAACCA	ACAACCTCAA	GATTTGAATG
msa363690.2{690_M781}	TCAAAGTCAA	GCTAATGCTT	CATACAACCA	ACAACCTCAA	GATTTGAATG
msa363690.2{690_090}	TCAAAGTCAA	GCTAATGCTT	CATACAACCA	ACAACCTCAA	GATTTGAATG
msa363690.2{690_CJB110}	TCAAAGTCAA	GCTAATGCTT	CATACAACCA	ACAACCTCAA	GATTTGAATG
msa363690.2{690_1169NT}	TCAAAGTCAA	GCTAATGCTT	CATACAACCA	ACAACCTCAA	GATTTGAATG
msa363690.2{690_18RS21}	TCAAAGTCAA	GCTAATGCTT	CATACAACCA	ACAACCTCAA	GATTTGAATG
msa363690.2{690_2603}	TCAAAGTCAA	GCTAATGCTT	CATACAACCA	ACAACCTCAA	GATTTGAATG
msa363690.2{690_A909}	TCAAAGTCAA	GCTAATGCTT	CATACAACCA	ACAACCTCAA	GATTTGAATG
msa363690.2{690_JM9130013}	TCAAAGTCAA	GCTAATGCTT	CATACAACCA	ACAACCTCAA	GATTTGAATG
msa363690.2{690_H36B}	TCAAAGTCAA	GCTAATGCTT	CATACAACCA	ACAACCTCAA	GATTTGAATG
Consensus	*****	*****	*****	*****	*****
551					
msa363690.2{690_COH1}	ATGCTTATGC	AGATGCACAG	GCAGAAGTAA	ATAAAGCACA	AAAAGCATTG
msa363690.2{690_M732}	ATGCTTATGC	AGATGCACAG	GCAGAAGTAA	ATAAAGCACA	AAAAGCATTG
msa363690.2{690_M781}	ATGCTTATGC	AGATGCACAG	GCAGAAGTAA	ATAAAGCACA	AAAAGCATTG
msa363690.2{690_090}	ATGCTTATGC	AGATGCACAG	GCAGAAGTAA	ATAAAGCACA	AAAAGCATTG
msa363690.2{690_CJB110}	ATGCTTATGC	AGATGCACAG	GCAGAAGTAA	ATAAAGCACA	AAAAGCATTG
msa363690.2{690_1169NT}	ATGCTTATGC	AGATGCACAG	GCAGAAGTAA	ATAAAGCACA	AAAAGCATTG
msa363690.2{690_18RS21}	ATGCTTATGC	AGATGCACAG	GCAGAAGTAA	ATAAAGCACA	AAAAGCATTG
msa363690.2{690_2603}	ATGCTTATGC	AGATGCACAG	GCAGAAGTAA	ATAAAGCACA	AAAAGCATTG
msa363690.2{690_A909}	ATGCTTATGC	AGATGCACAG	GCAGAAGTAA	ATAAAGCACA	AAAAGCATTG
msa363690.2{690_JM9130013}	ATGCTTATGC	AGATGCACAG	GCAGAAGTAA	ATAAAGCACA	AAAAGCATTG
msa363690.2{690_H36B}	ATGCTTATGC	AGATGCACAG	GCAGAAGTAA	ATAAAGCACA	AAAAGCATTG
Consensus	*****	*****	*****	*****	*****
601					
msa363690.2{690_COH1}	AATGATACTG	TTATTACAAG	TGACGTATCA	GGGACAGTTG	TTGAAGTTAA
msa363690.2{690_M732}	AATGATACTG	TTATTACAAG	TGACGTATCA	GGGACAGTTG	TTGAAGTTAA
msa363690.2{690_M781}	AATGATACTG	TTATTACAAG	TGACGTATCA	GGGACAGTTG	TTGAAGTTAA
msa363690.2{690_090}	AATGATACTG	TTATTACAAG	TGACGTATCA	GGGACAGTTG	TTGAAGTTAA
msa363690.2{690_CJB110}	AATGATACTG	TTATTACAAG	TGACGTATCA	GGGACAGTTG	TTGAAGTTAA
msa363690.2{690_1169NT}	AATGATACTG	TTATTACAAG	TGACGTATCA	GGGACAGTTG	TTGAAGTTAA
msa363690.2{690_18RS21}	AATGATACTG	TTATTACAAG	TGACGTATCA	GGGACAGTTG	TTGAAGTTAA
msa363690.2{690_2603}	AATGATACTG	TTATTACAAG	TGACGTATCA	GGGACAGTTG	TTGAAGTTAA
msa363690.2{690_A909}	AATGATACTG	TTATTACAAG	TGACGTATCA	GGGACAGTTG	TTGAAGTTAA
msa363690.2{690_JM9130013}	AATGATACTG	TTATTACAAG	TGACGTATCA	GGGACAGTTG	TTGAAGTTAA
msa363690.2{690_H36B}	AATGATACTG	TTATTACAAG	TGACGTATCA	GGGACAGTTG	TTGAAGTTAA
Consensus	*****	*****	*****	*****	*****
651					
msa363690.2{690_COH1}	TAGTGATATT	GATCCAGCTT	CAAAAACCTAG	TCAAGTACTT	GTCCATGTAG
msa363690.2{690_M732}	TAGTGATATT	GATCCAGCTT	CAAAAACCTAG	TCAAGTACTT	GTCCATGTAG
msa363690.2{690_M781}	TAGTGATATT	GATCCAGCTT	CAAAAACCTAG	TCAAGTACTT	GTCCATGTAG
msa363690.2{690_090}	TAGTGATATT	GATCCAGCTT	CAAAAACCTAG	TCAAGTACTT	GTCCATGTAG
msa363690.2{690_CJB110}	TAGTGATATT	GATCCAGCTT	CAAAAACCTAG	TCAAGTACTT	GTCCATGTAG
msa363690.2{690_1169NT}	TAGTGATATT	GATCCAGCTT	CAAAAACCTAG	TCAAGTACTT	GTCCATGTAG
msa363690.2{690_18RS21}	TAGTGATATT	GATCCAGCTT	CAAAAACCTAG	TCAAGTACTT	GTCCATGTAG
msa363690.2{690_2603}	TAGTGATATT	GATCCAGCTT	CAAAAACCTAG	TCAAGTACTT	GTCCATGTAG
msa363690.2{690_A909}	TAGTGATATT	GATCCAGCTT	CAAAAACCTAG	TCAAGTACTT	GTCCATGTAG
msa363690.2{690_JM9130013}	TAGTGATATT	GATCCAGCTT	CAAAAACCTAG	TCAAGTACTT	GTCCATGTAG
msa363690.2{690_H36B}	TAGTGATATT	GATCCAGCTT	CAAAAACCTAG	TCAAGTACTT	GTCCATGTAG
Consensus	*****	*****	*****	*****	*****
701					
msa363690.2{690_COH1}	CAACTGAaGG	TAAACTCCAA	GTACAAGGAA	CGATGAGTGA	GTATGATTTG
msa363690.2{690_M732}	CAACTGAaGG	TAAACTCCAA	GTACAAGGAA	CGATGAGTGA	GTATGATTTG
msa363690.2{690_M781}	CAACTGAaGG	TAAACTCCAA	GTACAAGGAA	CGATGAGTGA	GTATGATTTG
msa363690.2{690_090}	CAACTGAaGG	TAAACTCCAA	GTACAAGGAA	CGATGAGTGA	GTATGATTTG
msa363690.2{690_CJB110}	CAACTGAaGG	TAAACTCCAA	GTACAAGGAA	CGATGAGTGA	GTATGATTTG
msa363690.2{690_1169NT}	CAACTGAaGG	TAAACTCCAA	GTACAAGGAA	CGATGAGTGA	GTATGATTTG

Table 85: Comparative Sequences relating to SAG1361

msa363690.2{690_18RS21}	CAACTGAaGG	TAAACTCCAA	GTACAAGGAA	CGATGAGTGA	GTATGATTTG
msa363690.2{690_2603}	CAACTGAaGG	TAAACTCCAA	GTACAAGGAA	CGATGAGTGA	GTATGATTTG
msa363690.2{690_A909}	CAACTGAaGG	TAAACTCCAA	GTACAAGGAA	CGATGAGTGA	GTATGATTTG
msa363690.2{690_JM9130013}	CAACTGAaGG	TAAACTCCAA	GTACAAGGAA	CGATGAGTGA	GTATGATTTG
msa363690.2{690_H36B}	CAACTGAaGG	TAAACTCCAA	GTACAAGGAA	CGATGAGTGA	GTATGATTTG
Consensus	*****-*	*****	*****	*****	*****
751					
msa363690.2{690_COH1}	GCTAATGTtA	AAAAAGAtCA	GgCTGTTAAA	ATAAAATCTA	AGGTCTATCC
msa363690.2{690_M732}	GCTAATGTtA	AAAAAGAtCA	GgCTGTTAAA	ATAAAATCTA	AGGTCTATCC
msa363690.2{690_M781}	GCTAATGTtA	AAAAAGAtCA	GgCTGTTAAA	ATAAAATCTA	AGGTCTATCC
msa363690.2{690_090}	GCTAATGTtA	AAAAAGAcCA	GgCTGTTAAA	ATAAAATCTA	AGGTCTATCC
msa363690.2{690_CJB110}	GCTAATGTtA	AAAAAGAcCA	GgCTGTTAAA	ATAAAATCTA	AGGTCTATCC
msa363690.2{690_1169NT}	GCTAATGTtA	AAAAAGAcCA	GgCTGTTAAA	ATAAAATCTA	AGGTCTATCC
msa363690.2{690_18RS21}	GCTAATGTtA	AAAAAGAcCA	GgCTGTTAAA	ATAAAATCTA	AGGTCTATCC
msa363690.2{690_2603}	GCTAATGTtA	AAAAAGAcCA	GgCTGTTAAA	ATAAAATCTA	AGGTCTATCC
msa363690.2{690_A909}	GCTAATGTtA	AAAAAGAcCA	GtCTGTTAAA	ATAAAATCTA	AGGTCTATCC
msa363690.2{690_JM9130013}	GCTAATGTtA	AAAAAGAcCA	GtCTGTTAAA	ATAAAATCTA	AGGTCTATCC
msa363690.2{690_H36B}	GCTAATGTaA	AAAAAGAcCA	GgCTGTTAAA	ATAAAATCTA	AGGTCTATCC
Consensus	*****-*	*****-*	*-*****	*****	*****
801					
msa363690.2{690_COH1}	TGACAAGGAA	TGGGAAGGTA	AAATTTTCATA	TATCTCAAAT	TATCCAGAAG
msa363690.2{690_M732}	TGACAAGGAA	TGGGAAGGTA	AAATTTTCATA	TATCTCAAAT	TATCCAGAAG
msa363690.2{690_M781}	TGACAAGGAA	TGGGAAGGTA	AAATTTTCATA	TATCTCAAAT	TATCCAGAAG
msa363690.2{690_090}	TGACAAGGAA	TGGGAAGGTA	AAATTTTCATA	TATCTCAAAT	TATCCAGAAG
msa363690.2{690_CJB110}	TGACAAGGAA	TGGGAAGGTA	AAATTTTCATA	TATCTCAAAT	TATCCAGAAG
msa363690.2{690_1169NT}	TGACAAGGAA	TGGGAAGGTA	AAATTTTCATA	TATCTCAAAT	TATCCAGAAG
msa363690.2{690_18RS21}	TGACAAGGAA	TGGGAAGGTA	AAATTTTCATA	TATCTCAAAT	TATCCAGAAG
msa363690.2{690_2603}	TGACAAGGAA	TGGGAAGGTA	AAATTTTCATA	TATCTCAAAT	TATCCAGAAG
msa363690.2{690_A909}	TGACAAGGAA	TGGGAAGGTA	AAATTTTCATA	TATCTCAAAT	TATCCAGAAG
msa363690.2{690_JM9130013}	TGACAAGGAA	TGGGAAGGTA	AAATTTTCATA	TATCTCAAAT	TATCCAGAAG
msa363690.2{690_H36B}	TGACAAGGAA	TGGGAAGGTA	AAATTTTCATA	TATCTCAAAT	TATCCAGAAG
Consensus	*****	*****	*****	*****	*****
851					
msa363690.2{690_COH1}	CAGAAGCAAA	CAACAAATGAC	TCTAATAACG	GCTCTAGTGC	TGTAAATTAT
msa363690.2{690_M732}	CAGAAGCAAA	CAACAAATGAC	TCTAATAACG	GCTCTAGTGC	TGTAAATTAT
msa363690.2{690_M781}	CAGAAGCAAA	CAACAAATGAC	TCTAATAACG	GCTCTAGTGC	TGTAAATTAT
msa363690.2{690_090}	CAGAAGCAAA	CAACAAATGAC	TCTAATAACG	GCTCTAGTGC	TGTAAATTAT
msa363690.2{690_CJB110}	CAGAAGCAAA	CAACAAATGAC	TCTAATAACG	GCTCTAGTGC	TGTAAATTAT
msa363690.2{690_1169NT}	CAGAAGCAAA	CAACAAATGAC	TCTAATAACG	GCTCTAGTGC	TGTAAATTAT
msa363690.2{690_18RS21}	CAGAAGCAAA	CAACAAATGAC	TCTAATAACG	GCTCTAGTGC	TGTAAATTAT
msa363690.2{690_2603}	CAGAAGCAAA	CAACAAATGAC	TCTAATAACG	GCTCTAGTGC	TGTAAATTAT
msa363690.2{690_A909}	CAGAAGCAAA	CAACAAATGAC	TCTAATAACG	GCTCTAGTGC	TGTAAATTAT
msa363690.2{690_JM9130013}	CAGAAGCAAA	CAACAAATGAC	TCTAATAACG	GCTCTAGTGC	TGTAAATTAT
msa363690.2{690_H36B}	CAGAAGCAAA	CAACAAATGAC	TCTAATAACG	GCTCTAGTGC	TGTAAATTAT
Consensus	*****	*****	*****	*****	*****
901					
msa363690.2{690_COH1}	AAATATAAAG	TAGATATTAC	TAGCCCTCTC	GATGCATTAA	AACAAGGTTT
msa363690.2{690_M732}	AAATATAAAG	TAGATATTAC	TAGCCCTCTC	GATGCATTAA	AACAAGGTTT
msa363690.2{690_M781}	AAATATAAAG	TAGATATTAC	TAGCCCTCTC	GATGCATTAA	AACAAGGTTT
msa363690.2{690_090}	AAATATAAAG	TAGATATTAC	TAGCCCTCTC	GATGCATTAA	AACAAGGTTT
msa363690.2{690_CJB110}	AAATATAAAG	TAGATATTAC	TAGCCCTCTC	GATGCATTAA	AACAAGGTTT
msa363690.2{690_1169NT}	AAATATAAAG	TAGATATTAC	TAGCCCTCTC	GATGCATTAA	AACAAGGTTT
msa363690.2{690_18RS21}	AAATATAAAG	TAGATATTAC	TAGCCCTCTC	GATGCATTAA	AACAAGGTTT
msa363690.2{690_2603}	AAATATAAAG	TAGATATTAC	TAGCCCTCTC	GATGCATTAA	AACAAGGTTT
msa363690.2{690_A909}	AAATATAAAG	TAGATATTAC	TAGCCCTCTC	GATGCATTAA	AACAAGGTTT
msa363690.2{690_JM9130013}	AAATATAAAG	TAGATATTAC	TAGCCCTCTC	GATGCATTAA	AACAAGGTTT
msa363690.2{690_H36B}	AAATATAAAG	TAGATATTAC	TAGCCCTCTC	GATGCATTAA	AACAAGGTTT
Consensus	*****	*****	*****	*****	*****
951					
msa363690.2{690_COH1}	TACcGTATCA	GTTGAAGTAG	TTAATGGAGA	TAAGCACCTT	ATTGTcCCTA
msa363690.2{690_M732}	TACcGTATCA	GTTGAAGTAG	TTAATGGAGA	TAAGCACCTT	ATTGTcCCTA
msa363690.2{690_M781}	TACcGTATCA	GTTGAAGTAG	TTAATGGAGA	TAAGCACCTT	ATTGTcCCTA
msa363690.2{690_090}	TACcGTATCA	GTTGAAGTAG	TTAATGGAGA	TAAGCACCTT	ATTGTcCCTA
msa363690.2{690_CJB110}	TACcGTATCA	GTTGAAGTAG	TTAATGGAGA	TAAGCACCTT	ATTGTcCCTA
msa363690.2{690_1169NT}	TACcGTATCA	GTTGAAGTAG	TTAATGGAGA	TAAGCACCTT	ATTGTcCCTA
msa363690.2{690_18RS21}	TACcGTATCA	GTTGAAGTAG	TTAATGGAGA	TAAGCACCTT	ATTGTcCCTA
msa363690.2{690_2603}	TACcGTATCA	GTTGAAGTAG	TTAATGGAGA	TAAGCACCTT	ATTGTcCCTA
msa363690.2{690_A909}	TACtGTATCA	GTTGAAGTAG	TTAATGGAGA	TAAGCACCTT	ATTGTcCCTA
msa363690.2{690_JM9130013}	TACtGTATCA	GTTGAAGTAG	TTAATGGAGA	TAAGCACCTT	ATTGTcCCTA
msa363690.2{690_H36B}	TACtGTATCA	GTTGAAGTAG	TTAATGGAGA	TAAGCACCTT	ATTGTcCCTA
Consensus	***-*****	*****	*****	*****	*****-****
1001					
msa363690.2{690_COH1}	CAAGTTCTGT	GATAAACAAA	GATAATAAAC	ACTTTGTTTG	GGTATACAAT
msa363690.2{690_M732}	CAAGTTCTGT	GATAAACAAA	GATAATAAAC	ACTTTGTTTG	GGTATACAAT
msa363690.2{690_M781}	CAAGTTCTGT	GATAAACAAA	GATAATAAAC	ACTTTGTTTG	GGTATACAAT
msa363690.2{690_090}	CAAGTTCTGT	GATAAACAAA	GATAATAAAC	ACTTTGTTTG	GGTATACAAT
msa363690.2{690_CJB110}	CAAGTTCTGT	GATAAACAAA	GATAATAAAC	ACTTTGTTTG	GGTATACAAT

Table 85: Comparative Sequences relating to SAG1361

msa363690.2{690_1169NT}	CAAGTTCTGT	GATAAACAAA	GATAATAAAC	ACTTTGTTTG	GGTATACAAT
msa363690.2{690_18RS21}	CAAGTTCTGT	GATAAACAAA	GATAATAAAC	ACTTTGTTTG	GGTATACAAT
msa363690.2{690_2603}	CAAGTTCTGT	GATAAACAAA	GATAATAAAC	ACTTTGTTTG	GGTATACAAT
msa363690.2{690_A909}	CAAGTTCTGT	GATAAACAAA	GATAATAAAC	ACTTTGTTTG	GGTATACAAT
msa363690.2{690_JM9130013}	CAAGTTCTGT	GATAAACAAA	GATAATAAAC	ACTTTGTTTG	GGTATACAAT
msa363690.2{690_H36B}	CAAGTTCTGT	GATAAACAAA	GATAATAAAC	ACTTTGTTTG	GGTATACAAT
Consensus	*****	***-*****	*****	*****	*****
msa363690.2{690_COH1}	GATTCTAATC	GTAAAAATTC	CAAAGTTGAA	GTCAAAATTG	GTAAAGCTGA
msa363690.2{690_M732}	GATTCTAATC	GTAAAAATTC	CAAAGTTGAA	GTCAAAATTG	GTAAAGCTGA
msa363690.2{690_M781}	GATTCTAATC	GTAAAAATTC	CAAAGTTGAA	GTCAAAATTG	GTAAAGCTGA
msa363690.2{690_090}	GATTCTAATC	GTAAAAATTC	CAAAGTTGAA	GTCAAAATTG	GTAAAGCTGA
msa363690.2{690_CJB110}	GATTCTAATC	GTAAAAATTC	CAAAGTTGAA	GTCAAAATTG	GTAAAGCTGA
msa363690.2{690_1169NT}	GATTCTAATC	GTAAAAATTC	CAAAGTTGAA	GTCAAAATTG	GTAAAGCTGA
msa363690.2{690_18RS21}	GATTCTAATC	GTAAAAATTC	CAAAGTTGAA	GTCAAAATTG	GTAAAGCTGA
msa363690.2{690_2603}	GATTCTAATC	GTAAAAATTC	CAAAGTTGAA	GTCAAAATTG	GTAAAGCTGA
msa363690.2{690_A909}	GATTCTAATC	GTAAAAATTC	CAAAGTTGAA	GTCAAAATTG	GTAAAGCTGA
msa363690.2{690_JM9130013}	GATTCTAATC	GTAAAAATTC	CAAAGTTGAA	GTCAAAATTG	GTAAAGCTGA
msa363690.2{690_H36B}	GATTCTAATC	GTAAAAATTC	CAAAGTTGAA	GTCAAAATTG	GTAAAGCTGA
Consensus	*****	*****	*****	*****	*****
msa363690.2{690_COH1}	TGCTAAGACA	CAAGAAATTT	TATCAGGTTT	GAAAGCAGGA	CAAATCGTgG
msa363690.2{690_M732}	TGCTAAGACA	CAAGAAATTT	TATCAGGTTT	GAAAGCAGGA	CAAATCGTgG
msa363690.2{690_M781}	TGCTAAGACA	CAAGAAATTT	TATCAGGTTT	GAAAGCAGGA	CAAATCGTgG
msa363690.2{690_090}	TGCTAAGACA	CAAGAAATTT	TATCAGGTTT	GAAAGCAGGA	CAAATCGTgG
msa363690.2{690_CJB110}	TGCTAAGACA	CAAGAAATTT	TATCAGGTTT	GAAAGCAGGA	CAAATCGTgG
msa363690.2{690_1169NT}	TGCTAAGACA	CAAGAAATTT	TATCAGGTTT	GAAAGCAGGA	CAAATCGTgG
msa363690.2{690_18RS21}	TGCTAAGACA	CAAGAAATTT	TATCAGGTTT	GAAAGCAGGA	CAAATCGTgG
msa363690.2{690_2603}	TGCTAAGACA	CAAGAAATTT	TATCAGGTTT	GAAAGCAGGA	CAAATCGTgG
msa363690.2{690_A909}	TGCTAAGACA	CAAGAAATTT	TATCAGGTTT	GAAAGCAGGA	CAAATCGTgG
msa363690.2{690_JM9130013}	TGCTAAGACA	CAAGAAATTT	TATCAGGTTT	GAAAGCAGGA	CAAATCGTgG
msa363690.2{690_H36B}	TGCTAAGACA	CAAGAAATTT	TATCAGGTTT	GAAAGCAGGA	CAAATCGTaG
Consensus	*****	*****	*****	*****	*****-*
msa363690.2{690_COH1}	TTACTAATCC	AAGcAAAaCt	TTCAAGGATG	GGCAAAAAAT	TGATAATATT
msa363690.2{690_M732}	TTACTAATCC	AAGcAAAaCt	TTCAAGGATG	GGCAAAAAAT	TGATAATATT
msa363690.2{690_M781}	TTACTAATCC	AAGcAAAaCt	TTCAAGGATG	GGCAAAAAAT	TGATAATATT
msa363690.2{690_090}	TTACTAATCC	AAGtAAAaCc	TTCAAGGATG	GGCAAAAAAT	TGATAATATT
msa363690.2{690_CJB110}	TTACTAATCC	AAGtAAAaCc	TTCAAGGATG	GGCAAAAAAT	TGATAATATT
msa363690.2{690_1169NT}	TTACTAATCC	AAGtAAAaCc	TTCAAGGATG	GGCAAAAAAT	TGATAATATT
msa363690.2{690_18RS21}	TTACTAATCC	AAGtAAAaCc	TTCAAGGATG	GGCAAAAAAT	TGATAATATT
msa363690.2{690_2603}	TTACTAATCC	AAGtAAAaCc	TTCAAGGATG	GGCAAAAAAT	TGATAATATT
msa363690.2{690_A909}	TTACTAATCC	AAGcAAAaCt	TTCAAGGATG	GGCAAAAAAT	TGATAATATT
msa363690.2{690_JM9130013}	TTACTAATCC	AAGcAAAaCt	TTCAAGGATG	GGCAAAAAAT	TGATAATATT
msa363690.2{690_H36B}	TTACTAATCC	AAGtAAAaCt	TTCAAGGATG	GGCAAAAAAT	TGATAATATT
Consensus	*****	***-***-*	*****	*****	*****
msa363690.2{690_COH1}	GAATCAATcG	ATCTTAAgTC	TAATAAGAAA	TCAGAGgtga	a-
msa363690.2{690_M732}	GAATCAATcG	ATCTTAAgTC	TAATAAGAAA	TCAGAGgtga	a-
msa363690.2{690_M781}	GAATCAATcG	ATCTTAAgTC	TAATAAGAAA	TCAGAGgtga	a-
msa363690.2{690_090}	GAATCAATcG	ATCTTAAcTC	TAATAAGAAA	TCAGAGg---	--
msa363690.2{690_CJB110}	GAATCAATcG	ATCTTAAcTC	TAATAAGAAA	TCAGAGgtga	--
msa363690.2{690_1169NT}	GAATCAATcG	ATCTTAAcTC	TAATAAGAAA	TCAGAGgtga	a-
msa363690.2{690_18RS21}	GAATCAATcG	ATCTTAAcTC	TAATAAGAAA	TCAGAG-----	--
msa363690.2{690_2603}	GAATCAATcG	ATCTTAAcTC	TAATAAGAAA	TCAGAGgtga	aA
msa363690.2{690_A909}	GAATCAATaG	ATCTTAAgTC	TAATAAGAAA	TCAGAGgtga	aA
msa363690.2{690_JM9130013}	GAATCAATaG	ATCTTAAgTC	TAATAAGAAA	TCAGAGgtga	aA
msa363690.2{690_H36B}	GAATCAATcG	ATCTTAAgTC	TAATAAGAAA	TCAGAGgtg-	--
Consensus	*****-*	*****-*	*****	*****----	--*

SEQ ID NO. 8511

STRAIN 2603 frame: 1

MSKRQNLGISKKGAIISGLSVALIVVIGGFLWVQSQPNKSAVKTNKYKVFENVREGSVSSST
 LLTGKAKANQEYVYFDANKGNRATVTVKVGDKITAGQQLVQYDTTTAQAAAYDTANRQLN
 KVARQINNLTGSLPAMESSDQSSSSQGGTQSTSGATNRLQQNYQSQANASYNQQLQ
 DLNDAYADAQAEVNKAQKALNDTVITSDVSGTVEVNSDIDPASKTSQVLVHVATEGKLQ
 VQGTMSYDLANVKKDQAVKIKSKVYPDKKEWEGKISYISNYPEAEANNNDSSNGSSAVNY
 KYKVDITSPLDALKQGFTVSVEVNGDKHLIVPTSSVINKDNKHFVWVYNDNRKISKVE
 VKIGKADAKTQEILSGLKAGQIVVTNPSKTFKDGQKIDNIESIDLNSNKKSEVK

SEQ ID NO. 8512

STRAIN 090 frame: 1

FLWVQSQPNKSAVKTNKYKVFENVREGSVSSSTLLTGKAKANQEYVYFDANKGNRATVTVK
 VGDKITAGQQLVQYDTTTAQAAAYDTANRQLNKVARQINNLTGSLPAMESSDQSSSSQ
 GQGTQSTSGATNRLQQNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
 SGTVEVNSDIDPASKTSQVLVHVATEGKLQVQGTMSYDLANVKKDQAVKIKSKVYPDK
 EWEGKISYISNYPEAEANNNDSSNGSSAVNYKYKVDITSPLDALKQGFTVSVEVNGDKH
 LIVPTSSVINKDNKHFVWVYNDNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
 TFKDGQKIDNIESIDLNSNKKSE

Table 85: Comparative Sequences relating to SAG1361**SEQ ID NO. 8513**

STRAIN A909 frame: 1

FLWVQSQPNKSAVKTNKYKVFNVREGSVSSSTLLTGKAKANQEYVYFDANKGNRATVTVK
 VGDKITAGQQLVQYDTTTTAQAAYDTANRQLNKVARQINNLTGSLPAMESSDQSSSSSQ
 GQGAQSTSGATNRLQQNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
 SGTVVEVNSDIDPASKTSQVLVHVATEGKLQVQGTMSSEYDLANVKKDQSVKIKSKVYPDK
 EWEGKISYISNYPEAEANNNDSSNGSSAVNYKYKVDITSPDLALKQGFTVSVEVVNGDKH
 LIVPTSSVTNKDNKHFVWVYNDNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
 TFKDGQKIDNIESIDLKSNKKSEV

SEQ ID NO. 8514

STRAIN H36B frame: 1

FLWVQSQPNKSAVKTNKYKVFNVREGSVSSSTLLTGKAKANQEYVYFDANKGNRATVTVK
 VGDKITAGQQLVQYDTTTTAQAAYDTANRQLNKVARQINNLTGSLPAMESSDQSSSSSQ
 GQGTQSTSGATNRLQQNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
 SGTVVEVNSDIDPASKTSQVLVHVATEGKLQVQGTMSSEYDLANVKKDQAVKIKSKVYPDK
 EWEGKISYISNYPEAEANNNDSSNGSSAVNYKYKVDITSPDLALKQGFTVSVEVVNGDKH
 LIVPTSSVTNKDNKHFVWVYNDNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
 AFKDGQKIDNIESIDLKSNKKSEV

SEQ ID NO. 8515

STRAIN 18RS21 frame: 1

FLWVQSQPNKSAVKTNKYKVFNVREGSVSSSTLLTGKAKANQEYVYFDANKGNRATVTVK
 VGDKITAGQQLVQYDTTTTAQAAYDTANRQLNKVARQINNLTGSLPAMESSDQSSSSSQ
 GQGTQSTSGATNRLQQNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
 SGTVVEVNSDIDPASKTSQVLVHVATEGKLQVQGTMSSEYDLANVKKDQAVKIKSKVYPDK
 EWEGKISYISNYPEAEANNNDSSNGSSAVNYKYKVDITSPDLALKQGFTVSVEVVNGDKH
 LIVPTSSVINKDNKHFVWVYNDNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
 TFKDGQKIDNIESIDLNSNKKSE

SEQ ID NO. 8516

STRAIN M732 frame: 1

FLWVQSQPNKSAVKTNKYKVFNVREGSVSSSTLLTGKAKANQEYVYFDANKGNRATVTVK
 VGDKITAGQQLVQYDTTTTAQAAYDTANRQLNKVARQINNLTGSLPAMESSDQSSSSSQ
 GQGTQSTSGATNRLQQNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
 SGTVVEVNSDIDPASKTSQVLVHVATEGKLQVQGTMSSEYDLANVKKDQAVKIKSKVYPDK
 EWEGKISYISNYPEAEANNNDSSNGSSAVNYKYKVDITSPDLALKQGFTVSVEVVNGDKH
 LIVPTSSVINKDNKHFVWVYNDNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
 TFKDGQKIDNIESIDLKSNKKSEV

SEQ ID NO. 8517

STRAIN COH1 frame: 1

FLWVQSQPNKSAVKTNKYKVFNVREGSVSSSTLLTGKAKANQEYVYFDANKGNRATVTVK
 VGDKITAGQQLVQYDTTTTAQAAYDTANRQLNKVARQINNLTGSLPAMESSDQSSSSSQ
 GQGTQSTSGATNRLQQNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
 SGTVVEVNSDIDPASKTSQVLVHVATEGKLQVQGTMSSEYDLANVKKDQAVKIKSKVYPDK
 EWEGKISYISNYPEAEANNNDSSNGSSAVNYKYKVDITSPDLALKQGFTVSVEVVNGDKH
 LIVPTSSVINKDNKHFVWVYNDNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
 TFKDGQKIDNIESIDLKSNKKSEV

SEQ ID NO. 8518

STRAIN M781 frame: 1

FLWVQSQPNKSAVKTNKYKVFNVREGSVSSSTLLTGKAKANQEYVYFDANKGNRATVTVK
 VGDKITAGQQLVQYDTTTTAQAAYDTANRQLNKVARQINNLTGSLPAMESSDQSSSSSQ
 GQGTQSTSGATNRLQQNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
 SGTVVEVNSDIDPASKTSQVLVHVATEGKLQVQGTMSSEYDLANVKKDQAVKIKSKVYPDK
 EWEGKISYISNYPEAEANNNDSSNGSSAVNYKYKVDITSPDLALKQGFTVSVEVVNGDKH
 LIVPTSSVINKDNKHFVWVYNDNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
 TFKDGQKIDNIESIDLKSNKKSEV

SEQ ID NO. 8519

STRAIN M781 frame: 1

FLWVQSQPNKSAVKTNKYKVFNVREGSVSSSTLLTGKAKANQEYVYFDANKGNRATVTVK
 VGDKITAGQQLVQYDTTTTAQAAYDTANRQLNKVARQINNLTGSLPAMESSDQSSSSSQ
 GQGTQSTSGATNRLQQNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
 SGTVVEVNSDIDPASKTSQVLVHVATEGKLQVQGTMSSEYDLANVKKDQAVKIKSKVYPDK
 EWEGKISYISNYPEAEANNNDSSNGSSAVNYKYKVDITSPDLALKQGFTVSVEVVNGDKH
 LIVPTSSVINKDNKHFVWVYNDNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
 TFKDGQKIDNIESIDLKSNKKSEV

SEQ ID NO. 8520

STRAIN CJB110 frame: 1

FLWVQSQPNKSAVKTNKYKVFNVREGSVSSSTLLTGKAKANQEYVYFDANKGNRATVTVK
 VGDKITAGQQLVQYDTTTTAQAAYDTANRQLNKVARQINNLTGSLPAMESSDQSSSSSQ
 GQGTQSTSGATNRLQQNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
 SGTVVEVNSDIDPASKTSQVLVHVATEGKLQVQGTMSSEYDLANVKKDQAVKIKSKVYPDK
 EWEGKISYISNYPEAEANNNDSSNGSSAVNYKYKVDITSPDLALKQGFTVSVEVVNGDKH
 LIVPTSSVINKDNKHFVWVYNDNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
 TFKDGQKIDNIESIDLNSNKKSEV

SEQ ID NO. 8521

Table 85: Comparative Sequences relating to SAG1361

STRAIN 1169NT frame: 1

FLWVQSQPKNKSAVKTNKYKVFNVREGSVSSSTLLTGKAKANQEQYVYFDANKGNRATVTVK
 VGDKITAGQQLVQYDTTTTAQAAYDTANRQLNKVARQINNLTGSLPAMESSDQSSSSSQ
 GQGTQSTSGATNRLQQNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
 SGTVEVNSDIDPASKTSQVLVHVATEGKLQVQGTMSYDLANVKKDQAVKIKSKVYPDK
 EWEGKISYISNYPEAEANNNSNNGSSAVNYKYKVDITSPLDALKQGFVTSVEVNGDKH
 LIVPTSSVINKDNKHFVWVYNDNSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
 TFKDGGQKIDNIESIDLNSNKKSEV

SEQ ID NO. 8522

STRAIN JM9130013 frame: 1

FLWVQSQPKNKSAVKTNKYKVFNVREGSVSSSTLLTGKAKANQEQYVYFDANKGNRATVTVK
 VGDKITAGQQLVQYDTTTTAQAAYDTANRQLNKVARQINNLTGSLPAMESSDQSSSSSQ
 GQGAQSTSGATNRLQQNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
 SGTVEVNSDIDPASKTSQVLVHVATEGKLQVQGTMSYDLANVKKDQSVKIKSKVYPDK
 EWEGKISYISNYPEAEANNNSNNGSSAVNYKYKVDITSPLDALKQGFVTSVEVNGDKH
 LIVPTSSVTNKDNKHFVWVYNDNSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
 TFKDGGQKIDNIESIDLNSNKKSEVK

PRETTY of: /biotmp/msa375805.2{*} April 1, 2003 02:58 ..

	1			50
msa375805.2{690_COH1}	-----F	LWVQSQPKNK	AVKTNKYKVF	
msa375805.2{690_M732}	-----F	LWVQSQPKNK	AVKTNKYKVF	
msa375805.2{690_M781}	-----F	LWVQSQPKNK	AVKTNKYKVF	
msa375805.2{690_090}	-----F	LWVQSQPKNK	AVKTNKYKVF	
msa375805.2{690_CJB110}	-----F	LWVQSQPKNK	AVKTNKYKVF	
msa375805.2{690_1169NT}	-----F	LWVQSQPKNK	AVKTNKYKVF	
msa375805.2{690_18RS21}	-----F	LWVQSQPKNK	AVKTNKYKVF	
msa375805.2{690_2603}	mskrqnlgis kkgaiisgls valivviggF	LWVQSQPKNK	AVKTNKYKVF	
msa375805.2{690_A909}	-----F	LWVQSQPKNK	AVKTNKYKVF	
msa375805.2{690_JM9130013}	-----F	LWVQSQPKNK	AVKTNKYKVF	
msa375805.2{690_H36B}	-----F	LWVQSQPKNK	AVKTNKYKVF	
Consensus	*****	*****	*****	*****
	51			100
msa375805.2{690_COH1}	VREGSVSSST LLTGKAKANQ	EQYVYFDANK	GNRATVTVKV	GDKITAGQQL
msa375805.2{690_M732}	VREGSVSSST LLTGKAKANQ	EQYVYFDANK	GNRATVTVKV	GDKITAGQQL
msa375805.2{690_M781}	VREGSVSSST LLTGKAKANQ	EQYVYFDANK	GNRATVTVKV	GDKITAGQQL
msa375805.2{690_090}	VREGSVSSST LLTGKAKANQ	EQYVYFDANK	GNRATVTVKV	GDKITAGQQL
msa375805.2{690_CJB110}	VREGSVSSST LLTGKAKANQ	EQYVYFDANK	GNRATVTVKV	GDKITAGQQL
msa375805.2{690_1169NT}	VREGSVSSST LLTGKAKANQ	EQYVYFDANK	GNRATVTVKV	GDKITAGQQL
msa375805.2{690_18RS21}	VREGSVSSST LLTGKAKANQ	EQYVYFDANK	GNRATVTVKV	GDKITAGQQL
msa375805.2{690_2603}	VREGSVSSST LLTGKAKANQ	EQYVYFDANK	GNRATVTVKV	GDKITAGQQL
msa375805.2{690_A909}	VREGSVSSST LLTGKAKANQ	EQYVYFDANK	GNRATVTVKV	GDKITAGQQL
msa375805.2{690_JM9130013}	VREGSVSSST LLTGKAKANQ	EQYVYFDANK	GNRATVTVKV	GDKITAGQQL
msa375805.2{690_H36B}	VREGSVSSST LLTGKAKANQ	EQYVYFDANK	GNRATVTVKV	GDKITAGQQL
Consensus	*****	*****	*****	*****
	101			150
msa375805.2{690_COH1}	VQYDTTTTAQA AYDTANRQLN	KVARQINNLLK	TTGSfPAMEs	SDQSSSSSQG
msa375805.2{690_M732}	VQYDTTTTAQA AYDTANRQLN	KVARQINNLLK	TTGSfPAMEs	SDQSSSSSQG
msa375805.2{690_M781}	VQYDTTTTAQA AYDTANRQLN	KVARQINNLLK	TTGSfPAMEs	SDQSSSSSQG
msa375805.2{690_090}	VQYDTTTTAQA AYDTANRQLN	KVARQINNLLK	TTGSfPAME1	SDQSSSSSQG
msa375805.2{690_CJB110}	VQYDTTTTAQA AYDTANRQLN	KVARQINNLLK	TTGSfPAME1	SDQSSSSSQG
msa375805.2{690_1169NT}	VQYDTTTTAQA AYDTANRQLN	KVARQINNLLK	TTGSfPAMEs	SDQSSSSSQG
msa375805.2{690_18RS21}	VQYDTTTTAQA AYDTANRQLN	KVARQINNLLK	TTGSfPAMEs	SDQSSSSSQG
msa375805.2{690_2603}	VQYDTTTTAQA AYDTANRQLN	KVARQINNLLK	TTGSfPAMEs	SDQSSSSSQG
msa375805.2{690_A909}	VQYDTTTTAQA AYDTANRQLN	KVARQINNLLK	TTGSfPAMEs	SDQSSSSSQG
msa375805.2{690_JM9130013}	VQYDTTTTAQA AYDTANRQLN	KVARQINNLLK	TTGSfPAMEs	SDQSSSSSQG
msa375805.2{690_H36B}	VQYDTTTTAQA AYDTANRQLN	KVARQINNLLK	TTGSfPAMEs	SDQSSSSSQG
Consensus	*****	*****	*****	*****
	151			200
msa375805.2{690_COH1}	QGTQSTSGAT NRLQQNYQSQ	ANASYNQQLQ	DLNDAYADAQ	AEVNKAQKAL
msa375805.2{690_M732}	QGTQSTSGAT NRLQQNYQSQ	ANASYNQQLQ	DLNDAYADAQ	AEVNKAQKAL
msa375805.2{690_M781}	QGTQSTSGAT NRLQQNYQSQ	ANASYNQQLQ	DLNDAYADAQ	AEVNKAQKAL
msa375805.2{690_090}	QGTQSTSGAT NRLQQNYQSQ	ANASYNQQLQ	DLNDAYADAQ	AEVNKAQKAL
msa375805.2{690_CJB110}	QGTQSTSGAT NRLQQNYQSQ	ANASYNQQLQ	DLNDAYADAQ	AEVNKAQKAL
msa375805.2{690_1169NT}	QGTQSTSGAT NRLQQNYQSQ	ANASYNQQLQ	DLNDAYADAQ	AEVNKAQKAL
msa375805.2{690_18RS21}	QGTQSTSGAT NRLQQNYQSQ	ANASYNQQLQ	DLNDAYADAQ	AEVNKAQKAL
msa375805.2{690_2603}	QGTQSTSGAT NRLQQNYQSQ	ANASYNQQLQ	DLNDAYADAQ	AEVNKAQKAL
msa375805.2{690_A909}	QGTQSTSGAT NRLQQNYQSQ	ANASYNQQLQ	DLNDAYADAQ	AEVNKAQKAL
msa375805.2{690_JM9130013}	QGTQSTSGAT NRLQQNYQSQ	ANASYNQQLQ	DLNDAYADAQ	AEVNKAQKAL
msa375805.2{690_H36B}	QGTQSTSGAT NRLQQNYQSQ	ANASYNQQLQ	DLNDAYADAQ	AEVNKAQKAL
Consensus	**.....	*****	*****	*****
	201			250
msa375805.2{690_COH1}	NDTVITSDVS GTVVEVNSDI	DPASKTSQVL	VHVATEGKLQ	VQGTMSYDL
msa375805.2{690_M732}	NDTVITSDVS GTVVEVNSDI	DPASKTSQVL	VHVATEGKLQ	VQGTMSYDL
msa375805.2{690_M781}	NDTVITSDVS GTVVEVNSDI	DPASKTSQVL	VHVATEGKLQ	VQGTMSYDL
msa375805.2{690_090}	NDTVITSDVS GTVVEVNSDI	DPASKTSQVL	VHVATEGKLQ	VQGTMSYDL

Table 85: Comparative Sequences relating to SAG1361

msa375805.2{690_CJB110}	NDTVITSDVS	GTVEVNNDI	DPASKTSQVL	VHVATEGKLQ	VQGTMSYDL
msa375805.2{690_1169NT}	NDTVITSDVS	GTVEVNNDI	DPASKTSQVL	VHVATEGKLQ	VQGTMSYDL
msa375805.2{690_18RS21}	NDTVITSDVS	GTVEVNNDI	DPASKTSQVL	VHVATEGKLQ	VQGTMSYDL
msa375805.2{690_2603}	NDTVITSDVS	GTVEVNNDI	DPASKTSQVL	VHVATEGKLQ	VQGTMSYDL
msa375805.2{690_A909}	NDTVITSDVS	GTVEVNNDI	DPASKTSQVL	VHVATEGKLQ	VQGTMSYDL
msa375805.2{690_JM9130013}	NDTVITSDVS	GTVEVNNDI	DPASKTSQVL	VHVATEGKLQ	VQGTMSYDL
msa375805.2{690_H36B}	NDTVITSDVS	GTVEVNNDI	DPASKTSQVL	VHVATEGKLQ	VQGTMSYDL
Consensus	*****	*****	*****	*****	*****
251					
msa375805.2{690_COH1}	ANVKKDQaVK	IKSKVYPDKE	WEGKISYISN	YPEAEANNND	SNNGSSAVNY
msa375805.2{690_M732}	ANVKKDQaVK	IKSKVYPDKE	WEGKISYISN	YPEAEANNND	SNNGSSAVNY
msa375805.2{690_M781}	ANVKKDQaVK	IKSKVYPDKE	WEGKISYISN	YPEAEANNND	SNNGSSAVNY
msa375805.2{690_090}	ANVKKDQaVK	IKSKVYPDKE	WEGKISYISN	YPEAEANNND	SNNGSSAVNY
msa375805.2{690_CJB110}	ANVKKDQaVK	IKSKVYPDKE	WEGKISYISN	YPEAEANNND	SNNGSSAVNY
msa375805.2{690_1169NT}	ANVKKDQaVK	IKSKVYPDKE	WEGKISYISN	YPEAEANNND	SNNGSSAVNY
msa375805.2{690_18RS21}	ANVKKDQaVK	IKSKVYPDKE	WEGKISYISN	YPEAEANNND	SNNGSSAVNY
msa375805.2{690_2603}	ANVKKDQaVK	IKSKVYPDKE	WEGKISYISN	YPEAEANNND	SNNGSSAVNY
msa375805.2{690_A909}	ANVKKDQsVK	IKSKVYPDKE	WEGKISYISN	YPEAEANNND	SNNGSSAVNY
msa375805.2{690_JM9130013}	ANVKKDQsVK	IKSKVYPDKE	WEGKISYISN	YPEAEANNND	SNNGSSAVNY
msa375805.2{690_H36B}	ANVKKDQaVK	IKSKVYPDKE	WEGKISYISN	YPEAEANNND	SNNGSSAVNY
Consensus	*****-*	*****	*****	*****	*****
301					
msa375805.2{690_COH1}	KYKVDITSPL	DALKQGFTVS	VEVNGDKHL	IVPTSSViNK	DNKHFVWVYN
msa375805.2{690_M732}	KYKVDITSPL	DALKQGFTVS	VEVNGDKHL	IVPTSSViNK	DNKHFVWVYN
msa375805.2{690_M781}	KYKVDITSPL	DALKQGFTVS	VEVNGDKHL	IVPTSSViNK	DNKHFVWVYN
msa375805.2{690_090}	KYKVDITSPL	DALKQGFTVS	VEVNGDKHL	IVPTSSViNK	DNKHFVWVYN
msa375805.2{690_CJB110}	KYKVDITSPL	DALKQGFTVS	VEVNGDKHL	IVPTSSViNK	DNKHFVWVYN
msa375805.2{690_1169NT}	KYKVDITSPL	DALKQGFTVS	VEVNGDKHL	IVPTSSViNK	DNKHFVWVYN
msa375805.2{690_18RS21}	KYKVDITSPL	DALKQGFTVS	VEVNGDKHL	IVPTSSViNK	DNKHFVWVYN
msa375805.2{690_2603}	KYKVDITSPL	DALKQGFTVS	VEVNGDKHL	IVPTSSViNK	DNKHFVWVYN
msa375805.2{690_A909}	KYKVDITSPL	DALKQGFTVS	VEVNGDKHL	IVPTSSVtNK	DNKHFVWVYN
msa375805.2{690_JM9130013}	KYKVDITSPL	DALKQGFTVS	VEVNGDKHL	IVPTSSVtNK	DNKHFVWVYN
msa375805.2{690_H36B}	KYKVDITSPL	DALKQGFTVS	VEVNGDKHL	IVPTSSVtNK	DNKHFVWVYN
Consensus	*****	*****	*****	*****-*	*****
351					
msa375805.2{690_COH1}	DSNRKISKVE	VKIGKADAKT	QEILSGLKAG	QIVVTNPSKt	FKDGQKIDNI
msa375805.2{690_M732}	DSNRKISKVE	VKIGKADAKT	QEILSGLKAG	QIVVTNPSKt	FKDGQKIDNI
msa375805.2{690_M781}	DSNRKISKVE	VKIGKADAKT	QEILSGLKAG	QIVVTNPSKt	FKDGQKIDNI
msa375805.2{690_090}	DSNRKISKVE	VKIGKADAKT	QEILSGLKAG	QIVVTNPSKt	FKDGQKIDNI
msa375805.2{690_CJB110}	DSNRKISKVE	VKIGKADAKT	QEILSGLKAG	QIVVTNPSKt	FKDGQKIDNI
msa375805.2{690_1169NT}	DSNRKISKVE	VKIGKADAKT	QEILSGLKAG	QIVVTNPSKt	FKDGQKIDNI
msa375805.2{690_18RS21}	DSNRKISKVE	VKIGKADAKT	QEILSGLKAG	QIVVTNPSKt	FKDGQKIDNI
msa375805.2{690_2603}	DSNRKISKVE	VKIGKADAKT	QEILSGLKAG	QIVVTNPSKt	FKDGQKIDNI
msa375805.2{690_A909}	DSNRKISKVE	VKIGKADAKT	QEILSGLKAG	QIVVTNPSKt	FKDGQKIDNI
msa375805.2{690_JM9130013}	DSNRKISKVE	VKIGKADAKT	QEILSGLKAG	QIVVTNPSKt	FKDGQKIDNI
msa375805.2{690_H36B}	DSNRKISKVE	VKIGKADAKT	QEILSGLKAG	QIVVTNPSKa	FKDGQKIDNI
Consensus	*****	*****	*****	*****-*	*****
401					
msa375805.2{690_COH1}	ESIDLkSNKK	SEv~			
msa375805.2{690_M732}	ESIDLkSNKK	SEv~			
msa375805.2{690_M781}	ESIDLkSNKK	SEv~			
msa375805.2{690_090}	ESIDLnSNKK	SE~			
msa375805.2{690_CJB110}	ESIDLnSNKK	SEv~			
msa375805.2{690_1169NT}	ESIDLnSNKK	SEv~			
msa375805.2{690_18RS21}	ESIDLnSNKK	SE~			
msa375805.2{690_2603}	ESIDLnSNKK	SEvK			
msa375805.2{690_A909}	ESIDLkSNKK	SEvK			
msa375805.2{690_JM9130013}	ESIDLkSNKK	SEvK			
msa375805.2{690_H36B}	ESIDLkSNKK	SEv~			
Consensus	*****-****	***~*			
414					

Table 86: Comparative Sequences relating to SAG1393

SEQ ID NO. 8601

STRAIN 2603

atgaaaaaaattggaattattgtcctcacactactgaccttcttttttggtatcttgcgga
 caacaaactaaacaagaagcactaaaacaactatttctaaaatgcctaaaattgaaggc
 ttcacctattatggaaaaattcctgaaaatccgaaaaagtaattattttacatattct
 tacactgggtattttattaaaactaggtgttaatgtttcaagttacagtttagacttagaa
 aaagatagccccgttttttggtaaacaactgaaagaagctaaaaaattaactgctgatgat
 acagaagctattgccgcacaaaaacctgatttaatcatggttttcgatcaagatccaaac
 atcaatactctgaaaaaaattgcaccaacttttagttattaaatatggtgcacaaaattat
 ttagatatgatgccagccttggggaaagtattcggtaaagaaaaagaagctaatacagtgg
 gtttagccaatggaaaactaaaactctcgctgtcaaaaaagatttacaccatatcttaaag
 cctaacactacttttactattatggatttttatgataaaaatatctattttatatggtaat
 aattttggacgcggtggagaaactaatctatgattcactaggttatgctgccccagaaaaa
 gtcaaaaaagatgtctttaaaaaagggtgggttaccgtttcgcaagaagcaatcggtgat
 tacgttggagattatgcccttgttaataataacaaaacgactaaaaaagcagcttcatca
 cttaaagaaagtgtctggaagaatttaccagctgtcaaaaaagggcacatcatagaa
 agtaactacgacgtgttttatttctctgaccctctatctttagaagctcaattaaaatca
 tttacaaaggctatcaaagaaaatacaaat

SEQ ID NO. 8602

STRAIN 090

GAAGGCTTCACCTATTATGGAAAAATTCCTGAAAATCCGAAAAAAGTAAT
 TAATTTTACATATTCTTACACTGGGTATTTATTAAAACTAGGTGTTAATG
 TTTCAAGTTACAGTTTAGACTTAGAAAAAGATAGCCCCGTTTTTGGTAAg
 CAACTGAAAGAAGCTAAAAAATTAAGTCTGATGATACAGAAGCTATTGC
 CGCACAAAAACCTGATTTAATCATGGTTTTCGATCAAGATCCAAACATCA
 ATACTCTGAAAAAAATTCACCAACTTTAGTTATTAAATATGGTGCACAA
 AATTATTTAGATATGATGCCAGCCTTGGGGAAAGTATTCCGTAAAGAAAA
 AGAAGCTAATCAGTGGGTAGCCAATGGAAAACTAAAACCTCTCGCTGCCA
 AAAAAGATTTACACCATATCTTAAAGCCTAACACTACTTTTACTATTATG
 GATTTTATGATAAAAAATATCTATTTATATGGTAATAATTTTGGACGCGG
 tGGAGAACTAATCTATGATTCACTAGGTATGCTGCCCCAgAAAAAGTCA
 AAAAAGATGTcTTTAAAAAAGGGTGGTTTACCGTTTCgCAAGAAGCAATC
 GGtGATTACGTTGGAGATTATGCCCTTGTTAATATAAAACAAAACGACTAA
 AAAAGCAGCTTCatcACTTAAAGAAAGTGATGTCTGGAAGAATTTACCAG
 CTGTCaAAAAAGGGCACATCATAGAAAGTAacTACGACGTGTTTATTTTC
 TCTGACCCTCTATCTTTAGAAGCTCAATTAAAATCATTTACAAA

SEQ ID NO. 8603

STRAIN A909

GAAGGCTTCACCTATTATGGAAAAATTCCTG
 AAAATCCGAAAAAAGTAATTAATTTTACATATTCTTACACTGGATATTTA
 TTAAAACTAGGAGTTAATGTTTCAAGTTACAGTTTAGACTTAGAAAAAGA
 TAGCCCCGTTTTTGGTAAaCAACTGAAAGGAGCTAAAAAATTAAGTCTG
 ATGATACAGAAGCTATTGCCGCACAAAAACCTGATTTAaTCATGGTTTTT
 GATCAAGATCCAAACATCAATACTCTGAAAAAAATTCACCAACTTTAGT
 TATTAAATATGGTGCACAAAATTATTtagATaTGATGCCAGCTTTGGGGA
 AAGTATTCGGTAAAGAAAAAGAAGCTAATCAGTGGGTAGCCAaTGGAAA
 ACTAAAACTCTCGCTGCCAAAAAAGATTTACACCATATCTTAAACCTAA
 CACTACTTTTACCATTATGGATTTTATGATAAAAAATATCTATTTATATG
 GTAATAATTTTGGACGCGGTGGAGAATAATCTATGATTCACTAGGTAT
 GCTGCCCCAGAAAAAGTCAAAAAAGATGTCTTTAAAAAAGGGTGGTTTAC
 CGTTTCGCAAGAAGCAATCGGTgATTACGTTGGAGATTATGCCCTTGTTA
 ATATAACAAAACGACTAAAAAAGCAGCTTCATCACTTAAAGAAAGTGAT
 GTCTGGAAGAATTTACCAGCTGTCAAAAAAGGGCACATCATAGAAAGTAA
 CTACGACGTGTTTATTTCTCTGACCCTcTATCTTTAGAAGCTCAATTAA
 AATCATTTACAAA

SEQ ID NO. 8604

STRAIN H36B

GAAGGCTTCACCTATTATGGAAAA
 ATTCCTGAAAATCCGAAAAAAGTAATTAATTTTACATATTCTTACACTGG
 ATATTTATTAAAACTAGGAGTTAATGTTTCAAGTTACAGTTTAGACTTAG
 AAAAAGATAgCCCCGTTTTTGGTAAgCAACTGAAAGGAGCTAAAAAATTA
 ACTGCTGATGATACAGAAGCTATTGCCGCACAAAAACCTGATTTAaTCAT
 GGTTTTTGATCAAgATCCAAACATCAATACTCTGAAAAAAATTCACCAA
 CTTTAGTTATTAAATATGGTGCACAAAATTATTtagATaTgATGCCAGCT
 TTGGGGAAaAGTATTCGGTAAAGAAAAAGAAGCTAATCAGTGGGTAGCCA
 ATGGAAAACTAAAACCTCTCGCTGCCAAAAAAGATTTACACCATATCTTAA
 GGCCTaACAcTACTTTTACTATTATAGAtTTTTATGATAAAAAATATCTAT
 TTATATGGTAATAATTTTGGACGCGGtGGAgAACTAATCTATGATtCACT
 AGGTTATGCTGCCCCAgAAAAAGTCAAAAAAGATGTCTTTAAAAAAGGGT
 GGTTTACCGTTTCgCAAGAAGCAATCGGTgATTACGTTGGAGATTATGCC
 CTTGTTAATATAAAACAAAACGACTAAAAAAGCAGCTTCaTCACTTAAAGA
 AAGTGATGTTTGGGAAGAATTTACCAGCTGTCAAAAAAGGGCACATCATAG
 AAAGTAACTACGACGTGTTTATTTCTCTGACCCTCTATCTTTAGAAGCT
 CAATTAAAATCATTTACAAA

Table 86: Comparative Sequences relating to SAG1393**SEQ ID NO. 8605****STRAIN 18RS21**

GAAGGCTTCACCTATTATGGA
 AAAATTCCTGAAAATCCGAAAAAAGTAATTAATTTTACATATTCTTACAC
 TGGGTATTTATTAAAAC TAGGTGTTAATGTTTCAAGTTACAGTTTAGACT
 TAGAAAAAGATAGCCCCGTTTTTGGTAAACAAC TGAAAGAAGCTAAAAAA
 TTAAC TGCTGATGATACAGAAGCTATTGCCGCACAAAAACCTGATTTAAT
 CATGGTTTTTCGATCAAGATCCAAACATCAATACTCTGAAAAAAATTGCAC
 CAAC TTTAGTTATTAAATATGGTGCACAAAATTATTTAgATaTGATGCCA
 GCCTTGGGGAAAAGTATTTCGGTAAAGAAAAAgAAGCTAATCAGTGGGTTAG
 CCAATGGAAAACTAAAAC TCTCGCTGTCAAAAAAGATTTACACCATATCT
 TAAAGCCTAACACTACTTTTACTATTATGGATTTTTATGATAAAAAATATC
 TATTTATATGGTAATAATTTTGGACGCGGTGGAGAACTAATCTATGATTC
 ACTAGGTTATGCTGCCCCAgAAAAAGTCAAAAAAgATGTCTTTAAAAAAG
 GGTGGTTTTACCGTTTCGCAAGAAGCAATCGGTGATTACGTTGGAGATTAT
 GCCCTTGTTAATATAAAACAAAACgACTAAAAAAGCAGCTTCATCACTTAA
 AGAAAGTGATGTCTGGAAGAATTTACCAGCTGTCAAAAAAGGGCACATCA
 TAGAAAGTAACTACGACGTGTTTTATTTCTCTGACCCTCTATCTTTAGAA
 GCTCAATTAAAAATCATTTACAAA

SEQ ID NO. 8606**STRAIN M732**

GAAGGCTTCACCTATTATGG
 AAAAATTCCTGAAAATCCGAAAAAAGTAATTAATTTTACATATTCTTACA
 CTGGGTATTTATTAAAAC TAGGTGTTAATGTTTCAAGTTACAGTTTAGAC
 TTAGAAAAAGATAGCCCCGTTTTTGGTAAGCAACTGAAAGAAGCTAAAAA
 ATTAAC TGCTGATGATACAGAAGCTATTGCCGCACAAAAACCTGATTTAA
 TCATGGTTTTTCGATCAAGATCCAAACATCAATACTCTGAAAAAAATTGCA
 CCAAC TTTAGTTATTAAATATGGTGCACAAAATTATTTAgATATGATGCC
 AGCCTTGGGGAAAAGTATTTCGGTAAAGAAAAAGAAGCTAATCAGtGGGTTA
 GCCAATGGAAAACTAAAAC TCTCGCTGCCAAAAAAGATTTACACCATATC
 TTAAAGCCTAACACTACTTTTACTATTATGGATTTTTATGATAAAAAATAT
 CTATTTATATGGTAATAATTTTGGACgCGGtGGAgAACTAATCTATGATT
 CACTAGGTTATGCTGCCCCAGAAAAAGTCAAAAAAGATGTCTTTAAAAAA
 GGGTGGTTTACCGTTTCGCAAGAAGCAATCGGTGATTACGTTGGAGATTA
 TGCCCTTGTTAATATAAAACAAAACGACTAAAAAAGCAGCTTCATCACTTA
 AAGAAAGTGATGTCTGGAAGAATTTACCAGCTGTCAAAAAAGGGCACATC
 ATAGAAAGTAACTACGACGTGTTTTATTTCTCTGACCCTCTATCTTTAGA
 AGCTCAATTAAAAATCATTTACAAA

SEQ ID NO. 8607**STRAIN COH1**

GAAGGCTTCACCTATTATG
 GAAAAATTCCTGAAAATCCGAAAAAAGTAATTAATTTTACATATTCTTAC
 ACTGGGTATTTATTAAAAC TAGGTGTTAATGTTTCAAGTTACAGTTTAgA
 CTTAGAAAAAGATAGCCCCGTTTTTGGTAAGCAACTGAAAGAAGCTAAAA
 AATTAAC TGCTGATGATACAGAAGCTATTGCCGCACAAAAACCTGATTTA
 ATCATGGTTTTTCGATCAAGATCCAAACATCAATACTCTGAAAAAAATTGC
 ACCAAC TTTAGTTATTAAATATGGTGCACAAAATTATTTAgATATGATGC
 CAGCCTTGGGGAAAAGTaTTcGGTAAAGAAAAAGAAGCTAATCAGTGGGTT
 AGCCAATGGAAAACTAAAAC TCTCGCTGCCAAAAAAGATTTACACCATAT
 CTTAAAGCCTAACACTACTTTTACTATTATGGATTTTTATGATAAAAAATA
 TCTATTTATATGGTAATAATTTTGGACGCGGTGGAGAACTAATCTATGAT
 TCACTAGGTTATGCTGCCCCAGAAAAAGTCAAAAAAGATGTCTTTAAAAA
 AGGGTGGTTTTACCGTTTCGCAAGAAGCAATCGGTGATTACGTTGGAGATT
 ATGCCCTTGTTAATATAAAACAAAACGACTAAAAAAGCAGCTTCATCACTT
 AAAGAAAGTGATGTCTGGAAGAATTTACCAGCTGTCAAAAAAGGGCACAT
 CATAGAAAGTAACTACGACGTGTTTTATTTCTCTGACCCTCTATCTTTAG
 AAGCTCAATTAAAAATCATTTACAAA

SEQ ID NO. 8608**STRAIN M781**

GAAGGCTTCACCTATTATGG
 AAAAATTCCTGAAAATCCGAAAAAAGTAATTAATTTTACATATTCTTACA
 CTGGGTATTTATTAAAAC TAGGTGTTAATGTTTCAAGTTACAGTTTAGAC
 TTAgAAAAAGATAGCCCCGTTTTTGGTAAGCAACTGAAAGAAGCTAAAAA<
 ATTAAC TGCTGATGATACAGAAGCTATTGCCGCACAAAAACCTGATTTAA
 TCATGGTTTTTCGATCAAGATCCAAACATCAATACTCTGAAAAAAATTGCA
 CCAAC TTTAGTTATTAAATATGGTGCACAAAATTATTTAgATATGATGCC
 AGCCTTGGGGAAAAGTATTTCGGtAAAGAAAAAGAAGCTAATCAGTGGGTTA
 GCCAATGGAAAACTAAAAC TCTCGCTGCCAAAAAAGATTTACACCATATC
 TTAAAGCCTAACACTACTTTTACTATTATGGATTTTTATGATAAAAAATAT
 CTATTTATATGGTAATAATTTTGGACGCGGTGGAGAACTAATCTATGATT
 CACTAGGTTATGCTGCCCCAGAAAAAGTCAAAAAAGATGTCTTTAAAAAA
 GGGTGGTTTACCGTTTCGCAAGAAGCAATCGGTGATTACGTTGGAGATTA
 TGCCCTTGTTAATATAAAACAAAACGACTAAAAAAGCAGCTTCATCACTTA

Table 86: Comparative Sequences relating to SAG1393

AAGAAAGTGATGTCTGGAAGAATTTACCAGCTGTCAAAAAAGGGCACATC
ATAGAAAGTAACTACGACGTGTTTTATTTCTCTGACCCTCTATCTTTAGA
AGCTCAATTAATAATCATTTACAAA

SEQ ID NO. 8609

STRAIN CJB110

GAAGGCTTCACCTATTATGGA

AAAATTCCTGAAAATCCGAAAAAGTAATTAATTTTACATATTCTTACAC
TGGGTATTTATTAAACTAGGTGTTAATGTTTCAAGTTACAGTTTAGACT
TAGAAAAAGATAGCCCCGTTTTTGGTAAGCAACTGAAAGAAGCTAAAAAA
TTAACTGCTGATGATACAGAAGCTATTGCCGCACAAAAACCTGATTTAAT
CATGGTTTTTCGATCAAGATCCAAACATCAATACTCTGAAAAAATTGCAC
CACTTTTAGTTATTAATATGGTGCACAAAATTATTTAGATATGATGCCA
GCCTTGGGGAAAGTATTCGGTAAAGAAAAAGAAAGCTAATCAGTGGGTTAG
CCAATGGAAAACTAAACTCTCGCTGCCAAAAAGATTTACACCATATCT
TAAAGCCTAACACTACTTTTACTATTATGGATTTTATGATAAAAAATATC
TATTTATATGGTAATAATTTTGGACGCGGtGGAGAACTAATCTATGATTC
ACTAGGTTATGCTGCCCCAGAAAAAGTCAAAAAAGATGTCTTTAAAAAAG
GGTGGTTTACCGTTTCGCAAGAAGCAATCGGTGATTACGTTGGAGATTAT
GCCCTTGTTAATATAAACAAAACGACTAAAAAAGCAGCTTCATCACTTAA
AGAAAGTGATGTCTGGAAGAATTTACCAGCTGTCAAAAAAGGGCACATCA
TAGAAAGTAACTACGACGTGTTTTATTTCTCTGACCCTCTATCTTTAGAA
GCTCAATTAATAATCATTTACAAA

SEQ ID NO. 8610

STRAIN 1169NT

GAAGGCTTCACCTATTATGGAATAAT

CCTGAAAATCCGAAAAAGTAATTAATTTTACATATTCTTACACTGGGTA
TTTATTAAACTAGGTGTTAATGTTTCAAGTTACAGTTTAGACTTAGAAA
AAGATAGCCCCGTTTTTGGTAAGCAACTGAAAGAAGCTAAAAAATTAAT
GCTGATGATACAGAAGCTATTGCCGcACAAaaACCTGATTTAATCATGGT
TTTCGATCAAGATCCAAACATCAATACTCTGAAAAAATTGCACCAACTT
TAGTTATTAAATATGGTGCACAAAATTATTTAGATATGATGCCAGCCTTG
GGGAAAGTATTCGGTAAAGAAAAAGaaGCTAATCAGTGGGTTAGCCAATG
GAAACTAAACTCTCGCTGCCAAAAAGATTTACACCATATCTTAAAGC
CTAACACTACTTTTACTATTATGGATTTTATGATAAAAAATATCTATTTA
TATGGTAATAATTTTGGACGCGGTGGAGAACTAATCTATGATTCACTAGG
TTATGCTGCCCCAgAAAAAGTCAAAAAAGATGTCTTTAAAAAAGGGTGGT
TTACCGTTTCgCAAGAAGCAATCGGTGATTACGTTGGAGATTATGCCCTT
GTTAATATAAACAAAACGACTAAAAAAGCAGCTTCATCACTTAAAGAAAG
TGATGTCTGGAAGAATTTACCAGCTGTCAAAAAAGGGCACATCATAGAAA
GTAACCTACGACGTGTTTTATTTCTCTGACCCTCTATCTTTAGAAAGCTCAA
TTAAATCATTTACAAA

SEQ ID NO. 8611

STRAIN JM9130013

GAAGGCTTCACCTATTATG

GAAAAATTCCTGAAAATCCGAAAAAGTAATTAATTTTACATATTCTTAC
ACTGGATATTTATTAAACTAGGAGTTAATGTTTCAAGTTACAGTTTAGA
CTTAGAAAAAGATAGCCCCGTTTTTGGTAAGCAACTGAAAGGAGCTAAAA
AATTAACCTGCTGATGATACAGAAGCTATTGCCGCACAAAAACCTGATTTA
ATCATGGTTTTTGGATCAAGATCCAAACATCAATACTCTGAAAAAATTGC
ACCAACTTTAGTTATTAAATATGGTGCACAAAATTATTTAGATATGATGC
CAGCTTTGGGGAAAGTATTTCGGTAAAGAAAAAGAAAGCTAATCAGTGGGTT
AGCCAATGGAAAACTAAACTCTCGCTGCCAAAAAGATTTACACCATAT
CTTAAACCTAACACTACTTTTACCATTATGGATTTTATGATAAAAAATA
TCTATTTATATGGTAATAATTTTGGACGCGGtGGAGAACTAATCTATGAT
TCACTAGGTTATGCTGCCCCAgAAAAAGTCAAAAAAGATGTCTTTAAAAA
AGGGTGGTTTACCGTTTCgCAAGAAGCAATCGGTGATTACGTTGGAGATT
ATGCCCTTGTTAATATAAACAAAACGACTAAAAAAGCAGCTTCATCACTT
AAAGAAAGTGATGTCTGGAAGAATTTACCAGCTGTCAAAAAAGGGCACAT
CATAGAAAGTAACTACGACGTGTTTTATTTCTCTGACCCTCTATCTTTAG
AAGCTCAATTAATAATCATTTACAAA

PRETTY of: /biotmp/msa521731.2{*} April 28, 2003 08:07 ..

	1				50
msa521731.2{691_090}	-----	-----	-----	-----	-----
msa521731.2{691_1169NT}	-----	-----	-----	-----	-----
msa521731.2{691_CJB110}	-----	-----	-----	-----	-----
msa521731.2{691_COH1}	-----	-----	-----	-----	-----
msa521731.2{691_M732}	-----	-----	-----	-----	-----
msa521731.2{691_M781}	-----	-----	-----	-----	-----
msa521731.2{691_18RS21}	-----	-----	-----	-----	-----
msa521731.2{691_2603}	atgaaaaaaa	ttggaattat	tgtcctcaca	ctactgacct	tctttttggt

Table 86: Comparative Sequences relating to SAG1393

msa521731.2{691_A909}	-----	-----	-----	-----	-----
msa521731.2{691_JM9130013}	-----	-----	-----	-----	-----
msa521731.2{691_H36B}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	51				100
msa521731.2{691_090}	-----	-----	-----	-----	-----
msa521731.2{691_1169NT}	-----	-----	-----	-----	-----
msa521731.2{691_CJB110}	-----	-----	-----	-----	-----
msa521731.2{691_COH1}	-----	-----	-----	-----	-----
msa521731.2{691_M732}	-----	-----	-----	-----	-----
msa521731.2{691_M781}	-----	-----	-----	-----	-----
msa521731.2{691_18RS21}	-----	-----	-----	-----	-----
msa521731.2{691_2603}	atcttgcgga	caacaaacta	aacaagaaag	cactaaaaca	actatttcta
msa521731.2{691_A909}	-----	-----	-----	-----	-----
msa521731.2{691_JM9130013}	-----	-----	-----	-----	-----
msa521731.2{691_H36B}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	101				150
msa521731.2{691_090}	-----	----GAAGGC	TTCACCTATT	ATGGAAAAAT	TCCTGAAAAT
msa521731.2{691_1169NT}	-----	----GAAGGC	TTCACCTATT	ATGGAAAAAT	TCCTGAAAAT
msa521731.2{691_CJB110}	-----	----GAAGGC	TTCACCTATT	ATGGAAAAAT	TCCTGAAAAT
msa521731.2{691_COH1}	-----	----GAAGGC	TTCACCTATT	ATGGAAAAAT	TCCTGAAAAT
msa521731.2{691_M732}	-----	----GAAGGC	TTCACCTATT	ATGGAAAAAT	TCCTGAAAAT
msa521731.2{691_M781}	-----	----GAAGGC	TTCACCTATT	ATGGAAAAAT	TCCTGAAAAT
msa521731.2{691_18RS21}	-----	----GAAGGC	TTCACCTATT	ATGGAAAAAT	TCCTGAAAAT
msa521731.2{691_2603}	aaatgcctaa	aattGAAGGC	TTCACCTATT	ATGGAAAAAT	TCCTGAAAAT
msa521731.2{691_A909}	-----	----GAAGGC	TTCACCTATT	ATGGAAAAAT	TCCTGAAAAT
msa521731.2{691_JM9130013}	-----	----GAAGGC	TTCACCTATT	ATGGAAAAAT	TCCTGAAAAT
msa521731.2{691_H36B}	-----	----GAAGGC	TTCACCTATT	ATGGAAAAAT	TCCTGAAAAT
Consensus	*****	*****	*****	*****	*****
	151				200
msa521731.2{691_090}	CCGAAAAAAG	TAATTAATTT	TACATATTCT	TACACTGGgT	ATTTATTAAA
msa521731.2{691_1169NT}	CCGAAAAAAG	TAATTAATTT	TACATATTCT	TACACTGGgT	ATTTATTAAA
msa521731.2{691_CJB110}	CCGAAAAAAG	TAATTAATTT	TACATATTCT	TACACTGGgT	ATTTATTAAA
msa521731.2{691_COH1}	CCGAAAAAAG	TAATTAATTT	TACATATTCT	TACACTGGgT	ATTTATTAAA
msa521731.2{691_M732}	CCGAAAAAAG	TAATTAATTT	TACATATTCT	TACACTGGgT	ATTTATTAAA
msa521731.2{691_M781}	CCGAAAAAAG	TAATTAATTT	TACATATTCT	TACACTGGgT	ATTTATTAAA
msa521731.2{691_18RS21}	CCGAAAAAAG	TAATTAATTT	TACATATTCT	TACACTGGgT	ATTTATTAAA
msa521731.2{691_2603}	CCGAAAAAAG	TAATTAATTT	TACATATTCT	TACACTGGgT	ATTTATTAAA
msa521731.2{691_A909}	CCGAAAAAAG	TAATTAATTT	TACATATTCT	TACACTGGaT	ATTTATTAAA
msa521731.2{691_JM9130013}	CCGAAAAAAG	TAATTAATTT	TACATATTCT	TACACTGGaT	ATTTATTAAA
msa521731.2{691_H36B}	CCGAAAAAAG	TAATTAATTT	TACATATTCT	TACACTGGaT	ATTTATTAAA
Consensus	*****	*****	*****	*****-*	*****
	201				250
msa521731.2{691_090}	ACTAGGtGTT	AATGTTTCAA	GTTACAGTTT	AGACTTAGAA	AAAGATAGCC
msa521731.2{691_1169NT}	ACTAGGtGTT	AATGTTTCAA	GTTACAGTTT	AGACTTAGAA	AAAGATAGCC
msa521731.2{691_CJB110}	ACTAGGtGTT	AATGTTTCAA	GTTACAGTTT	AGACTTAGAA	AAAGATAGCC
msa521731.2{691_COH1}	ACTAGGtGTT	AATGTTTCAA	GTTACAGTTT	AGACTTAGAA	AAAGATAGCC
msa521731.2{691_M732}	ACTAGGtGTT	AATGTTTCAA	GTTACAGTTT	AGACTTAGAA	AAAGATAGCC
msa521731.2{691_M781}	ACTAGGtGTT	AATGTTTCAA	GTTACAGTTT	AGACTTAGAA	AAAGATAGCC
msa521731.2{691_18RS21}	ACTAGGtGTT	AATGTTTCAA	GTTACAGTTT	AGACTTAGAA	AAAGATAGCC
msa521731.2{691_2603}	ACTAGGtGTT	AATGTTTCAA	GTTACAGTTT	AGACTTAGAA	AAAGATAGCC
msa521731.2{691_A909}	ACTAGGaGTT	AATGTTTCAA	GTTACAGTTT	AGACTTAGAA	AAAGATAGCC
msa521731.2{691_JM9130013}	ACTAGGaGTT	AATGTTTCAA	GTTACAGTTT	AGACTTAGAA	AAAGATAGCC
msa521731.2{691_H36B}	ACTAGGaGTT	AATGTTTCAA	GTTACAGTTT	AGACTTAGAA	AAAGATAGCC
Consensus	*****-***	*****	*****	*****	*****
	251				300
msa521731.2{691_090}	CCGTTTTTGG	TAAgCAACTG	AAAGaAGCTA	AAAAATTAAC	TGCTGATGAT
msa521731.2{691_1169NT}	CCGTTTTTGG	TAAgCAACTG	AAAGaAGCTA	AAAAATTAAC	TGCTGATGAT
msa521731.2{691_CJB110}	CCGTTTTTGG	TAAgCAACTG	AAAGaAGCTA	AAAAATTAAC	TGCTGATGAT
msa521731.2{691_COH1}	CCGTTTTTGG	TAAgCAACTG	AAAGaAGCTA	AAAAATTAAC	TGCTGATGAT
msa521731.2{691_M732}	CCGTTTTTGG	TAAgCAACTG	AAAGaAGCTA	AAAAATTAAC	TGCTGATGAT
msa521731.2{691_M781}	CCGTTTTTGG	TAAgCAACTG	AAAGaAGCTA	AAAAATTAAC	TGCTGATGAT
msa521731.2{691_18RS21}	CCGTTTTTGG	TAAaCAACTG	AAAGaAGCTA	AAAAATTAAC	TGCTGATGAT
msa521731.2{691_2603}	CCGTTTTTGG	TAAaCAACTG	AAAGaAGCTA	AAAAATTAAC	TGCTGATGAT
msa521731.2{691_A909}	CCGTTTTTGG	TAAaCAACTG	AAAGgAGCTA	AAAAATTAAC	TGCTGATGAT
msa521731.2{691_JM9130013}	CCGTTTTTGG	TAAgCAACTG	AAAGgAGCTA	AAAAATTAAC	TGCTGATGAT
msa521731.2{691_H36B}	CCGTTTTTGG	TAAgCAACTG	AAAGgAGCTA	AAAAATTAAC	TGCTGATGAT
Consensus	*****	***-*****	****-*****	*****	*****
	301				350
msa521731.2{691_090}	ACAGAAGCTA	TTGCCGCACA	AAAACCTGAT	TTAATCATGG	TTTTcGATCA
msa521731.2{691_1169NT}	ACAGAAGCTA	TTGCCGCACA	AAAACCTGAT	TTAATCATGG	TTTTcGATCA

Table 86: Comparative Sequences relating to SAG1393

msa521731.2{691_CJB110}	ACAGAAGCTA	TTGCCGCACA	AAAACCTGAT	TTAATCATGG	TTTTcGATCA
msa521731.2{691_COH1}	ACAGAAGCTA	TTGCCGCACA	AAAACCTGAT	TTAATCATGG	TTTTcGATCA
msa521731.2{691_M732}	ACAGAAGCTA	TTGCCGCACA	AAAACCTGAT	TTAATCATGG	TTTTcGATCA
msa521731.2{691_M781}	ACAGAAGCTA	TTGCCGCACA	AAAACCTGAT	TTAATCATGG	TTTTcGATCA
msa521731.2{691_18RS21}	ACAGAAGCTA	TTGCCGCACA	AAAACCTGAT	TTAATCATGG	TTTTcGATCA
msa521731.2{691_2603}	ACAGAAGCTA	TTGCCGCACA	AAAACCTGAT	TTAATCATGG	TTTTcGATCA
msa521731.2{691_A909}	ACAGAAGCTA	TTGCCGCACA	AAAACCTGAT	TTAATCATGG	TTTTtGATCA
msa521731.2{691_JM9130013}	ACAGAAGCTA	TTGCCGCACA	AAAACCTGAT	TTAATCATGG	TTTTtGATCA
msa521731.2{691_H36B}	ACAGAAGCTA	TTGCCGCACA	AAAACCTGAT	TTAATCATGG	TTTTtGATCA
Consensus	*****	*****	*****	*****	****_*****
351					
msa521731.2{691_090}	AGATCCAAAC	ATCAATACTC	TGAAAAAAT	TGCACCAACT	TTAGTTATTA
msa521731.2{691_1169NT}	AGATCCAAAC	ATCAATACTC	TGAAAAAAT	TGCACCAACT	TTAGTTATTA
msa521731.2{691_CJB110}	AGATCCAAAC	ATCAATACTC	TGAAAAAAT	TGCACCAACT	TTAGTTATTA
msa521731.2{691_COH1}	AGATCCAAAC	ATCAATACTC	TGAAAAAAT	TGCACCAACT	TTAGTTATTA
msa521731.2{691_M732}	AGATCCAAAC	ATCAATACTC	TGAAAAAAT	TGCACCAACT	TTAGTTATTA
msa521731.2{691_M781}	AGATCCAAAC	ATCAATACTC	TGAAAAAAT	TGCACCAACT	TTAGTTATTA
msa521731.2{691_18RS21}	AGATCCAAAC	ATCAATACTC	TGAAAAAAT	TGCACCAACT	TTAGTTATTA
msa521731.2{691_2603}	AGATCCAAAC	ATCAATACTC	TGAAAAAAT	TGCACCAACT	TTAGTTATTA
msa521731.2{691_A909}	AGATCCAAAC	ATCAATACTC	TGAAAAAAT	TGCACCAACT	TTAGTTATTA
msa521731.2{691_JM9130013}	AGATCCAAAC	ATCAATACTC	TGAAAAAAT	TGCACCAACT	TTAGTTATTA
msa521731.2{691_H36B}	AGATCCAAAC	ATCAATACTC	TGAAAAAAT	TGCACCAACT	TTAGTTATTA
Consensus	*****	*****	*****	*****	*****
401					
msa521731.2{691_090}	AATATGGTGC	ACAAAATTAT	TTAGATATGA	TGCCAGCcTT	GGGGAAAGTA
msa521731.2{691_1169NT}	AATATGGTGC	ACAAAATTAT	TTAGATATGA	TGCCAGCcTT	GGGGAAAGTA
msa521731.2{691_CJB110}	AATATGGTGC	ACAAAATTAT	TTAGATATGA	TGCCAGCcTT	GGGGAAAGTA
msa521731.2{691_COH1}	AATATGGTGC	ACAAAATTAT	TTAGATATGA	TGCCAGCcTT	GGGGAAAGTA
msa521731.2{691_M732}	AATATGGTGC	ACAAAATTAT	TTAGATATGA	TGCCAGCcTT	GGGGAAAGTA
msa521731.2{691_M781}	AATATGGTGC	ACAAAATTAT	TTAGATATGA	TGCCAGCcTT	GGGGAAAGTA
msa521731.2{691_18RS21}	AATATGGTGC	ACAAAATTAT	TTAGATATGA	TGCCAGCcTT	GGGGAAAGTA
msa521731.2{691_2603}	AATATGGTGC	ACAAAATTAT	TTAGATATGA	TGCCAGCcTT	GGGGAAAGTA
msa521731.2{691_A909}	AATATGGTGC	ACAAAATTAT	TTAGATATGA	TGCCAGCcTT	GGGGAAAGTA
msa521731.2{691_JM9130013}	AATATGGTGC	ACAAAATTAT	TTAGATATGA	TGCCAGCcTT	GGGGAAAGTA
msa521731.2{691_H36B}	AATATGGTGC	ACAAAATTAT	TTAGATATGA	TGCCAGCcTT	GGGGAAAGTA
Consensus	*****	*****	*****	*****_**	*****
451					
msa521731.2{691_090}	TTCGGTAAAG	AAAAAGAAGC	TAATCAGTGG	GTTAGCCAAT	GGAAAACTAA
msa521731.2{691_1169NT}	TTCGGTAAAG	AAAAAGAAGC	TAATCAGTGG	GTTAGCCAAT	GGAAAACTAA
msa521731.2{691_CJB110}	TTCGGTAAAG	AAAAAGAAGC	TAATCAGTGG	GTTAGCCAAT	GGAAAACTAA
msa521731.2{691_COH1}	TTCGGTAAAG	AAAAAGAAGC	TAATCAGTGG	GTTAGCCAAT	GGAAAACTAA
msa521731.2{691_M732}	TTCGGTAAAG	AAAAAGAAGC	TAATCAGTGG	GTTAGCCAAT	GGAAAACTAA
msa521731.2{691_M781}	TTCGGTAAAG	AAAAAGAAGC	TAATCAGTGG	GTTAGCCAAT	GGAAAACTAA
msa521731.2{691_18RS21}	TTCGGTAAAG	AAAAAGAAGC	TAATCAGTGG	GTTAGCCAAT	GGAAAACTAA
msa521731.2{691_2603}	TTCGGTAAAG	AAAAAGAAGC	TAATCAGTGG	GTTAGCCAAT	GGAAAACTAA
msa521731.2{691_A909}	TTCGGTAAAG	AAAAAGAAGC	TAATCAGTGG	GTTAGCCAAT	GGAAAACTAA
msa521731.2{691_JM9130013}	TTCGGTAAAG	AAAAAGAAGC	TAATCAGTGG	GTTAGCCAAT	GGAAAACTAA
msa521731.2{691_H36B}	TTCGGTAAAG	AAAAAGAAGC	TAATCAGTGG	GTTAGCCAAT	GGAAAACTAA
Consensus	*****	*****	*****	*****	*****
501					
msa521731.2{691_090}	AACTCTCGCT	GcCAAAAAAG	ATTTACACCA	TATCTTAAag	CCTAACACTA
msa521731.2{691_1169NT}	AACTCTCGCT	GcCAAAAAAG	ATTTACACCA	TATCTTAAag	CCTAACACTA
msa521731.2{691_CJB110}	AACTCTCGCT	GcCAAAAAAG	ATTTACACCA	TATCTTAAag	CCTAACACTA
msa521731.2{691_COH1}	AACTCTCGCT	GcCAAAAAAG	ATTTACACCA	TATCTTAAag	CCTAACACTA
msa521731.2{691_M732}	AACTCTCGCT	GcCAAAAAAG	ATTTACACCA	TATCTTAAag	CCTAACACTA
msa521731.2{691_M781}	AACTCTCGCT	GcCAAAAAAG	ATTTACACCA	TATCTTAAag	CCTAACACTA
msa521731.2{691_18RS21}	AACTCTCGCT	GtCAAAAAAG	ATTTACACCA	TATCTTAAag	CCTAACACTA
msa521731.2{691_2603}	AACTCTCGCT	GtCAAAAAAG	ATTTACACCA	TATCTTAAag	CCTAACACTA
msa521731.2{691_A909}	AACTCTCGCT	GcCAAAAAAG	ATTTACACCA	TATCTTAAaa	CCTAACACTA
msa521731.2{691_JM9130013}	AACTCTCGCT	GcCAAAAAAG	ATTTACACCA	TATCTTAAaa	CCTAACACTA
msa521731.2{691_H36B}	AACTCTCGCT	GcCAAAAAAG	ATTTACACCA	TATCTTAAgg	CCTAACACTA
Consensus	*****	*_*****	*****	*****_--	*****
551					
msa521731.2{691_090}	CTTTTACtAT	TATgGATTTT	TATGATAAAA	ATATCTATTT	ATATGGTAAT
msa521731.2{691_1169NT}	CTTTTACtAT	TATgGATTTT	TATGATAAAA	ATATCTATTT	ATATGGTAAT
msa521731.2{691_CJB110}	CTTTTACtAT	TATgGATTTT	TATGATAAAA	ATATCTATTT	ATATGGTAAT
msa521731.2{691_COH1}	CTTTTACtAT	TATgGATTTT	TATGATAAAA	ATATCTATTT	ATATGGTAAT
msa521731.2{691_M732}	CTTTTACtAT	TATgGATTTT	TATGATAAAA	ATATCTATTT	ATATGGTAAT
msa521731.2{691_M781}	CTTTTACtAT	TATgGATTTT	TATGATAAAA	ATATCTATTT	ATATGGTAAT
msa521731.2{691_18RS21}	CTTTTACtAT	TATgGATTTT	TATGATAAAA	ATATCTATTT	ATATGGTAAT
msa521731.2{691_2603}	CTTTTACtAT	TATgGATTTT	TATGATAAAA	ATATCTATTT	ATATGGTAAT
msa521731.2{691_A909}	CTTTTACcAT	TATgGATTTT	TATGATAAAA	ATATCTATTT	ATATGGTAAT
msa521731.2{691_JM9130013}	CTTTTACcAT	TATgGATTTT	TATGATAAAA	ATATCTATTT	ATATGGTAAT

Table 86: Comparative Sequences relating to SAG1393

msa521731.2{691_H36B}	CTTTTACTAT	TATaGATTTT	TATGATAAAA	ATATCTATTT	ATATGGTAAT
Consensus	*****-**	***-*****	*****	*****	*****
msa521731.2{691_090}	AATTTTGGAC	GCGGTGGAGA	ACTAATCTAT	GATTCAC TAG	GTTATGCTGC
msa521731.2{691_1169NT}	AATTTTGGAC	GCGGTGGAGA	ACTAATCTAT	GATTCAC TAG	GTTATGCTGC
msa521731.2{691_CJB110}	AATTTTGGAC	GCGGTGGAGA	ACTAATCTAT	GATTCAC TAG	GTTATGCTGC
msa521731.2{691_COH1}	AATTTTGGAC	GCGGTGGAGA	ACTAATCTAT	GATTCAC TAG	GTTATGCTGC
msa521731.2{691_M732}	AATTTTGGAC	GCGGTGGAGA	ACTAATCTAT	GATTCAC TAG	GTTATGCTGC
msa521731.2{691_M781}	AATTTTGGAC	GCGGTGGAGA	ACTAATCTAT	GATTCAC TAG	GTTATGCTGC
msa521731.2{691_18RS21}	AATTTTGGAC	GCGGTGGAGA	ACTAATCTAT	GATTCAC TAG	GTTATGCTGC
msa521731.2{691_2603}	AATTTTGGAC	GCGGTGGAGA	ACTAATCTAT	GATTCAC TAG	GTTATGCTGC
msa521731.2{691_A909}	AATTTTGGAC	GCGGTGGAGA	ACTAATCTAT	GATTCAC TAG	GTTATGCTGC
msa521731.2{691_JM9130013}	AATTTTGGAC	GCGGTGGAGA	ACTAATCTAT	GATTCAC TAG	GTTATGCTGC
msa521731.2{691_H36B}	AATTTTGGAC	GCGGTGGAGA	ACTAATCTAT	GATTCAC TAG	GTTATGCTGC
Consensus	*****	*****	*****	*****	*****
msa521731.2{691_090}	CCCAGAAAAA	GTCAAAAAAG	ATGTCTTTAA	AAAAGGGTGG	TTTACCGTTT
msa521731.2{691_1169NT}	CCCAGAAAAA	GTCAAAAAAG	ATGTCTTTAA	AAAAGGGTGG	TTTACCGTTT
msa521731.2{691_CJB110}	CCCAGAAAAA	GTCAAAAAAG	ATGTCTTTAA	AAAAGGGTGG	TTTACCGTTT
msa521731.2{691_COH1}	CCCAGAAAAA	GTCAAAAAAG	ATGTCTTTAA	AAAAGGGTGG	TTTACCGTTT
msa521731.2{691_M732}	CCCAGAAAAA	GTCAAAAAAG	ATGTCTTTAA	AAAAGGGTGG	TTTACCGTTT
msa521731.2{691_M781}	CCCAGAAAAA	GTCAAAAAAG	ATGTCTTTAA	AAAAGGGTGG	TTTACCGTTT
msa521731.2{691_18RS21}	CCCAGAAAAA	GTCAAAAAAG	ATGTCTTTAA	AAAAGGGTGG	TTTACCGTTT
msa521731.2{691_2603}	CCCAGAAAAA	GTCAAAAAAG	ATGTCTTTAA	AAAAGGGTGG	TTTACCGTTT
msa521731.2{691_A909}	CCCAGAAAAA	GTCAAAAAAG	ATGTCTTTAA	AAAAGGGTGG	TTTACCGTTT
msa521731.2{691_JM9130013}	CCCAGAAAAA	GTCAAAAAAG	ATGTCTTTAA	AAAAGGGTGG	TTTACCGTTT
msa521731.2{691_H36B}	CCCAGAAAAA	GTCAAAAAAG	ATGTCTTTAA	AAAAGGGTGG	TTTACCGTTT
Consensus	*****	*****	*****	*****	*****
msa521731.2{691_090}	CGCAAGAAGC	AATCGGTGAT	TACGTTGGAG	ATTATGCCCT	TGTTAATATA
msa521731.2{691_1169NT}	CGCAAGAAGC	AATCGGTGAT	TACGTTGGAG	ATTATGCCCT	TGTTAATATA
msa521731.2{691_CJB110}	CGCAAGAAGC	AATCGGTGAT	TACGTTGGAG	ATTATGCCCT	TGTTAATATA
msa521731.2{691_COH1}	CGCAAGAAGC	AATCGGTGAT	TACGTTGGAG	ATTATGCCCT	TGTTAATATA
msa521731.2{691_M732}	CGCAAGAAGC	AATCGGTGAT	TACGTTGGAG	ATTATGCCCT	TGTTAATATA
msa521731.2{691_M781}	CGCAAGAAGC	AATCGGTGAT	TACGTTGGAG	ATTATGCCCT	TGTTAATATA
msa521731.2{691_18RS21}	CGCAAGAAGC	AATCGGTGAT	TACGTTGGAG	ATTATGCCCT	TGTTAATATA
msa521731.2{691_2603}	CGCAAGAAGC	AATCGGTGAT	TACGTTGGAG	ATTATGCCCT	TGTTAATATA
msa521731.2{691_A909}	CGCAAGAAGC	AATCGGTGAT	TACGTTGGAG	ATTATGCCCT	TGTTAATATA
msa521731.2{691_JM9130013}	CGCAAGAAGC	AATCGGTGAT	TACGTTGGAG	ATTATGCCCT	TGTTAATATA
msa521731.2{691_H36B}	CGCAAGAAGC	AATCGGTGAT	TACGTTGGAG	ATTATGCCCT	TGTTAATATA
Consensus	*****	*****	*****	*****	*****
msa521731.2{691_090}	AACAAAACGA	CTAAAAAAGC	AGCTTCATCA	CTTAAAGAAA	GTGATGTcTG
msa521731.2{691_1169NT}	AACAAAACGA	CTAAAAAAGC	AGCTTCATCA	CTTAAAGAAA	GTGATGTcTG
msa521731.2{691_CJB110}	AACAAAACGA	CTAAAAAAGC	AGCTTCATCA	CTTAAAGAAA	GTGATGTcTG
msa521731.2{691_COH1}	AACAAAACGA	CTAAAAAAGC	AGCTTCATCA	CTTAAAGAAA	GTGATGTcTG
msa521731.2{691_M732}	AACAAAACGA	CTAAAAAAGC	AGCTTCATCA	CTTAAAGAAA	GTGATGTcTG
msa521731.2{691_M781}	AACAAAACGA	CTAAAAAAGC	AGCTTCATCA	CTTAAAGAAA	GTGATGTcTG
msa521731.2{691_18RS21}	AACAAAACGA	CTAAAAAAGC	AGCTTCATCA	CTTAAAGAAA	GTGATGTcTG
msa521731.2{691_2603}	AACAAAACGA	CTAAAAAAGC	AGCTTCATCA	CTTAAAGAAA	GTGATGTcTG
msa521731.2{691_A909}	AACAAAACGA	CTAAAAAAGC	AGCTTCATCA	CTTAAAGAAA	GTGATGTcTG
msa521731.2{691_JM9130013}	AACAAAACGA	CTAAAAAAGC	AGCTTCATCA	CTTAAAGAAA	GTGATGTcTG
msa521731.2{691_H36B}	AACAAAACGA	CTAAAAAAGC	AGCTTCATCA	CTTAAAGAAA	GTGATGTcTG
Consensus	*****	*****	*****	*****	*****-**
msa521731.2{691_090}	GAAGAATTTA	CCAGCTGTCA	AAAAAGGGCA	CATCATAGAA	AGTAACTACG
msa521731.2{691_1169NT}	GAAGAATTTA	CCAGCTGTCA	AAAAAGGGCA	CATCATAGAA	AGTAACTACG
msa521731.2{691_CJB110}	GAAGAATTTA	CCAGCTGTCA	AAAAAGGGCA	CATCATAGAA	AGTAACTACG
msa521731.2{691_COH1}	GAAGAATTTA	CCAGCTGTCA	AAAAAGGGCA	CATCATAGAA	AGTAACTACG
msa521731.2{691_M732}	GAAGAATTTA	CCAGCTGTCA	AAAAAGGGCA	CATCATAGAA	AGTAACTACG
msa521731.2{691_M781}	GAAGAATTTA	CCAGCTGTCA	AAAAAGGGCA	CATCATAGAA	AGTAACTACG
msa521731.2{691_18RS21}	GAAGAATTTA	CCAGCTGTCA	AAAAAGGGCA	CATCATAGAA	AGTAACTACG
msa521731.2{691_2603}	GAAGAATTTA	CCAGCTGTCA	AAAAAGGGCA	CATCATAGAA	AGTAACTACG
msa521731.2{691_A909}	GAAGAATTTA	CCAGCTGTCA	AAAAAGGGCA	CATCATAGAA	AGTAACTACG
msa521731.2{691_JM9130013}	GAAGAATTTA	CCAGCTGTCA	AAAAAGGGCA	CATCATAGAA	AGTAACTACG
msa521731.2{691_H36B}	GAAGAATTTA	CCAGCTGTCA	AAAAAGGGCA	CATCATAGAA	AGTAACTACG
Consensus	*****	*****	*****	*****	*****
msa521731.2{691_090}	ACGTGTTTTA	TTTCTCTGAC	CCTCTATCTT	TAGAAGCTCA	ATTAAATCA
msa521731.2{691_1169NT}	ACGTGTTTTA	TTTCTCTGAC	CCTCTATCTT	TAGAAGCTCA	ATTAAATCA
msa521731.2{691_CJB110}	ACGTGTTTTA	TTTCTCTGAC	CCTCTATCTT	TAGAAGCTCA	ATTAAATCA
msa521731.2{691_COH1}	ACGTGTTTTA	TTTCTCTGAC	CCTCTATCTT	TAGAAGCTCA	ATTAAATCA

Table 86: Comparative Sequences relating to SAG1393

msa521731.2{691_M732}	ACGTGTTTTA	TTTCTCTGAC	CCTCTATCTT	TAGAAGCTCA	ATTAAAATCA
msa521731.2{691_M781}	ACGTGTTTTA	TTTCTCTGAC	CCTCTATCTT	TAGAAGCTCA	ATTAAAATCA
msa521731.2{691_18RS21}	ACGTGTTTTA	TTTCTCTGAC	CCTCTATCTT	TAGAAGCTCA	ATTAAAATCA
msa521731.2{691_2603}	ACGTGTTTTA	TTTCTCTGAC	CCTCTATCTT	TAGAAGCTCA	ATTAAAATCA
msa521731.2{691_A909}	ACGTGTTTTA	TTTCTCTGAC	CCTCTATCTT	TAGAAGCTCA	ATTAAAATCA
msa521731.2{691_JM9130013}	ACGTGTTTTA	TTTCTCTGAC	CCTCTATCTT	TAGAAGCTCA	ATTAAAATCA
msa521731.2{691_H36B}	ACGTGTTTTA	TTTCTCTGAC	CCTCTATCTT	TAGAAGCTCA	ATTAAAATCA
Consensus	*****	*****	*****	*****	*****
901					
msa521731.2{691_090}	TTTACAAA--	-----	-----	-----	-----
msa521731.2{691_1169NT}	TTTACAAA--	-----	-----	-----	-----
msa521731.2{691_CJB110}	TTTACAAA--	-----	-----	-----	-----
msa521731.2{691_COH1}	TTTACAAA--	-----	-----	-----	-----
msa521731.2{691_M732}	TTTACAAA--	-----	-----	-----	-----
msa521731.2{691_M781}	TTTACAAA--	-----	-----	-----	-----
msa521731.2{691_18RS21}	TTTACAAA--	-----	-----	-----	-----
msa521731.2{691_2603}	TTTACAAAgg	ctatcaaaga	aaatacaaat	-----	-----
msa521731.2{691_A909}	TTTACAAA--	-----	-----	-----	-----
msa521731.2{691_JM9130013}	TTTACAAA--	-----	-----	-----	-----
msa521731.2{691_H36B}	TTTACAAA--	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****

SEQ ID NO. 8612

STRAIN 2603 frame: 1

MKKIGIIVLTLLTFFLVSCGQQTQESTKTTISKMPKIEGFTYYGKIPENPKKVINFYTS
 YTGYYLLKLG VNVSSYS LDLEK DSPVFGKQLKEAKKLTA DDTEAIAAQKPD LIMVFDQDPN
 INTLKKIAPT LVIKYGAQNYLDMMPALGKVFGKEKEANQWVSQWKT KTLAVKKDLHHILK
 PNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAPEKVKKDVFKKGWFTVSQEAIGD
 YVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHIIESNYDVFFYFSDPLSLEAQLKS
 FTKAIKENTN

SEQ ID NO. 8613

STRAIN 090 frame: 1

EGFTYYGKIPENPKKVINFYTSYTGYYLLKLG VNVSSYS LDLEK DSPVFGKQLKEAKKLTA
 DDTEAIAAQKPD LIMVFDQDPNINTLKKIAPT LVIKYGAQNYLDMMPALGKVFGKEKEAN
 QWVSQWKT KTLAAKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
 EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
 IESNYDVFFYFSDPLSLEAQLKSFT

SEQ ID NO. 8614

STRAIN A909 frame: 1

EGFTYYGKIPENPKKVINFYTSYTGYYLLKLG VNVSSYS LDLEK DSPVFGKQLKGAKKLTA
 DDTEAIAAQKPD LIMVFDQDPNINTLKKIAPT LVIKYGAQNYLDMMPALGKVFGKEKEAN
 QWVSQWKT KTLAAKDLHHILRPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
 EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
 IESNYDVFFYFSDPLSLEAQLKSFT

SEQ ID NO. 8615

STRAIN H36B frame: 1

EGFTYYGKIPENPKKVINFYTSYTGYYLLKLG VNVSSYS LDLEK DSPVFGKQLKGAKKLTA
 DDTEAIAAQKPD LIMVFDQDPNINTLKKIAPT LVIKYGAQNYLDMMPALGKVFGKEKEAN
 QWVSQWKT KTLAAKDLHHILRPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
 EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
 IESNYDVFFYFSDPLSLEAQLKSFT

SEQ ID NO. 8616

STRAIN 18RS21 frame: 1

EGFTYYGKIPENPKKVINFYTSYTGYYLLKLG VNVSSYS LDLEK DSPVFGKQLKEAKKLTA
 DDTEAIAAQKPD LIMVFDQDPNINTLKKIAPT LVIKYGAQNYLDMMPALGKVFGKEKEAN
 QWVSQWKT KTLAVKKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
 EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
 IESNYDVFFYFSDPLSLEAQLKSFT

SEQ ID NO. 8617

STRAIN M732 frame: 1

EGFTYYGKIPENPKKVINFYTSYTGYYLLKLG VNVSSYS LDLEK DSPVFGKQLKEAKKLTA
 DDTEAIAAQKPD LIMVFDQDPNINTLKKIAPT LVIKYGAQNYLDMMPALGKVFGKEKEAN
 QWVSQWKT KTLAAKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
 EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
 IESNYDVFFYFSDPLSLEAQLKSFT

SEQ ID NO. 8618

STRAIN COH1 frame: 1

EGFTYYGKIPENPKKVINFYTSYTGYYLLKLG VNVSSYS LDLEK DSPVFGKQLKEAKKLTA
 DDTEAIAAQKPD LIMVFDQDPNINTLKKIAPT LVIKYGAQNYLDMMPALGKVFGKEKEAN

Table 86: Comparative Sequences relating to SAG1393

QWVSQWKTKTLAAKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
 EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
 IESNYDVFYFSDPLSLEAQLKSFT

SEQ ID NO. 8619

STRAIN M781 frame: 1

EGFTYYGKIPENPKKVINFYTSYTGYYLLKLG VNVSSYSLDLEKDS PVFGKQLKEAKKLT
 DDTEAIAAQKPD LIMVFDQDPNINTLKKIAPT LVIKYGAQNYLDMMPALGKVFGKEKEAN
 QWVSQWKTKTLAAKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
 EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
 IESNYDVFYFSDPLSLEAQLKSFT

SEQ ID NO. 8620

STRAIN CJB110 frame: 1

EGFTYYGKIPENPKKVINFYTSYTGYYLLKLG VNVSSYSLDLEKDS PVFGKQLKEAKKLT
 DDTEAIAAQKPD LIMVFDQDPNINTLKKIAPT LVIKYGAQNYLDMMPALGKVFGKEKEAN
 QWVSQWKTKTLAAKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
 EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
 IESNYDVFYFSDPLSLEAQLKSFT

SEQ ID NO. 8621

STRAIN 1169NT frame: 1

EGFTYYGKIPENPKKVINFYTSYTGYYLLKLG VNVSSYSLDLEKDS PVFGKQLKEAKKLT
 DDTEAIAAQKPD LIMVFDQDPNINTLKKIAPT LVIKYGAQNYLDMMPALGKVFGKEKEAN
 QWVSQWKTKTLAAKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
 EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
 IESNYDVFYFSDPLSLEAQLKSFT

SEQ ID NO. 8622

STRAIN JM9130013 frame: 1

EGFTYYGKIPENPKKVINFYTSYTGYYLLKLG VNVSSYSLDLEKDS PVFGKQLKGAKKLT
 DDTEAIAAQKPD LIMVFDQDPNINTLKKIAPT LVIKYGAQNYLDMMPALGKVFGKEKEAN
 QWVSQWKTKTLAAKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
 EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
 IESNYDVFYFSDPLSLEAQLKSFT

PRETTY of: /biotmp/msa522124.2{*} April 28, 2003 08:17 ..

	1				50
msa522124.2{691_090}	-----	-----	-----	-----EG	FTYYGKIPEN
msa522124.2{691_1169NT}	-----	-----	-----	-----EG	FTYYGKIPEN
msa522124.2{691_CJB110}	-----	-----	-----	-----EG	FTYYGKIPEN
msa522124.2{691_COH1}	-----	-----	-----	-----EG	FTYYGKIPEN
msa522124.2{691_M732}	-----	-----	-----	-----EG	FTYYGKIPEN
msa522124.2{691_M781}	-----	-----	-----	-----EG	FTYYGKIPEN
msa522124.2{691_18RS21}	-----	-----	-----	-----EG	FTYYGKIPEN
msa522124.2{691_2603}	mkkigiivlt	lltfflvscg	qgatkqestkt	tiskmpkieG	FTYYGKIPEN
msa522124.2{691_A909}	-----	-----	-----	-----EG	FTYYGKIPEN
msa522124.2{691_JM9130013}	-----	-----	-----	-----EG	FTYYGKIPEN
msa522124.2{691_H36B}	-----	-----	-----	-----EG	FTYYGKIPEN
Consensus	*****	*****	*****	*****	*****
	51				100
msa522124.2{691_090}	PKKVINFYTS	YTGYYLLKLG	VNVSSYSLDLE	KDSPVFGKQL	KeAKKLTADD
msa522124.2{691_1169NT}	PKKVINFYTS	YTGYYLLKLG	VNVSSYSLDLE	KDSPVFGKQL	KeAKKLTADD
msa522124.2{691_CJB110}	PKKVINFYTS	YTGYYLLKLG	VNVSSYSLDLE	KDSPVFGKQL	KeAKKLTADD
msa522124.2{691_COH1}	PKKVINFYTS	YTGYYLLKLG	VNVSSYSLDLE	KDSPVFGKQL	KeAKKLTADD
msa522124.2{691_M732}	PKKVINFYTS	YTGYYLLKLG	VNVSSYSLDLE	KDSPVFGKQL	KeAKKLTADD
msa522124.2{691_M781}	PKKVINFYTS	YTGYYLLKLG	VNVSSYSLDLE	KDSPVFGKQL	KeAKKLTADD
msa522124.2{691_18RS21}	PKKVINFYTS	YTGYYLLKLG	VNVSSYSLDLE	KDSPVFGKQL	KeAKKLTADD
msa522124.2{691_2603}	PKKVINFYTS	YTGYYLLKLG	VNVSSYSLDLE	KDSPVFGKQL	KeAKKLTADD
msa522124.2{691_A909}	PKKVINFYTS	YTGYYLLKLG	VNVSSYSLDLE	KDSPVFGKQL	KgAKKLTADD
msa522124.2{691_JM9130013}	PKKVINFYTS	YTGYYLLKLG	VNVSSYSLDLE	KDSPVFGKQL	KgAKKLTADD
msa522124.2{691_H36B}	PKKVINFYTS	YTGYYLLKLG	VNVSSYSLDLE	KDSPVFGKQL	KgAKKLTADD
Consensus	*****	*****	*****	*****	*-*****
	101				150
msa522124.2{691_090}	TEAIAAQKPD	LIMVFDQDPN	INTLKKIAPT	LVIKYGAQNY	LDMMPALGKV
msa522124.2{691_1169NT}	TEAIAAQKPD	LIMVFDQDPN	INTLKKIAPT	LVIKYGAQNY	LDMMPALGKV
msa522124.2{691_CJB110}	TEAIAAQKPD	LIMVFDQDPN	INTLKKIAPT	LVIKYGAQNY	LDMMPALGKV
msa522124.2{691_COH1}	TEAIAAQKPD	LIMVFDQDPN	INTLKKIAPT	LVIKYGAQNY	LDMMPALGKV
msa522124.2{691_M732}	TEAIAAQKPD	LIMVFDQDPN	INTLKKIAPT	LVIKYGAQNY	LDMMPALGKV
msa522124.2{691_M781}	TEAIAAQKPD	LIMVFDQDPN	INTLKKIAPT	LVIKYGAQNY	LDMMPALGKV
msa522124.2{691_18RS21}	TEAIAAQKPD	LIMVFDQDPN	INTLKKIAPT	LVIKYGAQNY	LDMMPALGKV
msa522124.2{691_2603}	TEAIAAQKPD	LIMVFDQDPN	INTLKKIAPT	LVIKYGAQNY	LDMMPALGKV
msa522124.2{691_A909}	TEAIAAQKPD	LIMVFDQDPN	INTLKKIAPT	LVIKYGAQNY	LDMMPALGKV
msa522124.2{691_JM9130013}	TEAIAAQKPD	LIMVFDQDPN	INTLKKIAPT	LVIKYGAQNY	LDMMPALGKV

Table 86: Comparative Sequences relating to SAG1393

msa522124.2{691_H36B}	TEAIAAQKPD	LIMVFDQDPN	INTLKKIAPT	LVIKYGAQNY	LDMPALGKV
Consensus	*****	*****	*****	*****	*****
msa522124.2{691_090}	151				200
msa522124.2{691_1169NT}	FGKEKEANQW	VSQWKTCTLA	akKDLHHILk	PNTTFTImDF	YDKNIYLYGN
msa522124.2{691_CJB110}	FGKEKEANQW	VSQWKTCTLA	akKDLHHILk	PNTTFTImDF	YDKNIYLYGN
msa522124.2{691_COH1}	FGKEKEANQW	VSQWKTCTLA	akKDLHHILk	PNTTFTImDF	YDKNIYLYGN
msa522124.2{691_M732}	FGKEKEANQW	VSQWKTCTLA	akKDLHHILk	PNTTFTImDF	YDKNIYLYGN
msa522124.2{691_M781}	FGKEKEANQW	VSQWKTCTLA	akKDLHHILk	PNTTFTImDF	YDKNIYLYGN
msa522124.2{691_18RS21}	FGKEKEANQW	VSQWKTCTLA	vKKDLHHILk	PNTTFTImDF	YDKNIYLYGN
msa522124.2{691_2603}	FGKEKEANQW	VSQWKTCTLA	vKKDLHHILk	PNTTFTImDF	YDKNIYLYGN
msa522124.2{691_A909}	FGKEKEANQW	VSQWKTCTLA	akKDLHHILk	PNTTFTImDF	YDKNIYLYGN
msa522124.2{691_JM9130013}	FGKEKEANQW	VSQWKTCTLA	akKDLHHILk	PNTTFTImDF	YDKNIYLYGN
msa522124.2{691_H36B}	FGKEKEANQW	VSQWKTCTLA	akKDLHHILr	PNTTFTIiDF	YDKNIYLYGN
Consensus	*****	*****	-*****-	*****-*	*****
msa522124.2{691_090}	201				250
msa522124.2{691_1169NT}	NFGRGGELIY	DSLGYAAPEK	VKKDVFKKGW	FTVSQEAIGD	YVG DYALVNI
msa522124.2{691_CJB110}	NFGRGGELIY	DSLGYAAPEK	VKKDVFKKGW	FTVSQEAIGD	YVG DYALVNI
msa522124.2{691_COH1}	NFGRGGELIY	DSLGYAAPEK	VKKDVFKKGW	FTVSQEAIGD	YVG DYALVNI
msa522124.2{691_M732}	NFGRGGELIY	DSLGYAAPEK	VKKDVFKKGW	FTVSQEAIGD	YVG DYALVNI
msa522124.2{691_M781}	NFGRGGELIY	DSLGYAAPEK	VKKDVFKKGW	FTVSQEAIGD	YVG DYALVNI
msa522124.2{691_18RS21}	NFGRGGELIY	DSLGYAAPEK	VKKDVFKKGW	FTVSQEAIGD	YVG DYALVNI
msa522124.2{691_2603}	NFGRGGELIY	DSLGYAAPEK	VKKDVFKKGW	FTVSQEAIGD	YVG DYALVNI
msa522124.2{691_A909}	NFGRGGELIY	DSLGYAAPEK	VKKDVFKKGW	FTVSQEAIGD	YVG DYALVNI
msa522124.2{691_JM9130013}	NFGRGGELIY	DSLGYAAPEK	VKKDVFKKGW	FTVSQEAIGD	YVG DYALVNI
msa522124.2{691_H36B}	NFGRGGELIY	DSLGYAAPEK	VKKDVFKKGW	FTVSQEAIGD	YVG DYALVNI
Consensus	*****	*****	*****	*****	*****
msa522124.2{691_090}	251				300
msa522124.2{691_1169NT}	NKTTKKAASS	LKESDVWKNL	PAVKKGHIIE	SNYDV FYFSD	PLSLEAQLKS
msa522124.2{691_CJB110}	NKTTKKAASS	LKESDVWKNL	PAVKKGHIIE	SNYDV FYFSD	PLSLEAQLKS
msa522124.2{691_COH1}	NKTTKKAASS	LKESDVWKNL	PAVKKGHIIE	SNYDV FYFSD	PLSLEAQLKS
msa522124.2{691_M732}	NKTTKKAASS	LKESDVWKNL	PAVKKGHIIE	SNYDV FYFSD	PLSLEAQLKS
msa522124.2{691_M781}	NKTTKKAASS	LKESDVWKNL	PAVKKGHIIE	SNYDV FYFSD	PLSLEAQLKS
msa522124.2{691_18RS21}	NKTTKKAASS	LKESDVWKNL	PAVKKGHIIE	SNYDV FYFSD	PLSLEAQLKS
msa522124.2{691_2603}	NKTTKKAASS	LKESDVWKNL	PAVKKGHIIE	SNYDV FYFSD	PLSLEAQLKS
msa522124.2{691_A909}	NKTTKKAASS	LKESDVWKNL	PAVKKGHIIE	SNYDV FYFSD	PLSLEAQLKS
msa522124.2{691_JM9130013}	NKTTKKAASS	LKESDVWKNL	PAVKKGHIIE	SNYDV FYFSD	PLSLEAQLKS
msa522124.2{691_H36B}	NKTTKKAASS	LKESDVWKNL	PAVKKGHIIE	SNYDV FYFSD	PLSLEAQLKS
Consensus	*****	*****	*****	*****	*****
msa522124.2{691_090}	301	310			
msa522124.2{691_1169NT}	FT-----				
msa522124.2{691_CJB110}	FT-----				
msa522124.2{691_COH1}	FT-----				
msa522124.2{691_M732}	FT-----				
msa522124.2{691_M781}	FT-----				
msa522124.2{691_18RS21}	FT-----				
msa522124.2{691_2603}	FTkaikentn				
msa522124.2{691_A909}	FT-----				
msa522124.2{691_JM9130013}	FT-----				
msa522124.2{691_H36B}	FT-----				
Consensus	*****				

SEQ ID NO. 8701
STRAIN 2603
ATGAAATTATCGAAGAAGTTATTGTTTTCGGCTGCTGTT
TTAACAATGGTGGCGGGGTCAACTGTTGAACCAGTAGCTCAGTTTGCGACTGGAATGAGT
ATTGTAAGAGCTGCAGAAGTGTCAACAAGACGCCAGCGAAAAACAACGATAAATATCTAT
AAATTACAAGCTGATAGTTTATAAATCGGAAATFACTTCTAATGGTGGTATCGAGAATAA
GACGGCGAAGTAATATCTAACTATGCTAAACTTGGTGACAATGTAAAGGTTTGCAAGGT
GTACAGTTTAAACGTTATAAAGTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTG
ACAACAGTTGAAGCAGCAGATGCAAAAGTTGGAACGATTCTTGAAGAAGGTGTCAGTCTA
CCTCAAAAACTAATGCTCAAGGTTTGGTCGTCGATGCTCTGGATTCAAAAAGTAATGTG
AGATACTTGTATGTAGAAGATTTAAAGAATTCACCTTCAAACATTACCAAAGCTTATGCT
GTACCGTTTGTGTGGAATTACCAGTTGCTAACTCTACAGGTACAGGTTTCTTTTCTGAA
ATTAATATTTACCCTAAAAACGTTGTAACTGATGAACCAAAAACAGATAAAGATGTTAAA
AAATTAGGTGAGGACGATGCAGGTTATACGATTGGTGAAGAATTCAAATGGTTCTTGAAA
TCTACAATCCCTGCCAATTTAGGTGACTATGAAAAATTTGAAATTACTGATAAATTTGCA
GATGGCTTGACTTATAAATCTGTTGGAAAAATCAAGATTGGTTGCAAAACACTGAATAGA
GATGAGCACTACACTATTGATGAACCAACAGTTGATAACCAAAATACAT'TAAAAATTACG
TTTAAACACAGAGAAATTTAAAGAAATTTGCTGAGCTACTTAAAGGAATGACCCCTTGT'TAAA
AATACAAGATGCTCTTGATAAAGCTACTGCAAAATACAGATGATGCGGCATTTT'TGAAAT
CCAGTTGCATCAACTATTAATGAAAAAGCAGTTT'TAGGAAAAGCAATTGAAAATACT'TTT
GAACTTCAATATGACCATACTCCTGATAAAGCTGACAATCCAAAACCATCTAATCCTCCA
AGAAAACCAGAAGTTCATACTGGTGGGAAACGATT'TGTAAAGAAAGACTCAACAGAAACA
CAAACACTAGGTGGTGCTGAGTTTGATTTGTTTGGCTTCTGATGGGACAGCAGTAAATGG
ACAGATGCTCTTATTAAGCGAATACTAATAAAAACTATATTGCTGGAGAAGCTGTTACT
GGGCAACCAATCAAATTTGAAATCACATAACAGACGGTACGTTT'TGAGATTAAAGGTTTGGCT
TATGCAGTTGATGCGAATGCAGAGGGTACAGCAGTAACTTACAAAT'TAAAAGAAACAAA
GCACCAGAAGGTTATGTAATCCCTGATAAAGAAATCGAGTTTACAGTATCACAAACATCT
TATAATACAAAACCAACTGACATCACGGTTGATAGTGCTGATGCAACACCTGATACAATT
AAAAACAACAAACGTCCTTCAATCCCTAATACTGGTGGTATTGGTACGGCTATCTTTGTC
GCTATCGGTGCTGCGGTGATGGCTTTTGCTGT'TAAGGGGATGAAGCGTCGTACAAAAGAT
AAC

SEQ ID NO. 8702
STRAIN 090
GCAGAAGTGTCCACAAGAACGCCAGCGAAAAC
AGCAGTAAATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATTA
CTTCTAATGGTGGTATCGAGATAAAGGACGGCGAAGTAATATCTAACTAT
GCTAAACCTTGGTGACAATGTAAAAGGTTGCAAGGTGTACAGTTTAAACG
TTATAAAGTCAAGACGGATATTTCTGTTGATGAATTTGAAAAAATTGACAA
CAGTTGAAGCAGCAGATGCAAAAGTTGGAACGATTCTTGAAGAAGGTGTC
AGTCTACCTCAAAAACTAATGCTCAAGGTTTGGTCGTCGATGCTCTGGA
TTCAAAAAGTAAATGTGAGATACTTGTATGTAGAAGATTTAAAGAATTAC
CTTCAAACATTACCAAAGCTTATGCTGTACCGTTTGTGTTGGAATTACCA
GTTGCTAACTCTACAGGTACAGGTTTCTTTCTGAAATTAATATTTTACCC
TAAAAACGTTGTAACTGATGAACCAAAAACAGATAAAGATGTTAAAAAAT
TAGGTCAGGACGATGCAGGTTATACGATTGGTGAAGAATTCAAATGGTTC
TTGAAATCTACAATCCCTGCCAATTTAGGTGACTATGAAAAATTTGAAAT
TACTGATAAATTTGCAGATGGCTTGACTTATAAATCTGTTGGAAAAATCA
AGATTGGTTTCAAAAACACTGAATAGAGATGAGCACTACACTATTGATGAA
CCAACAGTTGATAACCAAATACATATAAAAATTCGTTTAAACAGAGAA
ATTTAAAGAAATTTGCGACTACTTAAAGGAATGACCCCTGTTAAAAAT
AAGATGCTCTTGATAAAGCTACTGCAAATACAGATGATGCGGCATTTTTT
GAAATTCAGTTGCATCAACTATTAATGAAAAAGCAGTTTTAGGAAAAGC
AATTGAAAATACCTTTGAACTTCAATATGACCATACTCCTGATAAAGCTG
ACAATCCAAAACCATCTAATCCTCCAAGAAAACCAAGAGTTTCATACCTGGT
GGGAAACGATTTGTAAGAAGAACTCAACAGAGAAACAAACACTAGGTGG
TGCTGAGTTTGATTTGTTGGCTTCTGATGGGACAGCAGATAAATGGACAG
ATGCTCTTATTTAAAGCGAATACTAATAAAACTAATATTGCTGGAGAAGCT
GTTACTGGGCAACCAATCAAATTGAAATCACATACAGACGGTACGTTTGA
GATTAAAGGTTTGGCTTATGCAGTTGATGCGAATGCAGAGGGTACAGCAG
TAACCTTACAAATTTAAAGAAAACAAAAGCACCAGAAGGTTATGTAATCCCT
GATAAAGAAATCAGGTTTACAGTATCACAAACATCTTATAATACAAAACC
AACTGACATCAGGTTGTATAGTGCTGATGCAACACCTGATACAATTTAA
ACAACAAACGTCCTTCA

1151

Table 87: Comparative Sequences relating to SAG0645

GAAATTTAAAGAAATTGCTGAGCTACTTAAAGGAATGACCCCTTGTAAAA
 ATCAAGATGCTCTTGATAAAGCTACTGCAAATACAGATGATGCGGCATTT
 TTGGAAATTCAGTTGCATCAACTATTAATGAAAAAGCAGTTTATAGGAAA
 AGCAATTGAAAATACCTTTTGAACCTTCAATATGACCATACTCCTGATAAAG
 CTGACAATCCAAAACCATCTAATCCTCCAAGAAAACAGAAAGTTCATACT
 GGTGGGAAACGATTTGTAAAGAAAGACTCAACAGAAACACAAACACTAGG
 TGGTGCTGAGTTTGATTGTGGCTTCTGATGGGACAGCAGTAAATGGA
 CAGATGCTCTTATTAAAGCGAATACTAATAAAAACTATATTGCTGAGAA
 GCTGTTACTGGGCAACCAATCAAATTGAAATCACATACAGACGGTACGTT
 TGAGATTAAAGGTTTGGCTTATGCAGTTGATGCGAATGCAGAGGTACAG
 CAGTAACTTACAAATTAAAAGAAAACAAAGCACCAGAAGGTTATGTAATC
 CCTGATAAAGAAATCGAGTTTACAGTATCACAAACATCTTATAATACAAA
 ACCAACTGACATCACGGTTGATAGTGCTGATGCAACACCTGATACAATTA
 AAAACAACAA

SEQ ID NO. 8704

STRAIN 18RS21

GCAGAAGTGTCAAGAAGCGCCAGCGAAAAAC
 AGCAGTAAATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATTA
 CTTCTAATGGTGGTATCGAGAATAAAGACGGCGAAGTAATATCTAACTAT
 GCTAAACTTGGTGACAATGTAAAAGGTTTGCAAGGTGTACAGTTTAAACG
 TTATAAAGTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTGACAA
 CAGTTGAAGCAGCAGATGCAAAAGTTGGAACGATTCTTGAAGAAGGTGTC
 AGTCTACCTCAAAAACTAATGCTCAAGGTTTGGTCGTGATGCTCTGGA
 TTCAAAAAGTAATGTGAGATACTTGTATGTAGAAGATTTAAAGAATTCAC
 CTTCAAACATTACCAAAGCTTATGCTGTACCGTTTGTGTTGGAATTACCA
 GTTGCTAACTCTACAGGTACAGGTTTCTTTCTGAAATTAATATTTACCC
 TAAAAACGTTGTAAGTGAACCAAAAACAGATAAAGATGTTAAATAAT
 TAGGTGAGGACGATGCAGGTTATACGATTGGTGAAGAATTCAAATGGTTC
 TTGAAATCTACAATCCCTGCCAATTTAGGTGACTATGAAAAATTTGAAAT
 TACTGATAAATTTGCAGATGGCTTGACTTATAAATCTGTTGGAAAAATCA
 AGATTGGTTGCAAAACACTGAATAGAGATGAGCACTACACTATTGATGAA
 CCAACAGTTGATAACCAAAATACATTAATAAATTACGTTTAAACCAgAGAA
 ATTTAAAGAAATTGCTGAGCTACTTAAAGGAATGACCCCTTGTAAAAATC
 AAGATGCTCTTGATAAAGCTACTGCAAATACAGATGATGCGGCATTTTG
 GAAATTCAGTTGCATCAACTATTAATGAAAAAGCAGTTTATAGGAAAAGC
 AATTGAAAATACTTTTGAACCTTCAATATGACCATACTCCTGATAAAGCTG
 ACAATCCAAAACCATCTAATCCTCCAAGAAAACAGAAAGTTCATACTGGT
 GGGAAACGATTTGTAAAGAAAGACTCAACAGAAACACAAACACTAGGTGG
 TGCTGAGTTTGATTGTGGCTTCTGATGGGACAGCAGTAAATGGACAG
 ATGCTCTTATTAAAGCGAATACTAATAAAAACTATATTGCTGGAGAAGCT
 GTTACTGGGCAACCAATCAAATTGAAATCACATACAGACGGTACGTTTGA
 GATTAAAGGTTTGGCTTATGCAGTTGATGCGAATGCAGAGGGTACAGCAG
 TAACTTACAAATTAAAAGAAAACAAAGCACCAGAAGGTTATGTAATCCCT
 GATAAAGAAATCGAGTTTACAGTATCACAAACATCTTATAATACAAAACC
 AACTGACATCACGGTTGATAGTGCTGATGCAACACCTGATACAATTAATA
 ACAACAAACGTCCTTCA

SEQ ID NO. 8705

STRAIN M732

GCAGAAGTGTCAAGAAGCGCCAGCGAAAAACAACAGT
 AAATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATTAATTCTA
 ATGGTGGTATCGAGAATAAAGACGGCGAAGTAATATCTAACTATGCTAAA
 CTTGGTGACAATGTAAAAGGTTTGCAAGGTGTACAGTTTAAACGTTATAA
 AGTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTGACAACAGTGTG
 AAGCAGCAGATGCAAAAGTTGGAACGATTCTTGAAGAAGGTGTGAGTCTA
 CCTCAAAAACTAATGCTCAAGGTTTGGTCGTGATGCTCTGGATTCAAA
 AAGTAATGTGAGATACTTGTATGTAGAAGATTTAAAGAATTCACCTTCAA
 ACATTACCAAAGCTTATGCTGTACCGTTTGTGTTGGAATTACAGTTGCT
 AACTCTACAGGTACAGGTTTCTTTCTGAAATTAATATTTACCTTAAAAA
 CGTTGTAAGTGAACCAAAAACAGATAAAGATGTTAAAAAATTAGGTC
 AGGACGATGCAGGTTATACGATTGGTGAAGAATTCAAATGGTTCTTGAAA
 TCTACAATCCCTGCCAATTTAGGTGACTATGAAAAATTTGAAATTAAGTGA
 TAAATTTGCAGATGGCTTGACTTATAAATCTGTTGGAAAAATCAAGATTG
 GTTCGAAAACACTGAATAGAGATGAGCACTACACTATTGATGAACCAACA
 GTTGATAACCAAAATACATTAATAAATTACGTTTAAACCAAGAGAAATTTAA
 AGAAATTGCTGAGCTACTTAAAGGAATGACCCCTTGTAAAAATCAAGATG
 CTCTTGATAAAGCTACTGCAAATACAGATGATGCGGCATTTTGGAAAT
 CCAGTTGCATCAACTATTAATGAAAAAGCAGTTTATAGGAAAAGCAATTGA
 AAATACTTTTGAACCTTCAATATGACCATACTCCTGATAAAGCTGACAATC
 CAAAACCATCTAATCCTCCAAGAAAACAGAAAGTTCATACTGGTGGGAAA
 CGATTTGTAAAGAAAGACTCAACAGAAACACAAACACTAGGTGGTGTGA
 GTTTGATTTGTGGCTTCTGATGGGACAGCAGTAAATGGACAGATGCTC
 TTATTAAAGCGAATACTAATAAAAACTATATTGCTGGAGAAGCTGTACT
 GGGCAACCAATCAAATTGAAATCACATACAGACGGTACGTTTGAATTA
 AGGTTTGGCTTATGCAGTTGATGCGAATGCAGAGGGTACAGCAGTAACTT
 ACAAAATTAAGAAAACAAAGCACCAGAAGGTTATGTAATCCCTGATAAA
 GAAATCGAGTTTACAGTATCACAAACATCTTATAATACAAAACCAACTGA
 CATCACGGTTGATAGTGCTGATGCAACACCTGATACAATTAATAAACA
 AACGTCCTTCA

SEQ ID NO. 8706

STRAIN COH1

Table 87: Comparative Sequences relating to SAG0645

GCAGAAGTGT CACAAGAACGCCAGCGAAAAAC
 AGCAGTAAATATCTATAAAATTACAAGCTGATAGTTATAAATCGGAAATTA
 CTInTAATGGTGGTATCGAGAATAAAGACGGCGAAGTAATATCTAACTAT
 GCTAAACTTGGTGACAATGTAAAAGGTTTGCAAGGTGTACAGTTTAAACG
 TTATAAAGTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTGACAA
 CAGTTGAAGCAGCAGATGCAAAAGTTGGAACGATTCTTGAAGAAGGTGTC
 AGTCTACCTCAAAAAACTAATGCTCAAGGTTTGGTCGTCGATGCTCTGGA
 TTCAAAAAGTAATGTGAGATACTTGTATGTAGAAGATTTAAAGAATTAC
 CTTCAAAACATTACCAAAGCTTATGCTGTACCGTTTGTGTTGGAATTACCA
 GTTGCTAACTCTACAGGTACAGGTTTCCTTTCTGAAATTAATATTTACCC
 TAAAAACGTTGTAACCTGATGAACCAAAAAACAGATAAAGATGTTAAAAAAT
 TAGGTCAGGACGATGCAGGTTATACGATTGGTGAAGAATTCAAATGGTTC
 TTGAAATCTACAATCCCTGCCAATTTAGGTGACTATGAAAAATTTGAAAT
 TACTGATAAATTTGCAGATGGCTTGACTTATAAATCTGTTGGAATAATCA
 AGATTGGTTGCAAAACACTGAATAGAGATGAGCACTACACTATTGATGAA
 CCAACAGTTGATAACCAAAATACATTAAAAATTACGTTTAAACCAGAGAA
 ATTTAAAGAAATTTGCTGAGCTACTTAAAGGAATGACCCTTGTTAAAAATC
 AAGATGCTCTTGATAAAGCTACTGCAAATACAGATGATGCGGCATTTTGTG
 GAAATTCAGTTGCATCAACTATTAAATGAAAAAGCAGTTTATAGGAAAAGC
 AATTGAAAAATCTTTGAACTTCAATATGACCATACTCCTGATAAAGCTG
 ACAATCCAAAACCATCTAATCCTCCAAGAAAACAGAAAGTTTACTACTGGT
 GGGAAAACGATTGTAAAGAAAGACTCAACAGAAAACACAAACACTAGGTGG
 TGCTGAGTTTGATTTGTTGGCTTCTGATGGGACAGCAGTAAAATGGACAG
 ATGCTCTTATTAAAGCGAATACTAATAAAAACTATATTGCTGGAGAAGCT
 GTTACTGGGCAACCAATCAAATTTGAAATCACATACAGACGGTACGTTTGA
 GATTAAAGGTTTGGCTTATGCAGTTGATGCGAATGCAGAGGGTACAGCAG
 TAACCTTACAAATTAAGAAACAAAAGCACCAGAAGGTTATGTAATCCCT
 GATAAAGAAATCGAGTTTACAGTATCACAAACATCTTATAATACAAAACC
 AACTGACATCACGGTTGATAGTGCTGATGCAACACCTGATACAATTAATA
 ACAACAAACGTCCTTCA

SEQ ID NO. 8707

STRAIN M781

GCAGAAGTGT CACAAGAACGCCAGCGAAAAACAG
 CAGTAAATATCTATAAAATTACAAGCTGATAGTTATAAATCGGAAATTACT
 TCTAATGGTGGTATCGAGAATAAAGACGGCGAAGTAATATCTAACTATGC
 TAAACTTGGTGACAATGTAAAAGGTTTGCAAGGTGTACAGTTTAAACGTT
 ATAAAGTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTGACAACA
 GTTGAAGCAGCAGATGCAAAAGTTGGAACGATTCTTGAAGAAGGTGTCAG
 TCTACCTCAAAAAACTAATGCTCAAGGTTTGGTCGTCGATGCTCTGGATT
 CAAAAAGTAATGTGAGATACTTGTATGTAGAAGATTTAAAGAATTACCT
 TCAAAACATTACCAAAGCTTATGCTGTACCGTTTGTGTTGGAATTACAGT
 TGCTAACTCTACAGGTACAGGTTTCCTTTCTGAAATTAATATTTACCTTA
 AAAACGTTGTAACCTGATGAACCAAAAAACAGATAAAGATGTTAAAAAATTA
 GGTGAGGACGATGCAGGTTATACGATTGGTGAAGAATTCAAATGGTTCCT
 GAAATCTACAATCCCTGCCAATTTAGGTGACTATGAAAAATTTGAAATTA
 CTGATAAATTTGCAGATGGCTTGACTTATAAATCTGTTGGAATAATCAAG
 ATTGGTTGCAAAACACTGAATAGAGATGAGCACTACACTATTGATGAACC
 AACAGTTGATAACCAAAATACATTAAAAATTACGTTTAAACCAGAGAAAT
 TTAAAGAAATTTGCTGAGCTACTTAAAGGAATGACCCTTGTTAAAAATCAA
 GATGCTCTTGATAAAGCTACTGCAAATACAGATGATGCGGCATTTTGGGA
 AATTCCAGTTGCATCAACTATTAAATGAAAAAGCAGTTTATAGGAAAAGCAA
 TTGAAAATACCTTTGAACTTCAATATGACCATACTCCTGATAAAGCTGAC
 AATCCAAAACCATCTAATCCTCCAAGAAAACAGAAAGTTTACTACTGGTGG
 GAAACGATTGTAAAGAAAGACTCAACAGAAAACACAAACACTAGGTGGTG
 CTGAGTTTGATTTGTTGGCTTCTGATGGGACAGCAGTAAAATGGACAGAT
 GCTCTTATTAAAGCGAATACTAATAAAAACTATATTGCTGGAGAAGCTGT
 TACTGGGCAACCAATCAAATTTGAAATCACATACAGACGGTACGTTTGA
 TTAAAGGTTTGGCTTATGCAGTTGATGCGAATGCAGAGGGTACAGCAGTA
 ACTTACAAATTAAGAAACAAAAGCACCAGAAGGTTATGTAATCCCTGA
 TAAAGAAATCGAGTTTACAGTATCACAAACATCTTATAATACAAAACCAA
 CTGACATCACGGTTGATAGTGCTGATGCAACACCTGATACAATTAATAAC
 AACAAACGT

SEQ ID NO. 8708

STRAIN CJB110

GCAGAAGTGT CACAAGAACGCCAGCGAA
 AACAGCAGTAAATATCTATAAAATTACAAGCTGATAGTTATAAATTTGAAA
 TTACTTCTAATGGTGGTATCGAGAATAAAGACGGCGAAGTAATATCTAAC
 TATGCTAAACTTGGTGACAATGTAAAAGGTTTGCAAGGTGTACAGTTTAA
 ACGTTATAAAGTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTGA
 CAACAGTTGAAGCAGCAGATGCAAAAGTTGGAACGATTCTTGAAGAAGGT
 GTCAGTCTACCTCAAAAACTAATGCTCAAGGTTTGGTCGTCGATGCTCT
 GGATTCAAAAAGTAATGTGAGATACTTGTATGTAGAAGATTTAAAGAATT
 CACCTTCAAACATTACCAAAGCTTATGCTGTACCGTTTGTGTTGGAATTA
 CCAGTTGCTAACTCTACAGGTACAGGTTTCCTTTCTGAAATTAATATTTA
 CCTAAAAACGTTGTAACCTGATGAACCAAAAAACAGATAAAGATGTTAAAA
 AATTAGGTGAGGACGATGCAGGTTATACGATTGGTGAAGAATTCAAATGG
 TTCTTGAAATCTACAATCCCTGCCAATTTAGGTGACTATGAAAAATTTGA
 AATTACTGATAAATTTGCAGATGGCTTGACTTATAAATCTGTTGGAATAA
 TCAAGATTGGTTGCAAAACACTGAATAGAGATGAGCACTACACTATTGAT
 GAACCAACAGTTGATAACCAAAATACATTAAAAATTACGTTTAAACCAGA
 GAAATTTAAAGAAATTTGCTGAGCTACTTAAAGGAATGACCCTTGTTAAAA

Table 87: Comparative Sequences relating to SAG0645

ATCAAGATGCTCTTGATAAAGCTACTGCAAATACAGATGATGCGGCATT
 TTGGAAATTCAGTTGCATCACTATTAATGAAAAAGCAGTTTTAGGAAA
 AGCAATTGAAAATACCTTTGAACTTCAATATGACCATACTCCTGATAAAG
 CTGACAATcCAAAACCATCTAATCCTCCAAGAAAACAGAAAGTTCATACT
 GGTGGGAAACGATTTGTAAAGAAAGACTCAACAGAAACACAAACACTAGG
 TGGTGCTGAGTTTGATTTGTTGGCTTCTGATGGGACAGCAGTAAAATGGA
 CAGATGCTCTTATTAAAGCGAATACTAATAAAAACTATATTGCTGGAGAA
 GCTGTTACTGGGCAACCAATCAAATTGAAATCACATACAGACGGTACGTT
 TGAGATTAAAGGTTTGGCTTATGCAGTTGATGCGAATGCAGAGGGTACAG
 CAGTAACCTTACAAATTAAAAGAAAACAAAAGCACCAGAAGGTTATGTAATC
 CCTGATAAAGAAATCGAGTTTACAGTATCACAAACATCTTATAATCCAAA
 ACCAACTGACATCACGGTTGATAGTGCTGATGCAACACCTGATACAATTA
 AAAACAACAAACGTCCTTCA

SEQ ID NO. 8709

STRAIN JM9130013

GCAGAAGTGTCAACAAGAACGCCAGCGAAAACAGCAGTA
 AATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATTACTTCTAA
 TGGTGGTATCGAGAATAAAGACGGCGAAGTAATATCTAACTATGCTAAAC
 TTGGTGACAATGTAAAGGTTTGAAGGTGTACAGTTTAAACGTTATAAA
 GTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTGACAACAGTTGA
 AGCAGCAGATGCAAAAGTTGGAACGATTCTTGAAGAAGGTGTGAGTCTAC
 CTCAAAAAATCAATGCTCAAGGTTTGGTTCGTCGATGCTCTGGATTCAAAA
 AGTAATGTGAGATACTTGTATGTAGAAGATTTAAAGAATTCACCTTCAAA
 CATTACCAAAGCTTATGCTGTACCGTTTGTGTTGGAATTACCAGTTGCTA
 ACTCTACAGGTACAGGTTTCTCTTCTGAAATTAATATTTACCTAAAAAC
 GTTGTAACCTGATGAACCAAAAACAGATAAAGATGTTAAAAAATTAGGTCA
 GGACGATGCAAGGTTATACGATTGGTGAAGAATTCAAATGGTTCTTGAAAT
 CTACAATCCCTGCCAATTTAGGTGACTATGAAAAATTTGAAATTACTGAT
 AAAATTTGCAGATGGCTTGACTTATAAATCTGTTGGAAAAATCAAGATTGG
 TTCGAAAACACTGAATAGAGATGAGCACTACACTATTGATGAACCAACAG
 TTGATAACCAAAATACATTAAAAAATTACGTTTAAACCAGAGAAATTTAAA
 GAAATTGCTGAGCTACTTAAAGGAATGACCCTTGTTAAAAATCAAGATGC
 TCTTGATAAAGCTACTGCAAATACAGATGATGCGGCATTTTGGAAATTC
 CAGTTGCATCACTATTAATGAAAAAGCAGTTTATAGGAAAAGCAATTGAA
 AATACCTTTTGAACCTCAATATGACCATACTCCTGATAAAGCTGACAATCC
 AAAACCATCTAATcCTcCAAGAAAACAGAAAGTTCATACTGGTGGGAAAC
 GATTTGTAAAGAAAGACTCAACAGAAACACAAACACTAGGTGGTGCTGAG
 TTTGATTTGTTGGCTTCTGATGGGACAGCAGTAAAATGGACAGATGCTCT
 TATTAAAGCGAATACTAATAAAAACTATATTGCTGGAGAAGCTGTTACTG
 GGCAACCAATCAAATTGAAATCACATACAGACGGTACGTTTGAGATTAAA
 GGTTTGGCTTATGCAGTTGATGCGAATGCAGAGGGTACAGCAGTAACCTTA
 CAAATTTAAAGAAACAAAAGCACCAGAAGGTTATGTAATCCCTGATAAAG
 AAATCGAGTTTACAGTATCACAAACATCTTATAATACAAAACCAACTGAC
 ATCAGGTTGATAGTGCTGATGCAACACCTGATACAATTA AAAACAACAA
 ACGTCCTTCA

PRETTY of: /biotmp/msa123961.2{*} April 30, 2003 07:17 ..

	1				50
msa123961.2{80_2603}	atgaaattat	cgaagaagtt	attgttttcg	gctgctgttt	taacaatggt
msa123961.2{80_A909}	-----	-----	-----	-----	-----
msa123961.2{80_M732}	-----	-----	-----	-----	-----
msa123961.2{80_090}	-----	-----	-----	-----	-----
msa123961.2{80_COH1}	-----	-----	-----	-----	-----
msa123961.2{80_M781}	-----	-----	-----	-----	-----
msa123961.2{801_JM9130013}	-----	-----	-----	-----	-----
msa123961.2{80_18RS21}	-----	-----	-----	-----	-----
msa123961.2{80h_CJB110}	-----	-----	-----	-----	-----
Consensus	-----	-----	-----	-----	-----

	51				100
msa123961.2{80_2603}	ggcgggggtca	actggtgaac	cagtagctca	gtttgcgact	ggaatgagta
msa123961.2{80_A909}	-----	-----	-----	-----	-----
msa123961.2{80_M732}	-----	-----	-----	-----	-----
msa123961.2{80_090}	-----	-----	-----	-----	-----
msa123961.2{80_COH1}	-----	-----	-----	-----	-----
msa123961.2{80_M781}	-----	-----	-----	-----	-----
msa123961.2{801_JM9130013}	-----	-----	-----	-----	-----
msa123961.2{80_18RS21}	-----	-----	-----	-----	-----
msa123961.2{80h_CJB110}	-----	-----	-----	-----	-----
Consensus	-----	-----	-----	-----	-----

	101				150
msa123961.2{80_2603}	ttgtaagagc	tGCAGAAGTG	TCACAAGAAC	GCCCAGCGAA	AACAaCAGTA
msa123961.2{80_A909}	-----	-GCAGAAGTG	TCACAAGAAC	GCCCAGCGAA	AACAaCAGTA
msa123961.2{80_M732}	-----	-GCAGAAGTG	TCACAAGAAC	GCCCAGCGAA	AACAaCAGTA
msa123961.2{80_090}	-----	-GCAGAAGTG	TCACAAGAAC	GCCCAGCGAA	AACAaCAGTA
msa123961.2{80_COH1}	-----	-GCAGAAGTG	TCACAAGAAC	GCCCAGCGAA	AACAaCAGTA
msa123961.2{80_M781}	-----	-GCAGAAGTG	TCACAAGAAC	GCCCAGCGAA	AACAaCAGTA
msa123961.2{801_JM9130013}	-----	-GCAGAAGTG	TCACAAGAAC	GCCCAGCGAA	AACAaCAGTA
msa123961.2{80_18RS21}	-----	-GCAGAAGTG	TCACAAGAAC	GCCCAGCGAA	AACAaCAGTA

Table 87: Comparative Sequences relating to SAG0645

msa123961.2{80h_CJB110}	-----	-GCAGAAAGTG	TCACAAGAAC	GCCCAGCGAA	AACAGCAGTA
Consensus	-----	*****	*****	*****	*****
151					
msa123961.2{80_2603}	AATATCTATA	AATTACAAGC	TGATAGTTAT	AAATcGGAAA	TTACTTcTAA
msa123961.2{80_A909}	AATATCTATA	AATTACAAGC	TGATAGTTAT	AAATcGGAAA	TTACTTcTAA
msa123961.2{80_M732}	AATATCTATA	AATTACAAGC	TGATAGTTAT	AAATcGGAAA	TTACTTcTAA
msa123961.2{80_090}	AATATCTATA	AATTACAAGC	TGATAGTTAT	AAATcGGAAA	TTACTTcTAA
msa123961.2{80_COH1}	AATATCTATA	AATTACAAGC	TGATAGTTAT	AAATcGGAAA	TTACTTnTAA
msa123961.2{80_M781}	AATATCTATA	AATTACAAGC	TGATAGTTAT	AAATcGGAAA	TTACTTcTAA
msa123961.2{801_JM9130013}	AATATCTATA	AATTACAAGC	TGATAGTTAT	AAATcGGAAA	TTACTTcTAA
msa123961.2{80_18RS21}	AATATCTATA	AATTACAAGC	TGATAGTTAT	AAATcGGAAA	TTACTTcTAA
msa123961.2{80h_CJB110}	AATATCTATA	AATTACAAGC	TGATAGTTAT	AAATcGGAAA	TTACTTcTAA
Consensus	*****	*****	*****	*****	*****
201					
msa123961.2{80_2603}	TGGTGGTATC	GAGAATAAAG	ACGGCGAAGT	AATATCTAAC	TATGCTAAAC
msa123961.2{80_A909}	TGGTGGTATC	GAGAATAAAG	ACGGCGAAGT	AATATCTAAC	TATGCTAAAC
msa123961.2{80_M732}	TGGTGGTATC	GAGAATAAAG	ACGGCGAAGT	AATATCTAAC	TATGCTAAAC
msa123961.2{80_090}	TGGTGGTATC	GAGAATAAAG	ACGGCGAAGT	AATATCTAAC	TATGCTAAAC
msa123961.2{80_COH1}	TGGTGGTATC	GAGAATAAAG	ACGGCGAAGT	AATATCTAAC	TATGCTAAAC
msa123961.2{80_M781}	TGGTGGTATC	GAGAATAAAG	ACGGCGAAGT	AATATCTAAC	TATGCTAAAC
msa123961.2{801_JM9130013}	TGGTGGTATC	GAGAATAAAG	ACGGCGAAGT	AATATCTAAC	TATGCTAAAC
msa123961.2{80_18RS21}	TGGTGGTATC	GAGAATAAAG	ACGGCGAAGT	AATATCTAAC	TATGCTAAAC
msa123961.2{80h_CJB110}	TGGTGGTATC	GAGAATAAAG	ACGGCGAAGT	AATATCTAAC	TATGCTAAAC
Consensus	*****	*****	*****	*****	*****
251					
msa123961.2{80_2603}	TTGGTGACAA	TGTAAGAGGT	TTGCAAGGTG	TACAGTTTAA	ACGTTATAAA
msa123961.2{80_A909}	TTGGTGACAA	TGTAAGAGGT	TTGCAAGGTG	TACAGTTTAA	ACGTTATAAA
msa123961.2{80_M732}	TTGGTGACAA	TGTAAGAGGT	TTGCAAGGTG	TACAGTTTAA	ACGTTATAAA
msa123961.2{80_090}	TTGGTGACAA	TGTAAGAGGT	TTGCAAGGTG	TACAGTTTAA	ACGTTATAAA
msa123961.2{80_COH1}	TTGGTGACAA	TGTAAGAGGT	TTGCAAGGTG	TACAGTTTAA	ACGTTATAAA
msa123961.2{80_M781}	TTGGTGACAA	TGTAAGAGGT	TTGCAAGGTG	TACAGTTTAA	ACGTTATAAA
msa123961.2{801_JM9130013}	TTGGTGACAA	TGTAAGAGGT	TTGCAAGGTG	TACAGTTTAA	ACGTTATAAA
msa123961.2{80_18RS21}	TTGGTGACAA	TGTAAGAGGT	TTGCAAGGTG	TACAGTTTAA	ACGTTATAAA
msa123961.2{80h_CJB110}	TTGGTGACAA	TGTAAGAGGT	TTGCAAGGTG	TACAGTTTAA	ACGTTATAAA
Consensus	*****	*****	*****	*****	*****
301					
msa123961.2{80_2603}	GTCAAGACGG	ATATTTCTGT	TGATGAATTG	AAAAAATTGA	CAACAGTTGA
msa123961.2{80_A909}	GTCAAGACGG	ATATTTCTGT	TGATGAATTG	AAAAAATTGA	CAACAGTTGA
msa123961.2{80_M732}	GTCAAGACGG	ATATTTCTGT	TGATGAATTG	AAAAAATTGA	CAACAGTTGA
msa123961.2{80_090}	GTCAAGACGG	ATATTTCTGT	TGATGAATTG	AAAAAATTGA	CAACAGTTGA
msa123961.2{80_COH1}	GTCAAGACGG	ATATTTCTGT	TGATGAATTG	AAAAAATTGA	CAACAGTTGA
msa123961.2{80_M781}	GTCAAGACGG	ATATTTCTGT	TGATGAATTG	AAAAAATTGA	CAACAGTTGA
msa123961.2{801_JM9130013}	GTCAAGACGG	ATATTTCTGT	TGATGAATTG	AAAAAATTGA	CAACAGTTGA
msa123961.2{80_18RS21}	GTCAAGACGG	ATATTTCTGT	TGATGAATTG	AAAAAATTGA	CAACAGTTGA
msa123961.2{80h_CJB110}	GTCAAGACGG	ATATTTCTGT	TGATGAATTG	AAAAAATTGA	CAACAGTTGA
Consensus	*****	*****	*****	*****	*****
351					
msa123961.2{80_2603}	AGCAGCAGAT	GCAAAAGTTG	GAACGATTCT	TGAAGAAGGT	GTCAGTCTAC
msa123961.2{80_A909}	AGCAGCAGAT	GCAAAAGTTG	GAACGATTCT	TGAAGAAGGT	GTCAGTCTAC
msa123961.2{80_M732}	AGCAGCAGAT	GCAAAAGTTG	GAACGATTCT	TGAAGAAGGT	GTCAGTCTAC
msa123961.2{80_090}	AGCAGCAGAT	GCAAAAGTTG	GAACGATTCT	TGAAGAAGGT	GTCAGTCTAC
msa123961.2{80_COH1}	AGCAGCAGAT	GCAAAAGTTG	GAACGATTCT	TGAAGAAGGT	GTCAGTCTAC
msa123961.2{80_M781}	AGCAGCAGAT	GCAAAAGTTG	GAACGATTCT	TGAAGAAGGT	GTCAGTCTAC
msa123961.2{801_JM9130013}	AGCAGCAGAT	GCAAAAGTTG	GAACGATTCT	TGAAGAAGGT	GTCAGTCTAC
msa123961.2{80_18RS21}	AGCAGCAGAT	GCAAAAGTTG	GAACGATTCT	TGAAGAAGGT	GTCAGTCTAC
msa123961.2{80h_CJB110}	AGCAGCAGAT	GCAAAAGTTG	GAACGATTCT	TGAAGAAGGT	GTCAGTCTAC
Consensus	*****	*****	*****	*****	*****
401					
msa123961.2{80_2603}	CTCAAAAAAC	TAATGCTCAA	GGTTTGGTCG	TCGATGCTCT	GGATTCAAAA
msa123961.2{80_A909}	CTCAAAAAAC	TAATGCTCAA	GGTTTGGTCG	TCGATGCTCT	GGATTCAAAA
msa123961.2{80_M732}	CTCAAAAAAC	TAATGCTCAA	GGTTTGGTCG	TCGATGCTCT	GGATTCAAAA
msa123961.2{80_090}	CTCAAAAAAC	TAATGCTCAA	GGTTTGGTCG	TCGATGCTCT	GGATTCAAAA
msa123961.2{80_COH1}	CTCAAAAAAC	TAATGCTCAA	GGTTTGGTCG	TCGATGCTCT	GGATTCAAAA
msa123961.2{80_M781}	CTCAAAAAAC	TAATGCTCAA	GGTTTGGTCG	TCGATGCTCT	GGATTCAAAA
msa123961.2{801_JM9130013}	CTCAAAAAAC	TAATGCTCAA	GGTTTGGTCG	TCGATGCTCT	GGATTCAAAA
msa123961.2{80_18RS21}	CTCAAAAAAC	TAATGCTCAA	GGTTTGGTCG	TCGATGCTCT	GGATTCAAAA
msa123961.2{80h_CJB110}	CTCAAAAAAC	TAATGCTCAA	GGTTTGGTCG	TCGATGCTCT	GGATTCAAAA
Consensus	*****	*****	*****	*****	*****
451					
msa123961.2{80_2603}	AGTAATGTGA	GATACTTGTA	TGTAGAAGAT	TTAAAGAATT	CACCTTCAAA
msa123961.2{80_A909}	AGTAATGTGA	GATACTTGTA	TGTAGAAGAT	TTAAAGAATT	CACCTTCAAA
msa123961.2{80_M732}	AGTAATGTGA	GATACTTGTA	TGTAGAAGAT	TTAAAGAATT	CACCTTCAAA
msa123961.2{80_090}	AGTAATGTGA	GATACTTGTA	TGTAGAAGAT	TTAAAGAATT	CACCTTCAAA
msa123961.2{80_COH1}	AGTAATGTGA	GATACTTGTA	TGTAGAAGAT	TTAAAGAATT	CACCTTCAAA
msa123961.2{80_M781}	AGTAATGTGA	GATACTTGTA	TGTAGAAGAT	TTAAAGAATT	CACCTTCAAA
msa123961.2{801_JM9130013}	AGTAATGTGA	GATACTTGTA	TGTAGAAGAT	TTAAAGAATT	CACCTTCAAA

Table 87: Comparative Sequences relating to SAG0645

msa123961.2{80_18RS21}	AGTAATGTGA	GATACTTGTA	TGTAGAAGAT	TTAAAGAATT	CACCTTCAAA
msa123961.2{80h_CJB110}	AGTAATGTGA	GATACTTGTA	TGTAGAAGAT	TTAAAGAATT	CACCTTCAAA
Consensus	*****	*****	*****	*****	*****
msa123961.2{80_2603}	CATTACCAAA	GCTTATGCTG	TACCGTTTGT	GTTGGAATTA	CCAGTTGCTA
msa123961.2{80_A909}	CATTACCAAA	GCTTATGCTG	TACCGTTTGT	GTTGGAATTA	CCAGTTGCTA
msa123961.2{80_M732}	CATTACCAAA	GCTTATGCTG	TACCGTTTGT	GTTGGAATTA	CCAGTTGCTA
msa123961.2{80_090}	CATTACCAAA	GCTTATGCTG	TACCGTTTGT	GTTGGAATTA	CCAGTTGCTA
msa123961.2{80_COH1}	CATTACCAAA	GCTTATGCTG	TACCGTTTGT	GTTGGAATTA	CCAGTTGCTA
msa123961.2{80_M781}	CATTACCAAA	GCTTATGCTG	TACCGTTTGT	GTTGGAATTA	CCAGTTGCTA
msa123961.2{801_JM9130013}	CATTACCAAA	GCTTATGCTG	TACCGTTTGT	GTTGGAATTA	CCAGTTGCTA
msa123961.2{80_18RS21}	CATTACCAAA	GCTTATGCTG	TACCGTTTGT	GTTGGAATTA	CCAGTTGCTA
msa123961.2{80h_CJB110}	CATTACCAAA	GCTTATGCTG	TACCGTTTGT	GTTGGAATTA	CCAGTTGCTA
Consensus	*****	*****	*****	*****	*****
msa123961.2{80_2603}	ACTCTACAGG	TACAGGTTTC	CTTTCTGAAA	TTAATATTTA	CCCTAAAAAC
msa123961.2{80_A909}	ACTCTACAGG	TACAGGTTTC	CTTTCTGAAA	TTAATATTTA	CCCTAAAAAC
msa123961.2{80_M732}	ACTCTACAGG	TACAGGTTTC	CTTTCTGAAA	TTAATATTTA	CCCTAAAAAC
msa123961.2{80_090}	ACTCTACAGG	TACAGGTTTC	CTTTCTGAAA	TTAATATTTA	CCCTAAAAAC
msa123961.2{80_COH1}	ACTCTACAGG	TACAGGTTTC	CTTTCTGAAA	TTAATATTTA	CCCTAAAAAC
msa123961.2{80_M781}	ACTCTACAGG	TACAGGTTTC	CTTTCTGAAA	TTAATATTTA	CCCTAAAAAC
msa123961.2{801_JM9130013}	ACTCTACAGG	TACAGGTTTC	CTTTCTGAAA	TTAATATTTA	CCCTAAAAAC
msa123961.2{80_18RS21}	ACTCTACAGG	TACAGGTTTC	CTTTCTGAAA	TTAATATTTA	CCCTAAAAAC
msa123961.2{80h_CJB110}	ACTCTACAGG	TACAGGTTTC	CTTTCTGAAA	TTAATATTTA	CCCTAAAAAC
Consensus	*****	*****	*****	*****	*****
msa123961.2{80_2603}	GTTGTAAGT	ATGAACCAAA	AACAGATAAA	GATGTTAAAA	AATTAGGTCA
msa123961.2{80_A909}	GTTGTAAGT	ATGAACCAAA	AACAGATAAA	GATGTTAAAA	AATTAGGTCA
msa123961.2{80_M732}	GTTGTAAGT	ATGAACCAAA	AACAGATAAA	GATGTTAAAA	AATTAGGTCA
msa123961.2{80_090}	GTTGTAAGT	ATGAACCAAA	AACAGATAAA	GATGTTAAAA	AATTAGGTCA
msa123961.2{80_COH1}	GTTGTAAGT	ATGAACCAAA	AACAGATAAA	GATGTTAAAA	AATTAGGTCA
msa123961.2{80_M781}	GTTGTAAGT	ATGAACCAAA	AACAGATAAA	GATGTTAAAA	AATTAGGTCA
msa123961.2{801_JM9130013}	GTTGTAAGT	ATGAACCAAA	AACAGATAAA	GATGTTAAAA	AATTAGGTCA
msa123961.2{80_18RS21}	GTTGTAAGT	ATGAACCAAA	AACAGATAAA	GATGTTAAAA	AATTAGGTCA
msa123961.2{80h_CJB110}	GTTGTAAGT	ATGAACCAAA	AACAGATAAA	GATGTTAAAA	AATTAGGTCA
Consensus	*****	*****	*****	*****	*****
msa123961.2{80_2603}	GGACGATGCA	GGTTATACGA	TTGGTGAAGA	ATTCAAATGG	TTCTTGAAAT
msa123961.2{80_A909}	GGACGATGCA	GGTTATACGA	TTGGTGAAGA	ATTCAAATGG	TTCTTGAAAT
msa123961.2{80_M732}	GGACGATGCA	GGTTATACGA	TTGGTGAAGA	ATTCAAATGG	TTCTTGAAAT
msa123961.2{80_090}	GGACGATGCA	GGTTATACGA	TTGGTGAAGA	ATTCAAATGG	TTCTTGAAAT
msa123961.2{80_COH1}	GGACGATGCA	GGTTATACGA	TTGGTGAAGA	ATTCAAATGG	TTCTTGAAAT
msa123961.2{80_M781}	GGACGATGCA	GGTTATACGA	TTGGTGAAGA	ATTCAAATGG	TTCTTGAAAT
msa123961.2{801_JM9130013}	GGACGATGCA	GGTTATACGA	TTGGTGAAGA	ATTCAAATGG	TTCTTGAAAT
msa123961.2{80_18RS21}	GGACGATGCA	GGTTATACGA	TTGGTGAAGA	ATTCAAATGG	TTCTTGAAAT
msa123961.2{80h_CJB110}	GGACGATGCA	GGTTATACGA	TTGGTGAAGA	ATTCAAATGG	TTCTTGAAAT
Consensus	*****	*****	*****	*****	*****
msa123961.2{80_2603}	CTACAATCCC	TGCCAATTTA	GGTGACTATG	AAAAATTTGA	AATTACTGAT
msa123961.2{80_A909}	CTACAATCCC	TGCCAATTTA	GGTGACTATG	AAAAATTTGA	AATTACTGAT
msa123961.2{80_M732}	CTACAATCCC	TGCCAATTTA	GGTGACTATG	AAAAATTTGA	AATTACTGAT
msa123961.2{80_090}	CTACAATCCC	TGCCAATTTA	GGTGACTATG	AAAAATTTGA	AATTACTGAT
msa123961.2{80_COH1}	CTACAATCCC	TGCCAATTTA	GGTGACTATG	AAAAATTTGA	AATTACTGAT
msa123961.2{80_M781}	CTACAATCCC	TGCCAATTTA	GGTGACTATG	AAAAATTTGA	AATTACTGAT
msa123961.2{801_JM9130013}	CTACAATCCC	TGCCAATTTA	GGTGACTATG	AAAAATTTGA	AATTACTGAT
msa123961.2{80_18RS21}	CTACAATCCC	TGCCAATTTA	GGTGACTATG	AAAAATTTGA	AATTACTGAT
msa123961.2{80h_CJB110}	CTACAATCCC	TGCCAATTTA	GGTGACTATG	AAAAATTTGA	AATTACTGAT
Consensus	*****	*****	*****	*****	*****
msa123961.2{80_2603}	AAATTTGCAG	ATGGCTTGAC	TTATAAATCT	GTTGGAAAAA	TCAAGATTGG
msa123961.2{80_A909}	AAATTTGCAG	ATGGCTTGAC	TTATAAATCT	GTTGGAAAAA	TCAAGATTGG
msa123961.2{80_M732}	AAATTTGCAG	ATGGCTTGAC	TTATAAATCT	GTTGGAAAAA	TCAAGATTGG
msa123961.2{80_090}	AAATTTGCAG	ATGGCTTGAC	TTATAAATCT	GTTGGAAAAA	TCAAGATTGG
msa123961.2{80_COH1}	AAATTTGCAG	ATGGCTTGAC	TTATAAATCT	GTTGGAAAAA	TCAAGATTGG
msa123961.2{80_M781}	AAATTTGCAG	ATGGCTTGAC	TTATAAATCT	GTTGGAAAAA	TCAAGATTGG
msa123961.2{801_JM9130013}	AAATTTGCAG	ATGGCTTGAC	TTATAAATCT	GTTGGAAAAA	TCAAGATTGG
msa123961.2{80_18RS21}	AAATTTGCAG	ATGGCTTGAC	TTATAAATCT	GTTGGAAAAA	TCAAGATTGG
msa123961.2{80h_CJB110}	AAATTTGCAG	ATGGCTTGAC	TTATAAATCT	GTTGGAAAAA	TCAAGATTGG
Consensus	*****	*****	*****	*****	*****
msa123961.2{80_2603}	TTCGAAAACA	CTGAATAGAG	ATGAGCACTA	CACTATTGAT	GAACCAACAG
msa123961.2{80_A909}	TTCGAAAACA	CTGAATAGAG	ATGAGCACTA	CACTATTGAT	GAACCAACAG
msa123961.2{80_M732}	TTCGAAAACA	CTGAATAGAG	ATGAGCACTA	CACTATTGAT	GAACCAACAG
msa123961.2{80_090}	TTCGAAAACA	CTGAATAGAG	ATGAGCACTA	CACTATTGAT	GAACCAACAG
msa123961.2{80_COH1}	TTCGAAAACA	CTGAATAGAG	ATGAGCACTA	CACTATTGAT	GAACCAACAG
msa123961.2{80_M781}	TTCGAAAACA	CTGAATAGAG	ATGAGCACTA	CACTATTGAT	GAACCAACAG

Table 87: Comparative Sequences relating to SAG0645

msa123961.2{801_JM9130013}	TTCGAAAACA	CTGAATAGAG	ATGAGCACTA	CACTATTGAT	GAACCAACAG
msa123961.2{80_18RS21}	TTCGAAAACA	CTGAATAGAG	ATGAGCACTA	CACTATTGAT	GAACCAACAG
msa123961.2{80h_CJB110}	TTCGAAAACA	CTGAATAGAG	ATGAGCACTA	CACTATTGAT	GAACCAACAG
Consensus	*****	*****	*****	*****	*****
851					
msa123961.2{80_2603}	TTGATAACCA	AAATACATTA	AAAATTACGT	TTAAACCAGA	GAAATTTAAA
msa123961.2{80_A909}	TTGATAACCA	AAATACATTA	AAAATTACGT	TTAAACCAGA	GAAATTTAAA
msa123961.2{80_M732}	TTGATAACCA	AAATACATTA	AAAATTACGT	TTAAACCAGA	GAAATTTAAA
msa123961.2{80_090}	TTGATAACCA	AAATACATTA	AAAATTACGT	TTAAACCAGA	GAAATTTAAA
msa123961.2{80_COH1}	TTGATAACCA	AAATACATTA	AAAATTACGT	TTAAACCAGA	GAAATTTAAA
msa123961.2{80_M781}	TTGATAACCA	AAATACATTA	AAAATTACGT	TTAAACCAGA	GAAATTTAAA
msa123961.2{801_JM9130013}	TTGATAACCA	AAATACATTA	AAAATTACGT	TTAAACCAGA	GAAATTTAAA
msa123961.2{80_18RS21}	TTGATAACCA	AAATACATTA	AAAATTACGT	TTAAACCAGA	GAAATTTAAA
msa123961.2{80h_CJB110}	TTGATAACCA	AAATACATTA	AAAATTACGT	TTAAACCAGA	GAAATTTAAA
Consensus	*****	*****	*****	*****	*****
901					
msa123961.2{80_2603}	GAAATTGCTG	AGCTACTTAA	AGGAATGACC	CTTGTTAAAA	ATCAAGATGC
msa123961.2{80_A909}	GAAATTGCTG	AGCTACTTAA	AGGAATGACC	CTTGTTAAAA	ATCAAGATGC
msa123961.2{80_M732}	GAAATTGCTG	AGCTACTTAA	AGGAATGACC	CTTGTTAAAA	ATCAAGATGC
msa123961.2{80_090}	GAAATTGCTG	AGCTACTTAA	AGGAATGACC	CTTGTTAAAA	ATCAAGATGC
msa123961.2{80_COH1}	GAAATTGCTG	AGCTACTTAA	AGGAATGACC	CTTGTTAAAA	ATCAAGATGC
msa123961.2{80_M781}	GAAATTGCTG	AGCTACTTAA	AGGAATGACC	CTTGTTAAAA	ATCAAGATGC
msa123961.2{801_JM9130013}	GAAATTGCTG	AGCTACTTAA	AGGAATGACC	CTTGTTAAAA	ATCAAGATGC
msa123961.2{80_18RS21}	GAAATTGCTG	AGCTACTTAA	AGGAATGACC	CTTGTTAAAA	ATCAAGATGC
msa123961.2{80h_CJB110}	GAAATTGCTG	AGCTACTTAA	AGGAATGACC	CTTGTTAAAA	ATCAAGATGC
Consensus	*****	*****	*****	*****	*****
951					
msa123961.2{80_2603}	TCTTGATAAA	GCTACTGCAA	ATACAGATGA	TGCGGCATTT	TTGGAAATTC
msa123961.2{80_A909}	TCTTGATAAA	GCTACTGCAA	ATACAGATGA	TGCGGCATTT	TTGGAAATTC
msa123961.2{80_M732}	TCTTGATAAA	GCTACTGCAA	ATACAGATGA	TGCGGCATTT	TTGGAAATTC
msa123961.2{80_090}	TCTTGATAAA	GCTACTGCAA	ATACAGATGA	TGCGGCATTT	TTGGAAATTC
msa123961.2{80_COH1}	TCTTGATAAA	GCTACTGCAA	ATACAGATGA	TGCGGCATTT	TTGGAAATTC
msa123961.2{80_M781}	TCTTGATAAA	GCTACTGCAA	ATACAGATGA	TGCGGCATTT	TTGGAAATTC
msa123961.2{801_JM9130013}	TCTTGATAAA	GCTACTGCAA	ATACAGATGA	TGCGGCATTT	TTGGAAATTC
msa123961.2{80_18RS21}	TCTTGATAAA	GCTACTGCAA	ATACAGATGA	TGCGGCATTT	TTGGAAATTC
msa123961.2{80h_CJB110}	TCTTGATAAA	GCTACTGCAA	ATACAGATGA	TGCGGCATTT	TTGGAAATTC
Consensus	*****	*****	*****	*****	*****
1001					
msa123961.2{80_2603}	CAGTTGCATC	AACATTAAT	GAAAAAGCAG	TTTtagGAAA	AGCAATTGAA
msa123961.2{80_A909}	CAGTTGCATC	AACATTAAT	GAAAAAGCAG	TTTtagGAAA	AGCAATTGAA
msa123961.2{80_M732}	CAGTTGCATC	AACATTAAT	GAAAAAGCAG	TTTtagGAAA	AGCAATTGAA
msa123961.2{80_090}	CAGTTGCATC	AACATTAAT	GAAAAAGCAG	TTTtagGAAA	AGCAATTGAA
msa123961.2{80_COH1}	CAGTTGCATC	AACATTAAT	GAAAAAGCAG	TTTtagGAAA	AGCAATTGAA
msa123961.2{80_M781}	CAGTTGCATC	AACATTAAT	GAAAAAGCAG	TTTtagGAAA	AGCAATTGAA
msa123961.2{801_JM9130013}	CAGTTGCATC	AACATTAAT	GAAAAAGCAG	TTTtagGAAA	AGCAATTGAA
msa123961.2{80_18RS21}	CAGTTGCATC	AACATTAAT	GAAAAAGCAG	TTTtagGAAA	AGCAATTGAA
msa123961.2{80h_CJB110}	CAGTTGCATC	AACATTAAT	GAAAAAGCAG	TTTtagGAAA	AGCAATTGAA
Consensus	*****	*****	*****	*****	*****
1051					
msa123961.2{80_2603}	AATACTTTTG	AACCTCAATA	TGACCATACT	CCTGATAAAG	CTGACAAATCC
msa123961.2{80_A909}	AATACTTTTG	AACCTCAATA	TGACCATACT	CCTGATAAAG	CTGACAAATCC
msa123961.2{80_M732}	AATACTTTTG	AACCTCAATA	TGACCATACT	CCTGATAAAG	CTGACAAATCC
msa123961.2{80_090}	AATACTTTTG	AACCTCAATA	TGACCATACT	CCTGATAAAG	CTGACAAATCC
msa123961.2{80_COH1}	AATACTTTTG	AACCTCAATA	TGACCATACT	CCTGATAAAG	CTGACAAATCC
msa123961.2{80_M781}	AATACTTTTG	AACCTCAATA	TGACCATACT	CCTGATAAAG	CTGACAAATCC
msa123961.2{801_JM9130013}	AATACTTTTG	AACCTCAATA	TGACCATACT	CCTGATAAAG	CTGACAAATCC
msa123961.2{80_18RS21}	AATACTTTTG	AACCTCAATA	TGACCATACT	CCTGATAAAG	CTGACAAATCC
msa123961.2{80h_CJB110}	AATACTTTTG	AACCTCAATA	TGACCATACT	CCTGATAAAG	CTGACAAATCC
Consensus	*****	*****	*****	*****	*****
1101					
msa123961.2{80_2603}	AAAACCATCT	AATCCTCCAA	GAAAAACCAGA	AGTTCATACT	GGTGGGAAAC
msa123961.2{80_A909}	AAAACCATCT	AATCCTCCAA	GAAAAACCAGA	AGTTCATACT	GGTGGGAAAC
msa123961.2{80_M732}	AAAACCATCT	AATCCTCCAA	GAAAAACCAGA	AGTTCATACT	GGTGGGAAAC
msa123961.2{80_090}	AAAACCATCT	AATCCTCCAA	GAAAAACCAGA	AGTTCATACT	GGTGGGAAAC
msa123961.2{80_COH1}	AAAACCATCT	AATCCTCCAA	GAAAAACCAGA	AGTTCATACT	GGTGGGAAAC
msa123961.2{80_M781}	AAAACCATCT	AATCCTCCAA	GAAAAACCAGA	AGTTCATACT	GGTGGGAAAC
msa123961.2{801_JM9130013}	AAAACCATCT	AATCCTCCAA	GAAAAACCAGA	AGTTCATACT	GGTGGGAAAC
msa123961.2{80_18RS21}	AAAACCATCT	AATCCTCCAA	GAAAAACCAGA	AGTTCATACT	GGTGGGAAAC
msa123961.2{80h_CJB110}	AAAACCATCT	AATCCTCCAA	GAAAAACCAGA	AGTTCATACT	GGTGGGAAAC
Consensus	*****	*****	*****	*****	*****
1151					
msa123961.2{80_2603}	GATTTGTAAA	GAAAGACTCA	ACAGAAACAC	AAACACTAGG	TGGTGCTGAG
msa123961.2{80_A909}	GATTTGTAAA	GAAAGACTCA	ACAGAAACAC	AAACACTAGG	TGGTGCTGAG
msa123961.2{80_M732}	GATTTGTAAA	GAAAGACTCA	ACAGAAACAC	AAACACTAGG	TGGTGCTGAG
msa123961.2{80_090}	GATTTGTAAA	GAAAGACTCA	ACAGAAACAC	AAACACTAGG	TGGTGCTGAG
msa123961.2{80_COH1}	GATTTGTAAA	GAAAGACTCA	ACAGAAACAC	AAACACTAGG	TGGTGCTGAG

Table 87: Comparative Sequences relating to SAG0645

msa123961.2{80_M781}	GATTTGTAAA	GAAAGACTCA	ACAGAAACAC	AAACACTAGG	TGGTGCTGAG
msa123961.2{801_JM9130013}	GATTTGTAAA	GAAAGACTCA	ACAGAAACAC	AAACACTAGG	TGGTGCTGAG
msa123961.2{80_18RS21}	GATTTGTAAA	GAAAGACTCA	ACAGAAACAC	AAACACTAGG	TGGTGCTGAG
msa123961.2{80h_CJB110}	GATTTGTAAA	GAAAGACTCA	ACAGAAACAC	AAACACTAGG	TGGTGCTGAG
Consensus	*****	*****	*****	*****	*****
msa123961.2{80_2603}	TTTGATTTGT	TGGCTTCTGA	TGGGACAGCA	GTAAAATGGA	CAGATGCTCT
msa123961.2{80_A909}	TTTGATTTGT	TGGCTTCTGA	TGGGACAGCA	GTAAAATGGA	CAGATGCTCT
msa123961.2{80_M732}	TTTGATTTGT	TGGCTTCTGA	TGGGACAGCA	GTAAAATGGA	CAGATGCTCT
msa123961.2{80_090}	TTTGATTTGT	TGGCTTCTGA	TGGGACAGCA	GTAAAATGGA	CAGATGCTCT
msa123961.2{80_COH1}	TTTGATTTGT	TGGCTTCTGA	TGGGACAGCA	GTAAAATGGA	CAGATGCTCT
msa123961.2{80_M781}	TTTGATTTGT	TGGCTTCTGA	TGGGACAGCA	GTAAAATGGA	CAGATGCTCT
msa123961.2{801_JM9130013}	TTTGATTTGT	TGGCTTCTGA	TGGGACAGCA	GTAAAATGGA	CAGATGCTCT
msa123961.2{80_18RS21}	TTTGATTTGT	TGGCTTCTGA	TGGGACAGCA	GTAAAATGGA	CAGATGCTCT
msa123961.2{80h_CJB110}	TTTGATTTGT	TGGCTTCTGA	TGGGACAGCA	GTAAAATGGA	CAGATGCTCT
Consensus	*****	*****	*****	*****	*****
msa123961.2{80_2603}	TATTAAGCG	AATACTAATA	AAACTATAT	TGCTGGAGAA	GCTGTTACTG
msa123961.2{80_A909}	TATTAAGCG	AATACTAATA	AAACTATAT	TGCTGGAGAA	GCTGTTACTG
msa123961.2{80_M732}	TATTAAGCG	AATACTAATA	AAACTATAT	TGCTGGAGAA	GCTGTTACTG
msa123961.2{80_090}	TATTAAGCG	AATACTAATA	AAACTATAT	TGCTGGAGAA	GCTGTTACTG
msa123961.2{80_COH1}	TATTAAGCG	AATACTAATA	AAACTATAT	TGCTGGAGAA	GCTGTTACTG
msa123961.2{80_M781}	TATTAAGCG	AATACTAATA	AAACTATAT	TGCTGGAGAA	GCTGTTACTG
msa123961.2{801_JM9130013}	TATTAAGCG	AATACTAATA	AAACTATAT	TGCTGGAGAA	GCTGTTACTG
msa123961.2{80_18RS21}	TATTAAGCG	AATACTAATA	AAACTATAT	TGCTGGAGAA	GCTGTTACTG
msa123961.2{80h_CJB110}	TATTAAGCG	AATACTAATA	AAACTATAT	TGCTGGAGAA	GCTGTTACTG
Consensus	*****	*****	*****	*****	*****
msa123961.2{80_2603}	GGCAACCAAT	CAAATTGAAA	TCACATACAG	ACGGTACGTT	TGAGATTAAA
msa123961.2{80_A909}	GGCAACCAAT	CAAATTGAAA	TCACATACAG	ACGGTACGTT	TGAGATTAAA
msa123961.2{80_M732}	GGCAACCAAT	CAAATTGAAA	TCACATACAG	ACGGTACGTT	TGAGATTAAA
msa123961.2{80_090}	GGCAACCAAT	CAAATTGAAA	TCACATACAG	ACGGTACGTT	TGAGATTAAA
msa123961.2{80_COH1}	GGCAACCAAT	CAAATTGAAA	TCACATACAG	ACGGTACGTT	TGAGATTAAA
msa123961.2{80_M781}	GGCAACCAAT	CAAATTGAAA	TCACATACAG	ACGGTACGTT	TGAGATTAAA
msa123961.2{801_JM9130013}	GGCAACCAAT	CAAATTGAAA	TCACATACAG	ACGGTACGTT	TGAGATTAAA
msa123961.2{80_18RS21}	GGCAACCAAT	CAAATTGAAA	TCACATACAG	ACGGTACGTT	TGAGATTAAA
msa123961.2{80h_CJB110}	GGCAACCAAT	CAAATTGAAA	TCACATACAG	ACGGTACGTT	TGAGATTAAA
Consensus	*****	*****	*****	*****	*****
msa123961.2{80_2603}	GGTTTGGCTT	ATGCAGTTGA	TGCGAATGCA	GAGGGTACAG	CAGTAACTTA
msa123961.2{80_A909}	GGTTTGGCTT	ATGCAGTTGA	TGCGAATGCA	GAGGGTACAG	CAGTAACTTA
msa123961.2{80_M732}	GGTTTGGCTT	ATGCAGTTGA	TGCGAATGCA	GAGGGTACAG	CAGTAACTTA
msa123961.2{80_090}	GGTTTGGCTT	ATGCAGTTGA	TGCGAATGCA	GAGGGTACAG	CAGTAACTTA
msa123961.2{80_COH1}	GGTTTGGCTT	ATGCAGTTGA	TGCGAATGCA	GAGGGTACAG	CAGTAACTTA
msa123961.2{80_M781}	GGTTTGGCTT	ATGCAGTTGA	TGCGAATGCA	GAGGGTACAG	CAGTAACTTA
msa123961.2{801_JM9130013}	GGTTTGGCTT	ATGCAGTTGA	TGCGAATGCA	GAGGGTACAG	CAGTAACTTA
msa123961.2{80_18RS21}	GGTTTGGCTT	ATGCAGTTGA	TGCGAATGCA	GAGGGTACAG	CAGTAACTTA
msa123961.2{80h_CJB110}	GGTTTGGCTT	ATGCAGTTGA	TGCGAATGCA	GAGGGTACAG	CAGTAACTTA
Consensus	*****	*****	*****	*****	*****
msa123961.2{80_2603}	CAAATTAAAA	GAAACAAAAG	CACCAGAAGG	TTATGTAATC	CCTGATAAAG
msa123961.2{80_A909}	CAAATTAAAA	GAAACAAAAG	CACCAGAAGG	TTATGTAATC	CCTGATAAAG
msa123961.2{80_M732}	CAAATTAAAA	GAAACAAAAG	CACCAGAAGG	TTATGTAATC	CCTGATAAAG
msa123961.2{80_090}	CAAATTAAAA	GAAACAAAAG	CACCAGAAGG	TTATGTAATC	CCTGATAAAG
msa123961.2{80_COH1}	CAAATTAAAA	GAAACAAAAG	CACCAGAAGG	TTATGTAATC	CCTGATAAAG
msa123961.2{80_M781}	CAAATTAAAA	GAAACAAAAG	CACCAGAAGG	TTATGTAATC	CCTGATAAAG
msa123961.2{801_JM9130013}	CAAATTAAAA	GAAACAAAAG	CACCAGAAGG	TTATGTAATC	CCTGATAAAG
msa123961.2{80_18RS21}	CAAATTAAAA	GAAACAAAAG	CACCAGAAGG	TTATGTAATC	CCTGATAAAG
msa123961.2{80h_CJB110}	CAAATTAAAA	GAAACAAAAG	CACCAGAAGG	TTATGTAATC	CCTGATAAAG
Consensus	*****	*****	*****	*****	*****
msa123961.2{80_2603}	AAATCGAGTT	TACAGTATCA	CAAACATCTT	ATAATaCAA	ACCAACTGAC
msa123961.2{80_A909}	AAATCGAGTT	TACAGTATCA	CAAACATCTT	ATAATaCAA	ACCAACTGAC
msa123961.2{80_M732}	AAATCGAGTT	TACAGTATCA	CAAACATCTT	ATAATaCAA	ACCAACTGAC
msa123961.2{80_090}	AAATCGAGTT	TACAGTATCA	CAAACATCTT	ATAATaCAA	ACCAACTGAC
msa123961.2{80_COH1}	AAATCGAGTT	TACAGTATCA	CAAACATCTT	ATAATaCAA	ACCAACTGAC
msa123961.2{80_M781}	AAATCGAGTT	TACAGTATCA	CAAACATCTT	ATAATaCAA	ACCAACTGAC
msa123961.2{801_JM9130013}	AAATCGAGTT	TACAGTATCA	CAAACATCTT	ATAATaCAA	ACCAACTGAC
msa123961.2{80_18RS21}	AAATCGAGTT	TACAGTATCA	CAAACATCTT	ATAATaCAA	ACCAACTGAC
msa123961.2{80h_CJB110}	AAATCGAGTT	TACAGTATCA	CAAACATCTT	ATAATaCAA	ACCAACTGAC
Consensus	*****	*****	*****	*****	*****
msa123961.2{80_2603}	ATCACGGTTG	ATAGTGCTGA	TGCAACACCT	GATACAATTA	AAAACAACAA
msa123961.2{80_A909}	ATCACGGTTG	ATAGTGCTGA	TGCAACACCT	GATACAATTA	AAAACAACAA
msa123961.2{80_M732}	ATCACGGTTG	ATAGTGCTGA	TGCAACACCT	GATACAATTA	AAAACAACAA
msa123961.2{80_090}	ATCACGGTTG	ATAGTGCTGA	TGCAACACCT	GATACAATTA	AAAACAACAA

Table 87: Comparative Sequences relating to SAG0645

msa123961.2{80_COH1}	ATCACGGTTG	ATAGTGCTGA	TGCAACACCT	GATACAATTA	AAAACAACAA
msa123961.2{80_M781}	ATCACGGTTG	ATAGTGCTGA	TGCAACACCT	GATACAATTA	AAAACAACAA
msa123961.2{801_JM9130013}	ATCACGGTTG	ATAGTGCTGA	TGCAACACCT	GATACAATTA	AAAACAACAA
msa123961.2{80_18RS21}	ATCACGGTTG	ATAGTGCTGA	TGCAACACCT	GATACAATTA	AAAACAACAA
msa123961.2{80h_CJB110}	ATCACGGTTG	ATAGTGCTGA	TGCAACACCT	GATACAATTA	AAAACAACAA
Consensus	*****	*****	*****	*****	*****
1551					
msa123961.2{80_2603}	acgtccttca	atccctaata	ctgggtggtat	tggtacggct	atctttgtcg
msa123961.2{80_A909}	-----	-----	-----	-----	-----
msa123961.2{80_M732}	acgtccttca	-----	-----	-----	-----
msa123961.2{80_090}	acgtccttca	-----	-----	-----	-----
msa123961.2{80_COH1}	acgtccttca	-----	-----	-----	-----
msa123961.2{80_M781}	acgt-----	-----	-----	-----	-----
msa123961.2{801_JM9130013}	acgtccttca	-----	-----	-----	-----
msa123961.2{80_18RS21}	acgtccttca	-----	-----	-----	-----
msa123961.2{80h_CJB110}	acgtccttca	-----	-----	-----	-----
Consensus	-----	-----	-----	-----	-----
1601					
msa123961.2{80_2603}	ctatcggtgc	tgcggtgatg	gcttttgcgtg	ttaaggggat	gaagcgctcg
msa123961.2{80_A909}	-----	-----	-----	-----	-----
msa123961.2{80_M732}	-----	-----	-----	-----	-----
msa123961.2{80_090}	-----	-----	-----	-----	-----
msa123961.2{80_COH1}	-----	-----	-----	-----	-----
msa123961.2{80_M781}	-----	-----	-----	-----	-----
msa123961.2{801_JM9130013}	-----	-----	-----	-----	-----
msa123961.2{80_18RS21}	-----	-----	-----	-----	-----
msa123961.2{80h_CJB110}	-----	-----	-----	-----	-----
Consensus	-----	-----	-----	-----	-----
1651					
msa123961.2{80_2603}	acaaaagata	ac			
msa123961.2{80_A909}	-----	--			
msa123961.2{80_M732}	-----	--			
msa123961.2{80_090}	-----	--			
msa123961.2{80_COH1}	-----	--			
msa123961.2{80_M781}	-----	--			
msa123961.2{801_JM9130013}	-----	--			
msa123961.2{80_18RS21}	-----	--			
msa123961.2{80h_CJB110}	-----	--			
Consensus	-----	--			

SEQ ID NO. 8710

STRAIN 2603 frame: 1

MKLSKKLLFSAAVLTMVAGSTVEPVAQFATGMSIVRAAEVSQERPAKTTVNIYKLQADSY
 KSEITSNGGIENKDGEVISNYAKLGDNVKGLQGVQFKRYKVKTDISVDELKKLTTVEAAD
 AKVGTILEEGVSLPQKTNAQGLVVDALDSKSNVRYLYVEDLKNSPSNITKAYAVPFVLEL
 PVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLGQDDAGYTI GEEFKWFLKSTIPANL
 GDYEKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHYTIDEPTVDNQNTLKITFKPEKFK
 EIAELLKGMTLVKNQDALDKATANTDDAAFLEIPVASTINEKAVLGKAIENFELQYDHT
 PDKADNPKNPNPRKPEVHTGGKRFVKKDSTETQTLGGAEFDLLASDGTAVKWTDALIKA
 NTNKNYIAGEAVTGQPIKLKSHDTGTFEIKGLAYAVDANAEGTAVTYKLKETKAPEGYVI
 PDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNKRPSIPTGGIGTAIFVAIGAAM
 AFAVKGMKRRTKDN

SEQ ID NO. 8711

STRAIN 090 frame: 1

AEVSQERPAKTAVNIYKLQADSYKSEITSNGGIENKDGEVISNYAKLGDNVKGLQGVQFK
 RYKVKTDISVDELKKLTTVEAADAKVGTILEEGVSLPQKTNAQGLVVDALDSKSNVRYLY
 VEDLKNSPSNITKAYAVPFVLELPVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLGQ
 DDAGYTI GEEFKWFLKSTIPANLGDYEKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
 TIDEPTVDNQNTLKITFKPEKFK EIAELLKGMTLVKNQDALDKATANTDDAAFLEIPVAS
 TINEKAVLGKAIENFELQYDHTPDKADNPKNPNPRKPEVHTGGKRFVKKDSTETQTLG
 GAEFDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIKLKSHDTGTFEIKGLAYAVD
 ANAEGTAVTYKLKETKAPEGYVIPDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNK
 RPS

SEQ ID NO. 8712

STRAIN 18RS21 frame: 1

AEVSQERPAKTAVNIYKLQADSYKSEITSNGGIENKDGEVISNYAKLGDNVKGLQGVQFK
 RYKVKTDISVDELKKLTTVEAADAKVGTILEEGVSLPQKTNAQGLVVDALDSKSNVRYLY
 VEDLKNSPSNITKAYAVPFVLELPVANSTGTGFLSEINIYPKNVVTDEPKTDKDVK.LGQ
 DDAGYTI GEEFKWFLKSTIPANLGDYEKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
 TIDEPTVDNQNTLKITFKPEKFK EIAELLKGMTLVKNQDALDKATANTDDAAFLEIPVAS
 TINEKAVLGKAIENFELQYDHTPDKADNPKNPNPRKPEVHTGGKRFVKKDSTETQTLG
 GAEFDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIKLKSHDTGTFEIKGLAYAVD
 ANAEGTAVTYKLKETKAPEGYVIPDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNK
 RPS

SEQ ID NO. 8713

STRAIN M732 frame: 1

AEVSQERPAKTTVNIYKLQADSYKSEITSNGGIENKDGEVISNYAKLGDNVKGLQGVQFK

Table 87: Comparative Sequences relating to SAG0645

RYKVKTDISVDELKKLTVEAADAKVGITILEEGVSLPQKTNAQGLVVDALDSKSNVRYLY
VEDLKNSPSNITKAYAVPFVLELPVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLGQ
DDAGYTI GEEFKWFLKSTIPANLGDYEKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
TIDEPTVDNQNTLKITFKPEKFKEIAELLKGMTLVKNQDALDKATANTDDAAFLEIPVAS
TINEKAVLGKAIENTFELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVKKDSTETQTLG
GAEFDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIKLKSHTDGTFEIKGLAYAVD
ANAEGTAVTYKLKETKAPEGYVIPDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNK
RPS

SEQ ID NO. 8714

STRAIN M781 frame: 1

AEVSQERPAKTAVNIYKLQADSYKSEITSNGGIENKDGEVISNYAKLGDNVKGLQGVQFK
RYKVKTDISVDELKKLTVEAADAKVGITILEEGVSLPQKTNAQGLVVDALDSKSNVRYLY
VEDLKNSPSNITKAYAVPFVLELPVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLGQ
DDAGYTI GEEFKWFLKSTIPANLGDYEKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
TIDEPTVDNQNTLKITFKPEKFKEIAELLKGMTLVKNQDALDKATANTDDAAFLEIPVAS
TINEKAVLGKAIENTFELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVKKDSTETQTLG
GAEFDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIKLKSHTDGTFEIKGLAYAVD
ANAEGTAVTYKLKETKAPEGYVIPDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNK
R

SEQ ID NO. 8715

STRAIN COH1 frame: 1

AEVSQERPAKTAVNIYKLQADSYKSEITSNGGIENKDGEVISNYAKLGDNVKGLQGVQFK
RYKVKTDISVDELKKLTVEAADAKVGITILEEGVSLPQKTNAQGLVVDALDSKSNVRYLY
VEDLKNSPSNITKAYAVPFVLELPVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLGQ
DDAGYTI GEEFKWFLKSTIPANLGDYEKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
TIDEPTVDNQNTLKITFKPEKFKEIAELLKGMTLVKNQDALDKATANTDDAAFLEIPVAS
TINEKAVLGKAIENTFELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVKKDSTETQTLG
GAEFDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIKLKSHTDGTFEIKGLAYAVD
ANAEGTAVTYKLKETKAPEGYVIPDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNK
RPS

SEQ ID NO. 8716

STRAIN CJB110 frame: 1

AEVSQERPAKTAVNIYKLQADSYKSEITSNGGIENKDGEVISNYAKLGDNVKGLQGVQFK
RYKVKTDISVDELKKLTVEAADAKVGITILEEGVSLPQKTNAQGLVVDALDSKSNVRYLY
VEDLKNSPSNITKAYAVPFVLELPVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLGQ
DDAGYTI GEEFKWFLKSTIPANLGDYEKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
TIDEPTVDNQNTLKITFKPEKFKEIAELLKGMTLVKNQDALDKATANTDDAAFLEIPVAS
TINEKAVLGKAIENTFELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVKKDSTETQTLG
GAEFDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIKLKSHTDGTFEIKGLAYAVD
ANAEGTAVTYKLKETKAPEGYVIPDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNK
RPS

SEQ ID NO. 8717

STRAIN JM9130013 frame: 1

AEVSQERPAKTAVNIYKLQADSYKSEITSNGGIENKDGEVISNYAKLGDNVKGLQGVQFK
RYKVKTDISVDELKKLTVEAADAKVGITILEEGVSLPQKTNAQGLVVDALDSKSNVRYLY
VEDLKNSPSNITKAYAVPFVLELPVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLGQ
DDAGYTI GEEFKWFLKSTIPANLGDYEKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
TIDEPTVDNQNTLKITFKPEKFKEIAELLKGMTLVKNQDALDKATANTDDAAFLEIPVAS
TINEKAVLGKAIENTFELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVKKDSTETQTLG
GAEFDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIKLKSHTDGTFEIKGLAYAVD
ANAEGTAVTYKLKETKAPEGYVIPDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNK
RPS

SEQ ID NO. 8718

STRAIN A909 frame: 1

AEVSQERPAKTAVNIYKLQADSYKSEITSNGGIENKDGEVISNYAKLGDNVKGLQGVQFK
RYKVKTDISVDELKKLTVEAADAKVGITILEEGVSLPQKTNAQGLVVDALDSKSNVRYLY
VEDLKNSPSNITKAYAVPFVLELPVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLGQ
DDAGYTI GEEFKWFLKSTIPANLGDYEKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
TIDEPTVDNQNTLKITFKPEKFKEIAELLKGMTLVKNQDALDKATANTDDAAFLEIPVAS
TINEKAVLGKAIENTFELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVKKDSTETQTLG
GAEFDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIKLKSHTDGTFEIKGLAYAVD
ANAEGTAVTYKLKETKAPEGYVIPDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNK

PRETTY of: /biotmp/msa124060.2{*} April 30, 2003 07:19 ..

	1				50
msa124060.2{80_2603}	mklskklfs	aavltmvags	tvepvaqfat	gmsivraAEV	SQERPAKTtV
msa124060.2{80_M732}	-----	-----	-----	-----AEV	SQERPAKTtV
msa124060.2{80_A909}	-----	-----	-----	-----AEV	SQERPAKTtV
msa124060.2{80_090}	-----	-----	-----	-----AEV	SQERPAKTaV
msa124060.2{80_M781}	-----	-----	-----	-----AEV	SQERPAKTaV
msa124060.2{80_COH1}	-----	-----	-----	-----AEV	SQERPAKTaV
msa124060.2{801_JM9130013}	-----	-----	-----	-----AEV	SQERPAKTaV
msa124060.2{80_18RS21}	-----	-----	-----	-----AEV	SQERPAKTaV
msa124060.2{80h_CJB110}	-----	-----	-----	-----AEV	SQERPAKTaV
Consensus	-----	-----	-----	-----***	*****-*

Table 87: Comparative Sequences relating to SAG0645

	51				100
msa124060.2{80_2603}	NIYKLQADSY	KsEITsNGGI	ENKDGEVISN	YAKLGDNVKG	LQGVQFKRYK
msa124060.2{80_M732}	NIYKLQADSY	KsEITsNGGI	ENKDGEVISN	YAKLGDNVKG	LQGVQFKRYK
msa124060.2{80_A909}	NIYKLQADSY	KsEITsNGGI	ENKDGEVISN	YAKLGDNVKG	LQGVQFKRYK
msa124060.2{80_090}	NIYKLQADSY	KsEITsNGGI	ENKDGEVISN	YAKLGDNVKG	LQGVQFKRYK
msa124060.2{80_M781}	NIYKLQADSY	KsEITsNGGI	ENKDGEVISN	YAKLGDNVKG	LQGVQFKRYK
msa124060.2{80_COH1}	NIYKLQADSY	KsEITsNGGI	ENKDGEVISN	YAKLGDNVKG	LQGVQFKRYK
msa124060.2{801_JM9130013}	NIYKLQADSY	KsEITsNGGI	ENKDGEVISN	YAKLGDNVKG	LQGVQFKRYK
msa124060.2{80_18RS21}	NIYKLQADSY	KsEITsNGGI	ENKDGEVISN	YAKLGDNVKG	LQGVQFKRYK
msa124060.2{80h_CJB110}	NIYKLQADSY	KLEITsNGGI	ENKDGEVISN	YAKLGDNVKG	LQGVQFKRYK
Consensus	*****	*-***-****	*****	*****	*****
	101				150
msa124060.2{80_2603}	VKTDISVDEL	KKLTTVEAAD	AKVGTILEEG	VSLPQKTNAQ	GLVVDALDSK
msa124060.2{80_M732}	VKTDISVDEL	KKLTTVEAAD	AKVGTILEEG	VSLPQKTNAQ	GLVVDALDSK
msa124060.2{80_A909}	VKTDISVDEL	KKLTTVEAAD	AKVGTILEEG	VSLPQKTNAQ	GLVVDALDSK
msa124060.2{80_090}	VKTDISVDEL	KKLTTVEAAD	AKVGTILEEG	VSLPQKTNAQ	GLVVDALDSK
msa124060.2{80_M781}	VKTDISVDEL	KKLTTVEAAD	AKVGTILEEG	VSLPQKTNAQ	GLVVDALDSK
msa124060.2{80_COH1}	VKTDISVDEL	KKLTTVEAAD	AKVGTILEEG	VSLPQKTNAQ	GLVVDALDSK
msa124060.2{801_JM9130013}	VKTDISVDEL	KKLTTVEAAD	AKVGTILEEG	VSLPQKTNAQ	GLVVDALDSK
msa124060.2{80_18RS21}	VKTDISVDEL	KKLTTVEAAD	AKVGTILEEG	VSLPQKTNAQ	GLVVDALDSK
msa124060.2{80h_CJB110}	VKTDISVDEL	KKLTTVEAAD	AKVGTILEEG	VSLPQKTNAQ	GLVVDALDSK
Consensus	*****	*****	*****	*****	*****
	151				200
msa124060.2{80_2603}	SNVRYLYVED	LKNSPSNITK	AYAVPFVLEL	PVANSTGTGF	LSEINIYPKN
msa124060.2{80_M732}	SNVRYLYVED	LKNSPSNITK	AYAVPFVLEL	PVANSTGTGF	LSEINIYPKN
msa124060.2{80_A909}	SNVRYLYVED	LKNSPSNITK	AYAVPFVLEL	PVANSTGTGF	LSEINIYPKN
msa124060.2{80_090}	SNVRYLYVED	LKNSPSNITK	AYAVPFVLEL	PVANSTGTGF	LSEINIYPKN
msa124060.2{80_M781}	SNVRYLYVED	LKNSPSNITK	AYAVPFVLEL	PVANSTGTGF	LSEINIYPKN
msa124060.2{80_COH1}	SNVRYLYVED	LKNSPSNITK	AYAVPFVLEL	PVANSTGTGF	LSEINIYPKN
msa124060.2{801_JM9130013}	SNVRYLYVED	LKNSPSNITK	AYAVPFVLEL	PVANSTGTGF	LSEINIYPKN
msa124060.2{80_18RS21}	SNVRYLYVED	LKNSPSNITK	AYAVPFVLEL	PVANSTGTGF	LSEINIYPKN
msa124060.2{80h_CJB110}	SNVRYLYVED	LKNSPSNITK	AYAVPFVLEL	PVANSTGTGF	LSEINIYPKN
Consensus	*****	*****	*****	*****	*****
	201				250
msa124060.2{80_2603}	VVTDEPKTDK	DVKkLGQDDA	GYTIGEEFKW	FLKSTIPANL	GDYEKFEITD
msa124060.2{80_M732}	VVTDEPKTDK	DVKkLGQDDA	GYTIGEEFKW	FLKSTIPANL	GDYEKFEITD
msa124060.2{80_A909}	VVTDEPKTDK	DVKkLGQDDA	GYTIGEEFKW	FLKSTIPANL	GDYEKFEITD
msa124060.2{80_090}	VVTDEPKTDK	DVKkLGQDDA	GYTIGEEFKW	FLKSTIPANL	GDYEKFEITD
msa124060.2{80_M781}	VVTDEPKTDK	DVKkLGQDDA	GYTIGEEFKW	FLKSTIPANL	GDYEKFEITD
msa124060.2{80_COH1}	VVTDEPKTDK	DVKkLGQDDA	GYTIGEEFKW	FLKSTIPANL	GDYEKFEITD
msa124060.2{801_JM9130013}	VVTDEPKTDK	DVKkLGQDDA	GYTIGEEFKW	FLKSTIPANL	GDYEKFEITD
msa124060.2{80_18RS21}	VVTDEPKTDK	DVKkLGQDDA	GYTIGEEFKW	FLKSTIPANL	GDYEKFEITD
msa124060.2{80h_CJB110}	VVTDEPKTDK	DVKkLGQDDA	GYTIGEEFKW	FLKSTIPANL	GDYEKFEITD
Consensus	*****	***-*****	*****	*****	*****
	251				300
msa124060.2{80_2603}	KFADGLTYKS	VGKIKIGSKT	LNRDEHYTID	EPTVDNQNTL	KITFKPEKFK
msa124060.2{80_M732}	KFADGLTYKS	VGKIKIGSKT	LNRDEHYTID	EPTVDNQNTL	KITFKPEKFK
msa124060.2{80_A909}	KFADGLTYKS	VGKIKIGSKT	LNRDEHYTID	EPTVDNQNTL	KITFKPEKFK
msa124060.2{80_090}	KFADGLTYKS	VGKIKIGSKT	LNRDEHYTID	EPTVDNQNTL	KITFKPEKFK
msa124060.2{80_M781}	KFADGLTYKS	VGKIKIGSKT	LNRDEHYTID	EPTVDNQNTL	KITFKPEKFK
msa124060.2{80_COH1}	KFADGLTYKS	VGKIKIGSKT	LNRDEHYTID	EPTVDNQNTL	KITFKPEKFK
msa124060.2{801_JM9130013}	KFADGLTYKS	VGKIKIGSKT	LNRDEHYTID	EPTVDNQNTL	KITFKPEKFK
msa124060.2{80_18RS21}	KFADGLTYKS	VGKIKIGSKT	LNRDEHYTID	EPTVDNQNTL	KITFKPEKFK
msa124060.2{80h_CJB110}	KFADGLTYKS	VGKIKIGSKT	LNRDEHYTID	EPTVDNQNTL	KITFKPEKFK
Consensus	*****	*****	*****	*****	*****
	301				350
msa124060.2{80_2603}	EIAELLKGMT	LVKNQDALDK	ATANTDDAAF	LEIPVASTIN	EKAVLGKAIE
msa124060.2{80_M732}	EIAELLKGMT	LVKNQDALDK	ATANTDDAAF	LEIPVASTIN	EKAVLGKAIE
msa124060.2{80_A909}	EIAELLKGMT	LVKNQDALDK	ATANTDDAAF	LEIPVASTIN	EKAVLGKAIE
msa124060.2{80_090}	EIAELLKGMT	LVKNQDALDK	ATANTDDAAF	LEIPVASTIN	EKAVLGKAIE
msa124060.2{80_M781}	EIAELLKGMT	LVKNQDALDK	ATANTDDAAF	LEIPVASTIN	EKAVLGKAIE
msa124060.2{80_COH1}	EIAELLKGMT	LVKNQDALDK	ATANTDDAAF	LEIPVASTIN	EKAVLGKAIE
msa124060.2{801_JM9130013}	EIAELLKGMT	LVKNQDALDK	ATANTDDAAF	LEIPVASTIN	EKAVLGKAIE
msa124060.2{80_18RS21}	EIAELLKGMT	LVKNQDALDK	ATANTDDAAF	LEIPVASTIN	EKAVLGKAIE
msa124060.2{80h_CJB110}	EIAELLKGMT	LVKNQDALDK	ATANTDDAAF	LEIPVASTIN	EKAVLGKAIE
Consensus	*****	*****	*****	*****	*****
	351				400
msa124060.2{80_2603}	NTFELQYDHT	PKADNPVKPS	NPPRKPEVHT	GGKRFVKKDS	TETQTLGGAE
msa124060.2{80_M732}	NTFELQYDHT	PKADNPVKPS	NPPRKPEVHT	GGKRFVKKDS	TETQTLGGAE
msa124060.2{80_A909}	NTFELQYDHT	PKADNPVKPS	NPPRKPEVHT	GGKRFVKKDS	TETQTLGGAE
msa124060.2{80_090}	NTFELQYDHT	PKADNPVKPS	NPPRKPEVHT	GGKRFVKKDS	TETQTLGGAE
msa124060.2{80_M781}	NTFELQYDHT	PKADNPVKPS	NPPRKPEVHT	GGKRFVKKDS	TETQTLGGAE
msa124060.2{80_COH1}	NTFELQYDHT	PKADNPVKPS	NPPRKPEVHT	GGKRFVKKDS	TETQTLGGAE
msa124060.2{801_JM9130013}	NTFELQYDHT	PKADNPVKPS	NPPRKPEVHT	GGKRFVKKDS	TETQTLGGAE
msa124060.2{80_18RS21}	NTFELQYDHT	PKADNPVKPS	NPPRKPEVHT	GGKRFVKKDS	TETQTLGGAE
msa124060.2{80h_CJB110}	NTFELQYDHT	PKADNPVKPS	NPPRKPEVHT	GGKRFVKKDS	TETQTLGGAE
Consensus	*****	*****	*****	*****	*****

Table 87: Comparative Sequences relating to SAG0645

	401				450
msa124060.2{80_2603}	FDLLASDGTA	VKWTDALIKA	NTNKNYIAGE	AVTGQPIKLG	SHTDGTFEIK
msa124060.2{80_M732}	FDLLASDGTA	VKWTDALIKA	NTNKNYIAGE	AVTGQPIKLG	SHTDGTFEIK
msa124060.2{80_A909}	FDLLASDGTA	VKWTDALIKA	NTNKNYIAGE	AVTGQPIKLG	SHTDGTFEIK
msa124060.2{80_090}	FDLLASDGTA	VKWTDALIKA	NTNKNYIAGE	AVTGQPIKLG	SHTDGTFEIK
msa124060.2{80_M781}	FDLLASDGTA	VKWTDALIKA	NTNKNYIAGE	AVTGQPIKLG	SHTDGTFEIK
msa124060.2{80_COH1}	FDLLASDGTA	VKWTDALIKA	NTNKNYIAGE	AVTGQPIKLG	SHTDGTFEIK
msa124060.2{801_JM9130013}	FDLLASDGTA	VKWTDALIKA	NTNKNYIAGE	AVTGQPIKLG	SHTDGTFEIK
msa124060.2{80_18RS21}	FDLLASDGTA	VKWTDALIKA	NTNKNYIAGE	AVTGQPIKLG	SHTDGTFEIK
msa124060.2{80h_CJB110}	FDLLASDGTA	VKWTDALIKA	NTNKNYIAGE	AVTGQPIKLG	SHTDGTFEIK
Consensus	*****	*****	*****	*****	*****
	451				500
msa124060.2{80_2603}	GLAYAVDANA	EGTAVTYKLG	ETKAPEGYVI	PDKEIEFTVS	QTSYNtKPTD
msa124060.2{80_M732}	GLAYAVDANA	EGTAVTYKLG	ETKAPEGYVI	PDKEIEFTVS	QTSYNtKPTD
msa124060.2{80_A909}	GLAYAVDANA	EGTAVTYKLG	ETKAPEGYVI	PDKEIEFTVS	QTSYNtKPTD
msa124060.2{80_090}	GLAYAVDANA	EGTAVTYKLG	ETKAPEGYVI	PDKEIEFTVS	QTSYNtKPTD
msa124060.2{80_M781}	GLAYAVDANA	EGTAVTYKLG	ETKAPEGYVI	PDKEIEFTVS	QTSYNtKPTD
msa124060.2{80_COH1}	GLAYAVDANA	EGTAVTYKLG	ETKAPEGYVI	PDKEIEFTVS	QTSYNtKPTD
msa124060.2{801_JM9130013}	GLAYAVDANA	EGTAVTYKLG	ETKAPEGYVI	PDKEIEFTVS	QTSYNtKPTD
msa124060.2{80_18RS21}	GLAYAVDANA	EGTAVTYKLG	ETKAPEGYVI	PDKEIEFTVS	QTSYNtKPTD
msa124060.2{80h_CJB110}	GLAYAVDANA	EGTAVTYKLG	ETKAPEGYVI	PDKEIEFTVS	QTSYNpKPTD
Consensus	*****	*****	*****	*****	*****_****
	501				550
msa124060.2{80_2603}	ITVDSADATP	DTIKNNkrps	ipntggigta	ifvaigaavm	afavkgmkrr
msa124060.2{80_M732}	ITVDSADATP	DTIKNNkrps	-----	-----	-----
msa124060.2{80_A909}	ITVDSADATP	DTIKNN	-----	-----	-----
msa124060.2{80_090}	ITVDSADATP	DTIKNNkrps	-----	-----	-----
msa124060.2{80_M781}	ITVDSADATP	DTIKNNkr--	-----	-----	-----
msa124060.2{80_COH1}	ITVDSADATP	DTIKNNkrps	-----	-----	-----
msa124060.2{801_JM9130013}	ITVDSADATP	DTIKNNkrps	-----	-----	-----
msa124060.2{80_18RS21}	ITVDSADATP	DTIKNNkrps	-----	-----	-----
msa124060.2{80h_CJB110}	ITVDSADATP	DTIKNNkrps	-----	-----	-----
Consensus	*****	*****----	-----	-----	-----
	551				
msa124060.2{80_2603}	tkdn				
msa124060.2{80_M732}	----				
msa124060.2{80_A909}	----				
msa124060.2{80_090}	----				
msa124060.2{80_M781}	----				
msa124060.2{80_COH1}	----				
msa124060.2{801_JM9130013}	----				
msa124060.2{80_18RS21}	----				
msa124060.2{80h_CJB110}	----				
Consensus	----				

Table 88: Comparative Sequences relating to SAG0477

SEQ ID NO. 8801

STRAIN 2603

ATGCCTAAGAAGAAATCAGATACCCAGAAAAAGAAGAAGTTGTCTTAACGGAATGGCAA
 AAGCGTAACCTTGAATTTTTAAAAAACGCAAAGAAGATGAAGAAGAACAAAAACGTATT
 AACGAAAAATTACGCTTAGATAAAAGAAGTAAATTAAATATTTCTTCTCCTGAAGAACCT
 CAAAATACTACTAAAATTAAGAAGCTTCATTTTCCAAAGATTTCAAGACCTAAGATTGAA
 AAGAAACAGAAAAAAGAAAAAATAGTCAACAGCTTAGCCAAAACTAATCGCATTAGAACT
 GCACCTATATTTGTAGTAGCATTCTAGTCATTTTAGTTTCCGTTTTCCTACTAACTCCT
 TTTAGTAAGCAAAAAACAATAACAGTTAGTGGAAATCAGCATACACCTGATGATATTTTG
 ATAGAGAAAACGAATATTCAAAAAACGATTATTTCTTTCTTTAATTTTAAACATAAA
 GCTATTGAACAACGTTTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTAT
 CAATTTCCCAATAAGTTTCATATTCAAGTTCAAGAAAATAAGATTATTGCATATGCACAT
 ACAAGCAAGGATATCAACCTGTCTTGGAACTGGAAAAAAGGCTGATCCTGTAAATAGT
 TCAGAGCTACCAAGCACTTCTTAACAATTAACCTTGATAAGGAAGATAGTATTAAAGCTA
 TTAATTAAAGATTTAAAGGCTTTAGACCCTGATTTAATAAGTGAGATTTCAGGTGATAAGT
 TTAGCTGATTCTAAAACGACACCTGACCTCCTGCTGTTAGATATGCACGATGGAAATAGT
 ATTAGAATACCATTATCTAAATTTAAAGAAAGACTTCCTTTTACAAACAAATTAAGAAG
 AACCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAGTTTACACAACAACAAATACC
 ATTGAATCAACCCCTGTTAAAGCAGAAGATACAAAAAATAAATCAACTGATAAAACACAA
 ACACAAAATGGTCAGGTTGCGGAAAATAGTCAAGGACAAACAAATAACTCAAATACTAAT
 CAACAAGGACAACAGATAGCAACAGAGCAGGCACCTAACCTCAAAATGTTAAT

SEQ ID NO. 8802

STRAIN H36B

CCTAAGAAGAAATCAGATACCCAGAAAAAGAAGAAGTT
 GTCTTAACGGAATGGCAAAGCGTAACCTTGAATTTTTAAAAAACGCAA
 AGAAGATGAAGAAGAACAAAAACGTATTACGAAAAATTACGCTTAGATA
 AAAGAAGTAAATTAAATATTTCTTCTCCTGAAGAACCTCAAAATACTACT
 AAAATTAAAGAAGCTTCATTTTCCAAAGATTTCAAGACCTAAGATTGAAAA
 GAAACAGAAAAAAGAAAAAATAGTCAACAGCTTAGCCAAAACTAATCGCA
 TTAGAAGTGCACCTATATTTGTAGTAGCATTCTAGTCATTTTAGTTTCC
 GTTTTCTACTAACTCCTTTTAGTAAGCAAAAAACAATAACAGTTAGTGG
 AAATCAGCATACACCTGATGATATTTTGATAGAGAAAACGAATATTCAAA
 AAAACGATTATTTCTTTTCTTTAATTTTAAACATAAAGCTATTGAACAA
 CGTTTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTATCA
 ATTTCCCAATAAGTTTCATATTCAAGTTCAAGAAAATAAGATTATTGCAT
 ATGCACATACAAAGCAAGGATATCAACCTGTCTTGGAACTGGAAAAAAG
 GCTGATCCTGTAAATAGTTAGAGCTACCAAGCACTTCTTAACAATTAA
 CCTTGATAAGGAAGATAGTATTAAAGCTATTAAATTAAAGATTTAAAGGCTT
 TAGACCCTGATTTAATAAGTGAGATTTCAGGTGATAAGTTTAGCTGATTCT
 AAAACGACACCTGACCTCCTGCTGTTAGATATGCACGATGGAAATAGTAT
 TAGAATACCATTATCTAAATTTAAAGAAAGACTTCCTTTTACAAACAAA
 TTAAGAAGAACCCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAGTT
 TACACAACAACAAATACCATTGAATCAACCCCTGTTAAAGCAGAAGATAC
 AAAAAATAAATCAACTGATAAAACACAAACACAAAATGGTCAGGTTGCGG
 AAAATAGTCAAGGACAAACAAATAACTCAAATACTAATCAACAAGGACAA
 CAGATAGCAACAGAGCAGGCACCTAACCTCAAAATGTTAAT

SEQ ID NO. 8803

STRAIN 18RS21

CCTAAGAAGAAATCAGATACCCAGAAAAAGAAGAAGTT
 GTCTTAACGGAATGGCAAAGCGTAACCTTGAATTTTTAAAAAACGCAA
 AGAAGATGAAGAAGAACAAAAACGTATTACGAAAAATTACGCTTAGATA
 AAAGAAGTAAATTAAATATTTCTTCTCCTGAAGAACCTCAAAATACTACT
 AAAATTAAAGAAGCTTCATTTTCCAAAGATTTCAAGACCTAAGATTGAAAA
 GAAACAGAAAAAAGAAAAAATAGTCAACAGCTTAGCCAAAACTAATCGCA
 TTAGAAGTGCACCTATATTTGTAGTAGCATTCTAGTCATTTTAGTTTCC
 GTTTTCTACTAACTCCTTTTAGTAAGCAAAAAACAATAACAGTTAGTGG
 AAATCAGCATACACCTGATGATATTTTGATAGAGAAAACGAATATTCAAA
 AAAACGATTATTTCTTTTCTTTAATTTTAAACATAAAGCTATTGAACAA
 CGTTTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTATCA
 ATTTCCCAATAAGTTTCATATTCAAGTTCAAGAAAATAAGATTATTGCAT
 ATGCACATACAAAGCAAGGATATCAACCTGTCTTGGAACTGGAAAAAAG
 GCTGATCCTGTAAATAGTTAGAGCTACCAAGCACTTCTTAACAATTAA
 CCTTGATAAGGAAGATAGTATTAAAGCTATTAAATTAAAGATTTAAAGGCTT
 TAGACCCTGATTTAATAAGTGAGATTTCAGGTGATAAGTTTAGCTGATTCT
 AAAACGACACCTGACCTCCTGCTGTTAGATATGCACGATGGAAATAGTAT
 TAGAATACCATTATCTAAATTTAAAGAAAGACTTCCTTTTACAAACAAA
 TTAAGAAGAACCCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAGTT
 TACACAACAACAAATACCATTGAATCAACCCCTGTTAAAGCAGAAGATAC
 AAAAAATAAATCAACTGATAAAACACAAACACAAAATGGTCAGGTTGCGG
 AAAATAGTCAAGGACAAACAAATAACTCAAATACTAATCAACAAGGACAA
 CAGATAGCAACAGAGCAGGCACCTAACCTCAAAATGTTAAT

SEQ ID NO. 8804

STRAIN M732

CCTAAGAAGAAATCAGATACCCAGAAAAAGAAGAAG
 TTGTCTTAACGGAATGGCAAAGCGTAACCTTGAATTTTTAAAAAACGCG
 AAAGAAGATGAAGAAGAACAAAAACGTATTACGAAAAATTACGCTTAGA
 TAAAGAAGTAAATTAAATATTTCTTCTCCTGAAGAACCTCAAAATACTA
 CTAAAAATTAAAGAAGCTTCATTTTCCAAAGATTTCAAAACCTAAGATTGAA
 AAGAAACAGAAAAAAGAAAAAATAGTCAACAGCTTAGCCAAAACTAATCG
 CATTAGAAGTGCACCTATATTTGTAGTAGCATTCTAGTCATTTTAGTTT

Table 88: Comparative Sequences relating to SAG0477

CCGTTTTCTACTAAGTCTTTTAGTAAGCAAAAAACAATAACAGTTAGT
 GGAAATCAGCATACACCTGATGATATTTTATAGAAAAACGAATATTCA
 AAAAAACGATTATTTCTTTCTTTAATTTTAAACATAAAGCTATTGAAC
 AACGTTTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTAT
 CAATTTCCCAATAAGTTTCATATTCAAGTTCAAGAAAAATAAGATTATTGC
 ATATGCACATACAAAGCAAGGATATCAGCCTGTCTTGGAACTGGAAAA
 AGGCTGATCCTGTAAATAGTTTCAAGCTACCAAAGCACTTCTTAACAATT
 AACCTTGATAAGGAAGATAGTATTAAGCTATTAATTAAAGATTAAAGGC
 TTTAGACCCTGATTTAATAAGTGAGATTCAAGTGATAAGTTTAGCTGATT
 CTAAAACGACACCTGACCTCCTGCTGTTAGATATGCATGATGGAAATAGT
 ATTAGAATACCATTATCTAAATTTAAAGAAAGACTTCTTTTACAAACA
 AATTAAGAAGAACCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAG
 TTTACACAACAACAAGTACTATTGAATCAACCCCTGTGAAAGCGGAAGAT
 AAAAAAATAAATCAACTGATAAAACACAAACACAAAATGGTCAGGTTGC
 GGAAAATAGTCAAGGACAAACAAATAAATCAATACTAATCAACAAGGAC
 AACAGATAGCAACAGAGCAGGCACCCAACCTCAAAATGTTAAT

SEQ ID NO. 8805

STRAIN COH1

CCTAAGAAGAAATCAGATACCCAGAAAAAGAAGATT
 GTCTTAACGGAATGGCAAAAGCGTAACCTTGAATTTTAAAAAAACGCAA
 AGAAGATGAAGAAGAACAAAAACGTATTAAAGAAAAATACGCTTAGATA
 AAAGAAGTAAATTAATATTTCTTCTCCTGAAGAACCTCAAAATACTACT
 AAAATTAAGAAGCTTCATTTTCAAAGATTTCAAAACCTAAGATTGAAAA
 GAAACAGAAAAAGAAAAAATAGTCAACAGCTTAGCCAAAACCTAATCGCA
 TTAGAAGTGCACCTATATTTGTAGTAGCATTCTAGTCATTTTAGTTTCC
 GTTTTCTACTAAGTCTTTTGTAGTAAGCAAAAAACAATAACAGTTAGTGG
 AAATCAGCATACACCTGATGATATTTTATAGAAAAACGAATATTCAAA
 AAAACGATTATTTCTTTCTTTAATTTTAAACATAAAGCTATTGAACAA
 CGTTTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTATCA
 ATTTCCCAATAAGTTTCATATTCAAGTTCAAGAAAAATAAGATTATTGCAT
 ATGCACATACAAAGCAAGGATATCAGCCTGTCTTGGAACTGGAAAAAG
 GCTGATCCTGTAAATAGTTTCAAGCTACCAAAGCACTTCTTAACAATTAA
 CCTTGATAAGGAAGATAGTATTAAGCTATTAATTAAAGATTAAAGGCTT
 TAGACCCTGATTTAATAAGTGAGATTCAAGTGATAAGTTTAGCTGATTCT
 AAAACGACACCTGACCTCCTGCTGTTAGATATGCATGATGGAAATAGTAT
 TAGAATACCATTATCTAAATTTAAAGAAAGACTTCTTTTACAAACAAA
 TTAAGAAGAACCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAGTT
 TACACAACAACAAGTACTATTGAATCAACCCCTGTGAAAGCGGAAGATAC
 AAAAAATAAATCAACTGATAAAACACAAACACAAAATGGTCAGGTTGCGG
 AAAATAGTCAAGGACAAACAAATAAATCAATACTAATCAACAAGGACAA
 CAGATAGCAACAGAGCAGGCACCCAACCTCAAAATGTTAAT

SEQ ID NO. 8806

STRAIN M781

CCTAAGAAGAAATCAGATACCCAGAAAAAGAAG
 TTGTCTTAACGGAATGGCAAAAGCGTAACCTTGAATTTTAAAAAAACGC
 AAAGAAGATGAAGAAGAACAAAAACGTATTAAAGAAAAATTACGCTTAGA
 TAAAGAAGTAAATTAATATTTCTTCTCCTGAAGAACCTCAAAATACTA
 CTAAATTAAGAAGCTTCATTTTCAAAGATTTCAAAACCTAAGATTGAA
 AAGAAACAGAAAAAGAAAAAATAGTCAACAGCTTAGCCAAAACCTAATCG
 CATTAGAAGTGCACCTATATTTGTAGTAGCATTCTAGTCATTTTAGTTT
 CCGTTTTCTACTAAGTCTTTTGTAGTAAGCAAAAAACAATAACAGTTAGT
 GGAAATCAGCATACACCTGATGATATTTTATAGAAAAACGAATATTCA
 AAAAAACGATTATTTCTTTCTTTAATTTTAAACATAAAGCTATTGAAC
 AACGTTTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTAT
 CAATTTCCCAATAAGTTTCATATTCAAGTTCAAGAAAAATAAGATTATTGC
 ATATGCACATACAAAGCAAGGATATCAGCCTGTCTTGGAACTGGAAAA
 AGGCTGATCCTGTAAATAGTTTCAAGCTACCAAAGCACTTCTTAACAATT
 AACCTTGATAAGGAAGATAGTATTAAGCTATTAATTAAAGATTAAAGGC
 TTTAGACCCTGATTTAATAAGTGAGATTCAAGTGATAAGTTTAGCTGATT
 CTAAAACGACACCTGACCTCCTGCTGTTAGATATGCATGATGGAAATAGT
 ATTAGAATACCATTATCTAAATTTAAAGAAAGACTTCTTTTACAAACA
 AATTAAGAAGAACCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAG
 TTTACACAACAACAAGTACTATTGAATCAACCCCTGTGAAAGCGGAAGAT
 AAAAAAATAAATCAACTGATAAAACACAAACACAAAATGGTCAGGTTGC
 GGAAAATAGTCAAGGACAAACAAATAAATCAATACTAATCAACAAGGAC
 AACAGATAGCAACAGAGCAGGCACCCAACCTCAAAATGTTAAT

SEQ ID NO. 8807

STRAIN CJB110

CCTAAGAAGAAATCAGATACCCAGAAAAAGAAG
 TTGTCTTAACGGAATGGCAAAAGCGTAACCTTGAATTTTAAAAAAACGC
 AAAGAAGATGAAGAAGAACAAAAACGTATTAAAGAAAAATTACGCTTAGA
 TAAAGAAGTAAATTAATATTTCTTCTCCTGAAGAACCTCAAAATACTA
 CTAAATTAAGAAGCTTCATTTTCAAAGATTTCAAAACCTAAGATTGAA
 AAGAAACAGAAAAAGAAAAAATAGTCAACAGCTTAGCCAAAACCTAATCG
 CATTAGAAGTGCACCTATATTTGTAGTAGCATTCTAGTCATTTTAGTTT
 CCGTTTTCTACTAAGTCTTTTGTAGTAAGCAAAAAACAATAACAGTTAGT
 GGAAATCAGCATACACCTGATGATATTTTATAGAAAAACGAATATTCA
 AAAAAACGATTATTTCTTTCTTTAATTTTAAACATAAAGCTATTGAAC
 AACGTTTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTAT
 CAATTTCCCAATAAGTTTCATATTCAAGTTCAAGAAAAATAAGATTATTGC

Table 88: Comparative Sequences relating to SAG0477

ATATGCACATACAAAGCAAGGATATCAGCCTGTCTTGGAACCTGGAAAAA
 AGGCTGATCCTGTAAATAGTTTCAGAGCTACCAAAGCACTTCTTAACAATT
 AACCTTGATAAGGAAGATAGTATTAAAGCTATTAAATTAAGATTAAAGGC
 TTAGACCCTGATTTAATAAGTGAGATTGAGGTGATAAGTTTAGCTGATT
 CTAACACGACACCTGACCTCCTGCTGTTAGATATGCATGATGGAAATAGT
 ATTAGAATACCATTATCTAAATTTAAAGAAAGACTTCCTTTTACAAACA
 AATTAAGAAGAACCCTTAAGGAACCCTTCTATTGTTGATATGGAAGTGGGAG
 TTACACAACAACAAGTACTATTGAATCAACCCCTGTGAAAGCGGAAGAT
 AAAAAAATAAATCAACTGATAAAACACAAACACAAAATGGTCAGGTTGC
 GGAAAATAGTCAAGGACAAACAAATAACTCAAATACTAATCAACAAGGAC
 AACAGATAGCAACAGAGCAGGCACCCAACCCTCAAATGTTAAT

SEQ ID NO. 8808

STRAIN 1169NT

CCTAAGAAGAAATCAGATACCCAGAAAAAGAAGAAGT
 TGTCTTAACGGAATGGCAAAAGCGTAACCTTGAATTTTAAAAAACGCA
 AAGAAGATGAAGAAGAACAACAAACGTAATTAACGAAAAATTACGCTTAGAT
 AAAAGAAGTAAATTAATATTTCTTCTCCTGAAGAACCCTAAAAATACTAC
 TAAAAATTAAGAAGCTTCATTTTCCAAAGATTTCAAACCTAAGATTGAAA
 AGAAACAGAAAAAAGAAAAATAGTCAACAGCTTAGCCAAAACCTAATCGC
 ATTAGAACTGCACCTATATTTATAGTAGCATTCCTAGTCATTTTAGTTTC
 CGTTTTCCTACTAACTCCTTTTAGTAAGCAAAAAACAATAACAGTTAGTG
 GAAATCAGCATACACCTGATGATAATTTTGATAGAGAAAACGAATATTCAA
 AAAAAACGATTATTTCTTTCTTTAATTTTAAACATAAAGCTATTGAACA
 ACGTTTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTATC
 AATTTCCCAACAAGTTTCATATTCAAGTTCAAGAAAAATAAGATTATTGCA
 TATGCACATACAAAGCAAGGATATCAGCCTGTCTTGGAACCTGGAAAAA
 GGCTGATCCTGTAAATAGTTTCAGAGCTACCAAAGCACTTCTTAACAATTA
 ACCTTGATAAGGAAGATAGTATTAAAGCTATTAAATTAAGATTAAAGGCT
 TTAGACCCTGATTTAATAAGTGAGATTGAGGTGATAAGTTTAGCTGATTTC
 TAAAACGACACCTGACCTCCTGCTGTTAGATATGCACGATGGAAATAGTA
 TTAGAATACCATTATCTAAATTTAAAGAAAGACTTCCTTTTACAAACAA
 ATTAAGAAGAACCCTTAAGGAACCCTTCTATTGTTGATATGGAAGTGGGAGT
 TTACACAACAACAAGTACTATTGAATCAACCCCTGTGAAAGCGGAAGATA
 CAAAAAATAAATCAACTGATAAAACACAAACCAAAATGGTCAGGTTGCG
 GAAAAATAGTCAAGGACAAACAAATAACTCAAATACTAATCAACAAGGACA
 ACAACAGATAGCAACGAGCAGGCACCCAACCCTCAAATGTTAAT

SEQ ID NO. 8809

STRAIN JM9130013

CCTAAGAAGAAATCAGATACCCAGAAAAAGAAGAAGT
 GTCTTAACGGAATGGCAAAAGCGTAACCTTGAATTTTAAAAAACGCAA
 AGAAGATGAAGAAGAACAACAAACGTAATTAACGAAAAATTACGCTTAGATA
 AAAGAAGTAAATTAATATTTCTTCTCCTGAAGAACCCTAAAAATACTACT
 AAAATTAAGAAGCTTCATTTTCCAAAGATTTCAAGACCTAAGATTGAAAA
 GAAACAGAAAAAAGAAAAATAGTCAACAGCTTAGCCAAAACCTAATCGCA
 TTAGAAGTGCACCTATATTTGTAGTAGCATTCCTAGTCATTTTAGTTTCC
 GTTTTCTACTAACTCCTTTTAGTAAGCAAAAAACAATAACAGTTAGTGG
 AAATCAGCATACACCTGATGATAATTTTGATAGAGAAAACGAATATTCAA
 AAAACGATTATTTCTTTCTTTAATTTTAAACATAAAGCTATTGAACAA
 CGTTTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTATCA
 ATTTCCCAATAAGTTTCATATTCAAGTTCAAGAAAAATAAGATTATTGCAT
 ATGCACATACAAAGCAAGGATATCAACCTGTCTTGGAACCTGGAAAAAAG
 GCTGATCCTGTAAATAGTTTCAGAGCTACCAAAGCACTTCTTAACAATTAA
 CCTTGATAAGGAAGATAGTATTAAAGCTATTAAATTAAGATTAAAGGCTT
 TAGACCCTGATTTAATAAGTGAGATTGAGGTGATAAGTTTAGCTGATTCT
 AAAACGACACCTGACCTCCTGCTGTTAGATATGCACGATGGAAATAGTAT
 TAGAATACCATATCTAAATTTAAAGAAAGACTTCCTTTTACAAACAAA
 TTAAGAAGAACCCTTAAGGAACCCTTCTATTGTTGATATGGAAGTGGGAGTT
 TACACAACAACAATAACCATTTGAATCAACCCCTGTTAAAGCAGAAGATAC
 AAAAAATAAATCAACTGATAAAACACAAACACAAAATGGTCAGGTTGCGG
 AAAATAGTCAAGGACAAACAAATAACTCAAATACTAATCAACAAGGACAA
 CAGATAGCAACAGAGCAGGCACCTAACCCCTCAAATGTTAAT

SEQ ID NO. 8810

STRAIN A909

CCTAAGAAGAAATCAGATACCCAGAAAAAGAAGAAGTTGTC
 TTAACGGAATGGCAAAAGCGTAACCTTGAATTTTaaAAAAACGCAAGA
 AGATGAAGAAGAAaCAAAAACGTAATTAACGAAAAATTACGCTTAGATAAAA
 GAAGTAAATTAATATTTCTTCTCCTGAAGAACCCTAAAAATACTACTAAA
 ATTAAGAAGCTTCATTTTCCAAAGATTTCAAGACCTAAGATTGAAAAGAA
 ACAGAAAAAAGAAAAATAGTCAACAGCTTAGCCAAAACCTAATCGCATT
 GAACTGCACCTATATTTGTAGTAGCATTCCTAGTCATTTTAGTTTCCGTT
 TTCTTACTAACTCCTTTTAGTAAGCAAAAAACAATAACAGTTAGTGGAAA
 TCAGCATACACCTGATGATAATTTTGATAGAGAAAACGAATATTCAAAAA
 ACGATTATTTCTTTCTTTAATTTTAAACATAAAGCTATTGAACAACGT
 TTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTATCAATT
 TCCCAATAAGTTTCATATTCAAGTTCAAGAAAAATAAGATTATTGCATATG
 CACATACAAAGCAAGGATATCAACCTGTCTTGGAACCTGGAAAAAAGGCT
 GATCCTGTAAATAGTTTCAGAGCTACCAAAGCACTTCTTAACAATTAACCT
 TGATAAGGAAGATAGTATTAAAGCTATTAAATTAAGATTAAAGGCTTTAG
 ACCCTGATTTAATAAGTGAGATTGAGGTGATAAGTTTAGCTGATTCTAAA
 ACGACACCTGACCTCCTGCTGTTAGATATGCACGATGGAAATAGTATTAs

Table 88: Comparative Sequences relating to SAG0477

AATACCATTATCTAAATTTAAAGAAAGACTTCCTTTTACAAACAAATTA
 AGAAGAACCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAGTTTAC
 ACAACAACAATACCTTGAATCAACCCCTGTTAAAGCAGAAGATACAAA
 AAATAAATCAACTGATAAAACACAA_mCACAAAATGGTCAGGTTGCGGAAA
 ATAGTCAAGGACAAACAAATAACTCAAATACTAATCAACAAGGACAACAG
 ATAGCAACAGAGCAGGCACCTAACCCCTCAAATGTTAAT

SEQ ID NO. 8811

STRAIN 090

TAAGAAGAAATCAGATACCCAGAAAAAGAAGAGTTGTCTTAACGGAAT
 GGCAAAAGCGTAACCTTGAATTTTAAAAAAGCGCAAGAAGATGAAGAA
 GAACAAAAACGTATTAACGAAAAATTACGCTTAGATAAAAGAAGTaaATT
 AAATATTTCTTCTCCTGAAGAACCTCAAAATACTACTAAAATTAAGAGC
 TTCATTTTCCAAAGATTTCAAAACCTAAGATTGAAAAAGAAACAGAAAAAA
 GAAAAAATAGTCAACAGCTTAGCCAAAATAATCGCATTAGAAGTGCACC
 TATATTTGTAGTAGCATTCTAGTCATTTTAGTTTCCGTTTCTTACTFAA
 CTCCTTTTAGTAAGCAAAAAACAATAACAGTTAGTGGAATCAGCATACA
 CCTGATGATATTTTGTAGAAAAACGAATATTCAAAAAACGATTATTT
 CTTTTCTTTAATTTTAAACATAAAGCTATGAACAACGTTTAGCTGCAG
 AAGATGTATGGGTAAAAACAGCTCAGATGACTTATCAATTTCCCAATAAG
 TTTTCATATTCAGTTCAAGAAAAATAAGATTATTGCATATGCACATACAAA
 GCAAGGATATCAGCCTGTCTTGGAAGCTGGAAAAAAGGCTGATCCTGTAA
 ATAGTTCAGAGCTACCAAAGCACTTCTTAACAATTAACCTTGATAAGGAA
 GATAGTATTAAGCTATTAATTAAGATTTAAAGGCTTTAGACCTTGATTT
 AATAAGTGAGATTGAGGTGATAAGTTTAGCTGATTTCTAAAACGACACCTG
 ACCTCCTGCTGTTAGATATGCATGATGGAAATAGTATTAGAATACCATTA
 TCTAAATTTAAAGAAAGACTTCCTTTTACAAACAAATTAAGAAGAACCT
 TAAGGAACCTTCTATTGTTGATATGGAAGTGGGAGTTTACACAACAACAA
 GTACTATTGAATCAACCCCTGTGAAAGCGGAAGATACAAAAAATAATCA
 ACTGATAAAACACAAACACAAATGGTCAGGTTGCGGAAAATAGTCAAGG
 ACAAACAAATAACTCAAATACTAATCAACAAGGACAACAGATAGCAACAG
 AGCAGGCACCCAACCTCAAATGTTAAT

PRETTY of: /biotmp/msa24691.2{*} August 5, 2002 05:14 ..

	1		50
msa252409.2{85_090.con }	--TAAGAAGA	AATCAGATAC	CCCAGAAAAA GAAGAAGTTG TCTTAACGGA
msa252409.2{85_CJB110 }	CCTAAGAAGA	AATCAGATAC	CCCAGAAAAA GAAGAAGTTG TCTTAACGGA
msa252409.2{85_COH1 }	CCTAAGAAGA	AATCAGATAC	CCCAGAAAAA GAAGAAGTTG TCTTAACGGA
msa252409.2{85_M732 }	CCTAAGAAGA	AATCAGATAC	CCCAGAAAAA GAAGAAGTTG TCTTAACGGA
msa252409.2{85_M781 }	CCTAAGAAGA	AATCAGATAC	CCCAGAAAAA GAAGAAGTTG TCTTAACGGA
msa252409.2{85_18RS21 }	CCTAAGAAGA	AATCAGATAC	CCCAGAAAAA GAAGAAGTTG TCTTAACGGA
msa252409.2{85_2603 }	CCTAAGAAGA	AATCAGATAC	CCCAGAAAAA GAAGAAGTTG TCTTAACGGA
msa252409.2{85_A909 }	CCTAAGAAGA	AATCAGATAC	CCCAGAAAAA GAAGAAGTTG TCTTAACGGA
msa252409.2{85_H36B }	CCTAAGAAGA	AATCAGATAC	CCCAGAAAAA GAAGAAGTTG TCTTAACGGA
msa252409.2{85_JM9130013 }	CCTAAGAAGA	AATCAGATAC	CCCAGAAAAA GAAGAAGTTG TCTTAACGGA
msa252409.2{85_1169NT }	CCTAAGAAGA	AATCAGATAC	CCCAGAAAAA GAAGAAGTTG TCTTAACGGA
Consensus	*****	*****	*****
	51		100
msa252409.2{85_090.con }	ATGGCAAAAAG	CGTAACCTTG	AATTTTAA AAAACGCAA GAAGATGAAG
msa252409.2{85_CJB110 }	ATGGCAAAAAG	CGTAACCTTG	AATTTTAA AAAACGCAA GAAGATGAAG
msa252409.2{85_COH1 }	ATGGCAAAAAG	CGTAACCTTG	AATTTTAA AAAACGCAA GAAGATGAAG
msa252409.2{85_M732 }	ATGGCAAAAAG	CGTAACCTTG	AATTTTAA AAAACGCAA GAAGATGAAG
msa252409.2{85_M781 }	ATGGCAAAAAG	CGTAACCTTG	AATTTTAA AAAACGCAA GAAGATGAAG
msa252409.2{85_18RS21 }	ATGGCAAAAAG	CGTAACCTTG	AATTTTAA AAAACGCAA GAAGATGAAG
msa252409.2{85_2603 }	ATGGCAAAAAG	CGTAACCTTG	AATTTTAA AAAACGCAA GAAGATGAAG
msa252409.2{85_A909 }	ATGGCAAAAAG	CGTAACCTTG	AATTTTAA AAAACGCAA GAAGATGAAG
msa252409.2{85_H36B }	ATGGCAAAAAG	CGTAACCTTG	AATTTTAA AAAACGCAA GAAGATGAAG
msa252409.2{85_JM9130013 }	ATGGCAAAAAG	CGTAACCTTG	AATTTTAA AAAACGCAA GAAGATGAAG
msa252409.2{85_1169NT }	ATGGCAAAAAG	CGTAACCTTG	AATTTTAA AAAACGCAA GAAGATGAAG
Consensus	*****	*****	*****
	101		150
msa252409.2{85_090.con }	AAGAACAAAA	ACGTATTAA	GAAAAATTAC GCTTAGATAA AAGAAGTAAA
msa252409.2{85_CJB110 }	AAGAACAAAA	ACGTATTAA	GAAAAATTAC GCTTAGATAA AAGAAGTAAA
msa252409.2{85_COH1 }	AAGAACAAAA	ACGTATTAA	GAAAAATTAC GCTTAGATAA AAGAAGTAAA
msa252409.2{85_M732 }	AAGAACAAAA	ACGTATTAA	GAAAAATTAC GCTTAGATAA AAGAAGTAAA
msa252409.2{85_M781 }	AAGAACAAAA	ACGTATTAA	GAAAAATTAC GCTTAGATAA AAGAAGTAAA
msa252409.2{85_18RS21 }	AAGAACAAAA	ACGTATTAA	GAAAAATTAC GCTTAGATAA AAGAAGTAAA
msa252409.2{85_2603 }	AAGAACAAAA	ACGTATTAA	GAAAAATTAC GCTTAGATAA AAGAAGTAAA
msa252409.2{85_A909 }	AAGAACAAAA	ACGTATTAA	GAAAAATTAC GCTTAGATAA AAGAAGTAAA
msa252409.2{85_H36B }	AAGAACAAAA	ACGTATTAA	GAAAAATTAC GCTTAGATAA AAGAAGTAAA
msa252409.2{85_JM9130013 }	AAGAACAAAA	ACGTATTAA	GAAAAATTAC GCTTAGATAA AAGAAGTAAA
msa252409.2{85_1169NT }	AAGAACAAAA	ACGTATTAA	GAAAAATTAC GCTTAGATAA AAGAAGTAAA
Consensus	*****	*****	*****
	151		200
msa252409.2{85_090.con }	TTAAATATTT	CTTCTCCTGA	AGAACCTCAA AATACTACTA AAATTAAGAA
msa252409.2{85_CJB110 }	TTAAATATTT	CTTCTCCTGA	AGAACCTCAA AATACTACTA AAATTAAGAA
msa252409.2{85_COH1 }	TTAAATATTT	CTTCTCCTGA	AGAACCTCAA AATACTACTA AAATTAAGAA
msa252409.2{85_M732 }	TTAAATATTT	CTTCTCCTGA	AGAACCTCAA AATACTACTA AAATTAAGAA

Table 88: Comparative Sequences relating to SAG0477

msa252409.2{85_M781}	TTAAATATTT	CTTCTCCTGA	AGAACCCTCAA	AATACTACTA	AAATTAAGAA
msa252409.2{85_18RS21}	TTAAATATTT	CTTCTCCTGA	AGAACCCTCAA	AATACTACTA	AAATTAAGAA
msa252409.2{85_2603}	TTAAATATTT	CTTCTCCTGA	AGAACCCTCAA	AATACTACTA	AAATTAAGAA
msa252409.2{85_A909}	TTAAATATTT	CTTCTCCTGA	AGAACCCTCAA	AATACTACTA	AAATTAAGAA
msa252409.2{85_H36B}	TTAAATATTT	CTTCTCCTGA	AGAACCCTCAA	AATACTACTA	AAATTAAGAA
msa252409.2{85_JM9130013}	TTAAATATTT	CTTCTCCTGA	AGAACCCTCAA	AATACTACTA	AAATTAAGAA
msa252409.2{85_1169NT}	TTAAATATTT	CTTCTCCTGA	AGAACCCTCAA	AATACTACTA	AAATTAAGAA
Consensus	*****	*****	*****	*****	*****
201					
msa252409.2{85_090.con}	GCTTCATTTT	CCAAAGATTT	CAAAACCTAA	GATTGAAAAG	AAACAGAAAA
msa252409.2{85_CJB110}	GCTTCATTTT	CCAAAGATTT	CAAAACCTAA	GATTGAAAAG	AAACAGAAAA
msa252409.2{85_COH1}	GCTTCATTTT	CCAAAGATTT	CAAAACCTAA	GATTGAAAAG	AAACAGAAAA
msa252409.2{85_M732}	GCTTCATTTT	CCAAAGATTT	CAAAACCTAA	GATTGAAAAG	AAACAGAAAA
msa252409.2{85_M781}	GCTTCATTTT	CCAAAGATTT	CAAAACCTAA	GATTGAAAAG	AAACAGAAAA
msa252409.2{85_18RS21}	GCTTCATTTT	CCAAAGATTT	CAAAACCTAA	GATTGAAAAG	AAACAGAAAA
msa252409.2{85_2603}	GCTTCATTTT	CCAAAGATTT	CAAAACCTAA	GATTGAAAAG	AAACAGAAAA
msa252409.2{85_A909}	GCTTCATTTT	CCAAAGATTT	CAAAACCTAA	GATTGAAAAG	AAACAGAAAA
msa252409.2{85_H36B}	GCTTCATTTT	CCAAAGATTT	CAAAACCTAA	GATTGAAAAG	AAACAGAAAA
msa252409.2{85_JM9130013}	GCTTCATTTT	CCAAAGATTT	CAAAACCTAA	GATTGAAAAG	AAACAGAAAA
msa252409.2{85_1169NT}	GCTTCATTTT	CCAAAGATTT	CAAAACCTAA	GATTGAAAAG	AAACAGAAAA
Consensus	*****	*****	***-*****	*****	*****
251					
msa252409.2{85_090.con}	AAGAAAAAAT	AGTCAACAGC	TTAGCCAAAA	CTAATCGCAT	TAGAACTGCA
msa252409.2{85_CJB110}	AAGAAAAAAT	AGTCAACAGC	TTAGCCAAAA	CTAATCGCAT	TAGAACTGCA
msa252409.2{85_COH1}	AAGAAAAAAT	AGTCAACAGC	TTAGCCAAAA	CTAATCGCAT	TAGAACTGCA
msa252409.2{85_M732}	AAGAAAAAAT	AGTCAACAGC	TTAGCCAAAA	CTAATCGCAT	TAGAACTGCA
msa252409.2{85_M781}	AAGAAAAAAT	AGTCAACAGC	TTAGCCAAAA	CTAATCGCAT	TAGAACTGCA
msa252409.2{85_18RS21}	AAGAAAAAAT	AGTCAACAGC	TTAGCCAAAA	CTAATCGCAT	TAGAACTGCA
msa252409.2{85_2603}	AAGAAAAAAT	AGTCAACAGC	TTAGCCAAAA	CTAATCGCAT	TAGAACTGCA
msa252409.2{85_A909}	AAGAAAAAAT	AGTCAACAGC	TTAGCCAAAA	CTAATCGCAT	TAGAACTGCA
msa252409.2{85_H36B}	AAGAAAAAAT	AGTCAACAGC	TTAGCCAAAA	CTAATCGCAT	TAGAACTGCA
msa252409.2{85_JM9130013}	AAGAAAAAAT	AGTCAACAGC	TTAGCCAAAA	CTAATCGCAT	TAGAACTGCA
msa252409.2{85_1169NT}	AAGAAAAAAT	AGTCAACAGC	TTAGCCAAAA	CTAATCGCAT	TAGAACTGCA
Consensus	*****	*****	*****	*****	*****
301					
msa252409.2{85_090.con}	CCTATATTTg	TAGTAGCATT	CCTAGTCATT	TTAGTTTCCG	TTTTCTACT
msa252409.2{85_CJB110}	CCTATATTTg	TAGTAGCATT	CCTAGTCATT	TTAGTTTCCG	TTTTCTACT
msa252409.2{85_COH1}	CCTATATTTg	TAGTAGCATT	CCTAGTCATT	TTAGTTTCCG	TTTTCTACT
msa252409.2{85_M732}	CCTATATTTg	TAGTAGCATT	CCTAGTCATT	TTAGTTTCCG	TTTTCTACT
msa252409.2{85_M781}	CCTATATTTg	TAGTAGCATT	CCTAGTCATT	TTAGTTTCCG	TTTTCTACT
msa252409.2{85_18RS21}	CCTATATTTg	TAGTAGCATT	CCTAGTCATT	TTAGTTTCCG	TTTTCTACT
msa252409.2{85_2603}	CCTATATTTg	TAGTAGCATT	CCTAGTCATT	TTAGTTTCCG	TTTTCTACT
msa252409.2{85_A909}	CCTATATTTg	TAGTAGCATT	CCTAGTCATT	TTAGTTTCCG	TTTTCTACT
msa252409.2{85_H36B}	CCTATATTTg	TAGTAGCATT	CCTAGTCATT	TTAGTTTCCG	TTTTCTACT
msa252409.2{85_JM9130013}	CCTATATTTg	TAGTAGCATT	CCTAGTCATT	TTAGTTTCCG	TTTTCTACT
msa252409.2{85_1169NT}	CCTATATTTa	TAGTAGCATT	CCTAGTCATT	TTAGTTTCCG	TTTTCTACT
Consensus	*****	*****	*****	*****	*****
351					
msa252409.2{85_090.con}	AACTCCTTTT	AGTAAGCAAA	AAACAATAAC	AGTTAGTGGA	AATCAGCATA
msa252409.2{85_CJB110}	AACTCCTTTT	AGTAAGCAAA	AAACAATAAC	AGTTAGTGGA	AATCAGCATA
msa252409.2{85_COH1}	AACTCCTTTT	AGTAAGCAAA	AAACAATAAC	AGTTAGTGGA	AATCAGCATA
msa252409.2{85_M732}	AACTCCTTTT	AGTAAGCAAA	AAACAATAAC	AGTTAGTGGA	AATCAGCATA
msa252409.2{85_M781}	AACTCCTTTT	AGTAAGCAAA	AAACAATAAC	AGTTAGTGGA	AATCAGCATA
msa252409.2{85_18RS21}	AACTCCTTTT	AGTAAGCAAA	AAACAATAAC	AGTTAGTGGA	AATCAGCATA
msa252409.2{85_2603}	AACTCCTTTT	AGTAAGCAAA	AAACAATAAC	AGTTAGTGGA	AATCAGCATA
msa252409.2{85_A909}	AACTCCTTTT	AGTAAGCAAA	AAACAATAAC	AGTTAGTGGA	AATCAGCATA
msa252409.2{85_H36B}	AACTCCTTTT	AGTAAGCAAA	AAACAATAAC	AGTTAGTGGA	AATCAGCATA
msa252409.2{85_JM9130013}	AACTCCTTTT	AGTAAGCAAA	AAACAATAAC	AGTTAGTGGA	AATCAGCATA
msa252409.2{85_1169NT}	AACTCCTTTT	AGTAAGCAAA	AAACAATAAC	AGTTAGTGGA	AATCAGCATA
Consensus	*****	*****	*****	*****	*****
401					
msa252409.2{85_090.con}	CACCTGATGA	TATTTTGATA	GAAAAACGA	ATATTCAAAA	AAACGATTAT
msa252409.2{85_CJB110}	CACCTGATGA	TATTTTGATA	GAAAAACGA	ATATTCAAAA	AAACGATTAT
msa252409.2{85_COH1}	CACCTGATGA	TATTTTGATA	GAAAAACGA	ATATTCAAAA	AAACGATTAT
msa252409.2{85_M732}	CACCTGATGA	TATTTTGATA	GAAAAACGA	ATATTCAAAA	AAACGATTAT
msa252409.2{85_M781}	CACCTGATGA	TATTTTGATA	GAAAAACGA	ATATTCAAAA	AAACGATTAT
msa252409.2{85_18RS21}	CACCTGATGA	TATTTTGATA	GAAAAACGA	ATATTCAAAA	AAACGATTAT
msa252409.2{85_2603}	CACCTGATGA	TATTTTGATA	GAAAAACGA	ATATTCAAAA	AAACGATTAT
msa252409.2{85_A909}	CACCTGATGA	TATTTTGATA	GAAAAACGA	ATATTCAAAA	AAACGATTAT
msa252409.2{85_H36B}	CACCTGATGA	TATTTTGATA	GAAAAACGA	ATATTCAAAA	AAACGATTAT
msa252409.2{85_JM9130013}	CACCTGATGA	TATTTTGATA	GAAAAACGA	ATATTCAAAA	AAACGATTAT
msa252409.2{85_1169NT}	CACCTGATGA	TATTTTGATA	GAAAAACGA	ATATTCAAAA	AAACGATTAT
Consensus	*****	*****	***-*****	*****	*****
451					
msa252409.2{85_090.con}	TTCTTTTCTT	TAATTTTTTAA	ACATAAAGCT	ATTGAACAAC	GTTTAGCTGC
msa252409.2{85_CJB110}	TTCTTTTCTT	TAATTTTTTAA	ACATAAAGCT	ATTGAACAAC	GTTTAGCTGC
msa252409.2{85_COH1}	TTCTTTTCTT	TAATTTTTTAA	ACATAAAGCT	ATTGAACAAC	GTTTAGCTGC

Table 88: Comparative Sequences relating to SAG0477

msa252409.2{85_M732}	TTCTTTTCTT	TAATTTTAA	ACATAAAGCT	ATTGAACAAC	GTTTAGCTGC
msa252409.2{85_M781}	TTCTTTTCTT	TAATTTTAA	ACATAAAGCT	ATTGAACAAC	GTTTAGCTGC
msa252409.2{85_18RS21}	TTCTTTTCTT	TAATTTTAA	ACATAAAGCT	ATTGAACAAC	GTTTAGCTGC
msa252409.2{85_2603}	TTCTTTTCTT	TAATTTTAA	ACATAAAGCT	ATTGAACAAC	GTTTAGCTGC
msa252409.2{85_A909}	TTCTTTTCTT	TAATTTTAA	ACATAAAGCT	ATTGAACAAC	GTTTAGCTGC
msa252409.2{85_H36B}	TTCTTTTCTT	TAATTTTAA	ACATAAAGCT	ATTGAACAAC	GTTTAGCTGC
msa252409.2{85_JM9130013}	TTCTTTTCTT	TAATTTTAA	ACATAAAGCT	ATTGAACAAC	GTTTAGCTGC
msa252409.2{85_1169NT}	TTCTTTTCTT	TAATTTTAA	ACATAAAGCT	ATTGAACAAC	GTTTAGCTGC
Consensus	*****	*****	*****	*****	*****
msa252409.2{85_090.con_}	AGAAGATGTA	TGGGTAAAAA	CAGCTCAGAT	GACTTATCAA	TTTCCCAAtA
msa252409.2{85_CJB110}	AGAAGATGTA	TGGGTAAAAA	CAGCTCAGAT	GACTTATCAA	TTTCCCAAtA
msa252409.2{85_COH1}	AGAAGATGTA	TGGGTAAAAA	CAGCTCAGAT	GACTTATCAA	TTTCCCAAtA
msa252409.2{85_M732}	AGAAGATGTA	TGGGTAAAAA	CAGCTCAGAT	GACTTATCAA	TTTCCCAAtA
msa252409.2{85_M781}	AGAAGATGTA	TGGGTAAAAA	CAGCTCAGAT	GACTTATCAA	TTTCCCAAtA
msa252409.2{85_18RS21}	AGAAGATGTA	TGGGTAAAAA	CAGCTCAGAT	GACTTATCAA	TTTCCCAAtA
msa252409.2{85_2603}	AGAAGATGTA	TGGGTAAAAA	CAGCTCAGAT	GACTTATCAA	TTTCCCAAtA
msa252409.2{85_A909}	AGAAGATGTA	TGGGTAAAAA	CAGCTCAGAT	GACTTATCAA	TTTCCCAAtA
msa252409.2{85_H36B}	AGAAGATGTA	TGGGTAAAAA	CAGCTCAGAT	GACTTATCAA	TTTCCCAAtA
msa252409.2{85_JM9130013}	AGAAGATGTA	TGGGTAAAAA	CAGCTCAGAT	GACTTATCAA	TTTCCCAAtA
msa252409.2{85_1169NT}	AGAAGATGTA	TGGGTAAAAA	CAGCTCAGAT	GACTTATCAA	TTTCCCAAtA
Consensus	*****	*****	*****	*****	*****
msa252409.2{85_090.con_}	AGTTTCATAT	TCAAGTTCAA	GAAAATAAGA	TTATTGCATA	TGCACATACA
msa252409.2{85_CJB110}	AGTTTCATAT	TCAAGTTCAA	GAAAATAAGA	TTATTGCATA	TGCACATACA
msa252409.2{85_COH1}	AGTTTCATAT	TCAAGTTCAA	GAAAATAAGA	TTATTGCATA	TGCACATACA
msa252409.2{85_M732}	AGTTTCATAT	TCAAGTTCAA	GAAAATAAGA	TTATTGCATA	TGCACATACA
msa252409.2{85_M781}	AGTTTCATAT	TCAAGTTCAA	GAAAATAAGA	TTATTGCATA	TGCACATACA
msa252409.2{85_18RS21}	AGTTTCATAT	TCAAGTTCAA	GAAAATAAGA	TTATTGCATA	TGCACATACA
msa252409.2{85_2603}	AGTTTCATAT	TCAAGTTCAA	GAAAATAAGA	TTATTGCATA	TGCACATACA
msa252409.2{85_A909}	AGTTTCATAT	TCAAGTTCAA	GAAAATAAGA	TTATTGCATA	TGCACATACA
msa252409.2{85_H36B}	AGTTTCATAT	TCAAGTTCAA	GAAAATAAGA	TTATTGCATA	TGCACATACA
msa252409.2{85_JM9130013}	AGTTTCATAT	TCAAGTTCAA	GAAAATAAGA	TTATTGCATA	TGCACATACA
msa252409.2{85_1169NT}	AGTTTCATAT	TCAAGTTCAA	GAAAATAAGA	TTATTGCATA	TGCACATACA
Consensus	*****	*****	*****	*****	*****
msa252409.2{85_090.con_}	AAGCAAGGAT	ATCAgCCTGT	CTTGGAAACT	GGAAAAAAGG	CTGATCCTGT
msa252409.2{85_CJB110}	AAGCAAGGAT	ATCAgCCTGT	CTTGGAAACT	GGAAAAAAGG	CTGATCCTGT
msa252409.2{85_COH1}	AAGCAAGGAT	ATCAgCCTGT	CTTGGAAACT	GGAAAAAAGG	CTGATCCTGT
msa252409.2{85_M732}	AAGCAAGGAT	ATCAgCCTGT	CTTGGAAACT	GGAAAAAAGG	CTGATCCTGT
msa252409.2{85_M781}	AAGCAAGGAT	ATCAgCCTGT	CTTGGAAACT	GGAAAAAAGG	CTGATCCTGT
msa252409.2{85_18RS21}	AAGCAAGGAT	ATCAaCCTGT	CTTGGAAACT	GGAAAAAAGG	CTGATCCTGT
msa252409.2{85_2603}	AAGCAAGGAT	ATCAaCCTGT	CTTGGAAACT	GGAAAAAAGG	CTGATCCTGT
msa252409.2{85_A909}	AAGCAAGGAT	ATCAaCCTGT	CTTGGAAACT	GGAAAAAAGG	CTGATCCTGT
msa252409.2{85_H36B}	AAGCAAGGAT	ATCAaCCTGT	CTTGGAAACT	GGAAAAAAGG	CTGATCCTGT
msa252409.2{85_JM9130013}	AAGCAAGGAT	ATCAaCCTGT	CTTGGAAACT	GGAAAAAAGG	CTGATCCTGT
msa252409.2{85_1169NT}	AAGCAAGGAT	ATCAgCCTGT	CTTGGAAACT	GGAAAAAAGG	CTGATCCTGT
Consensus	*****	*****	*****	*****	*****
msa252409.2{85_090.con_}	AAATAGTTCA	GAGCTACCAA	AGCACTTCTT	AACAATTAAC	CTTGATAAGG
msa252409.2{85_CJB110}	AAATAGTTCA	GAGCTACCAA	AGCACTTCTT	AACAATTAAC	CTTGATAAGG
msa252409.2{85_COH1}	AAATAGTTCA	GAGCTACCAA	AGCACTTCTT	AACAATTAAC	CTTGATAAGG
msa252409.2{85_M732}	AAATAGTTCA	GAGCTACCAA	AGCACTTCTT	AACAATTAAC	CTTGATAAGG
msa252409.2{85_M781}	AAATAGTTCA	GAGCTACCAA	AGCACTTCTT	AACAATTAAC	CTTGATAAGG
msa252409.2{85_18RS21}	AAATAGTTCA	GAGCTACCAA	AGCACTTCTT	AACAATTAAC	CTTGATAAGG
msa252409.2{85_2603}	AAATAGTTCA	GAGCTACCAA	AGCACTTCTT	AACAATTAAC	CTTGATAAGG
msa252409.2{85_A909}	AAATAGTTCA	GAGCTACCAA	AGCACTTCTT	AACAATTAAC	CTTGATAAGG
msa252409.2{85_H36B}	AAATAGTTCA	GAGCTACCAA	AGCACTTCTT	AACAATTAAC	CTTGATAAGG
msa252409.2{85_JM9130013}	AAATAGTTCA	GAGCTACCAA	AGCACTTCTT	AACAATTAAC	CTTGATAAGG
msa252409.2{85_1169NT}	AAATAGTTCA	GAGCTACCAA	AGCACTTCTT	AACAATTAAC	CTTGATAAGG
Consensus	*****	*****	*****	*****	*****
msa252409.2{85_090.con_}	AAGATAGTAT	TAAGCTATTA	ATTAAAGATT	TAAAGGCTTT	AGACCCTGAT
msa252409.2{85_CJB110}	AAGATAGTAT	TAAGCTATTA	ATTAAAGATT	TAAAGGCTTT	AGACCCTGAT
msa252409.2{85_COH1}	AAGATAGTAT	TAAGCTATTA	ATTAAAGATT	TAAAGGCTTT	AGACCCTGAT
msa252409.2{85_M732}	AAGATAGTAT	TAAGCTATTA	ATTAAAGATT	TAAAGGCTTT	AGACCCTGAT
msa252409.2{85_M781}	AAGATAGTAT	TAAGCTATTA	ATTAAAGATT	TAAAGGCTTT	AGACCCTGAT
msa252409.2{85_18RS21}	AAGATAGTAT	TAAGCTATTA	ATTAAAGATT	TAAAGGCTTT	AGACCCTGAT
msa252409.2{85_2603}	AAGATAGTAT	TAAGCTATTA	ATTAAAGATT	TAAAGGCTTT	AGACCCTGAT
msa252409.2{85_A909}	AAGATAGTAT	TAAGCTATTA	ATTAAAGATT	TAAAGGCTTT	AGACCCTGAT
msa252409.2{85_H36B}	AAGATAGTAT	TAAGCTATTA	ATTAAAGATT	TAAAGGCTTT	AGACCCTGAT
msa252409.2{85_JM9130013}	AAGATAGTAT	TAAGCTATTA	ATTAAAGATT	TAAAGGCTTT	AGACCCTGAT
msa252409.2{85_1169NT}	AAGATAGTAT	TAAGCTATTA	ATTAAAGATT	TAAAGGCTTT	AGACCCTGAT
Consensus	*****	*****	*****	*****	*****
msa252409.2{85_090.con_}	TTAATAAGTG	AGATTTCAGG	GATAAGTTTA	GCTGATTCTA	AAACGACACC
msa252409.2{85_CJB110}	TTAATAAGTG	AGATTTCAGG	GATAAGTTTA	GCTGATTCTA	AAACGACACC

Table 88: Comparative Sequences relating to SAG0477

msa252409.2{85_COH1}	TTAATAAGTG	AGATTCAGGT	GATAAGTTTA	GCTGATTCTA	AAACGACACC		
msa252409.2{85_M732}	TTAATAAGTG	AGATTCAGGT	GATAAGTTTA	GCTGATTCTA	AAACGACACC		
msa252409.2{85_M781}	TTAATAAGTG	AGATTCAGGT	GATAAGTTTA	GCTGATTCTA	AAACGACACC		
msa252409.2{85_18RS21}	TTAATAAGTG	AGATTCAGGT	GATAAGTTTA	GCTGATTCTA	AAACGACACC		
msa252409.2{85_2603}	TTAATAAGTG	AGATTCAGGT	GATAAGTTTA	GCTGATTCTA	AAACGACACC		
msa252409.2{85_A909}	TTAATAAGTG	AGATTCAGGT	GATAAGTTTA	GCTGATTCTA	AAACGACACC		
msa252409.2{85_H36B}	TTAATAAGTG	AGATTCAGGT	GATAAGTTTA	GCTGATTCTA	AAACGACACC		
msa252409.2{85_JM9130013}	TTAATAAGTG	AGATTCAGGT	GATAAGTTTA	GCTGATTCTA	AAACGACACC		
msa252409.2{85_1169NT}	TTAATAAGTG	AGATTCAGGT	GATAAGTTTA	GCTGATTCTA	AAACGACACC		
Consensus	*****	*****	*****	*****	*****		
msa252409.2{85_090.con}	801	TGACCTCCTG	CTGTTAGATA	TGCATGATGG	AAATAGTATT	850	AgAATACCAT
msa252409.2{85_CJB110}	TGACCTCCTG	CTGTTAGATA	TGCATGATGG	AAATAGTATT	AgAATACCAT		
msa252409.2{85_COH1}	TGACCTCCTG	CTGTTAGATA	TGCATGATGG	AAATAGTATT	AgAATACCAT		
msa252409.2{85_M732}	TGACCTCCTG	CTGTTAGATA	TGCATGATGG	AAATAGTATT	AgAATACCAT		
msa252409.2{85_M781}	TGACCTCCTG	CTGTTAGATA	TGCATGATGG	AAATAGTATT	AgAATACCAT		
msa252409.2{85_18RS21}	TGACCTCCTG	CTGTTAGATA	TGCATGATGG	AAATAGTATT	AgAATACCAT		
msa252409.2{85_2603}	TGACCTCCTG	CTGTTAGATA	TGCATGATGG	AAATAGTATT	AgAATACCAT		
msa252409.2{85_A909}	TGACCTCCTG	CTGTTAGATA	TGCATGATGG	AAATAGTATT	AgAATACCAT		
msa252409.2{85_H36B}	TGACCTCCTG	CTGTTAGATA	TGCATGATGG	AAATAGTATT	AgAATACCAT		
msa252409.2{85_JM9130013}	TGACCTCCTG	CTGTTAGATA	TGCATGATGG	AAATAGTATT	AgAATACCAT		
msa252409.2{85_1169NT}	TGACCTCCTG	CTGTTAGATA	TGCATGATGG	AAATAGTATT	AgAATACCAT		
Consensus	*****	*****	****-*****	*****	*-*****		
msa252409.2{85_090.con}	851	TATCTAAATT	TAAAGAAAGA	CTTCCTTTTT	ACAAACAAAT	900	TAAGAAGAAC
msa252409.2{85_CJB110}	TATCTAAATT	TAAAGAAAGA	CTTCCTTTTT	ACAAACAAAT	TAAGAAGAAC		
msa252409.2{85_COH1}	TATCTAAATT	TAAAGAAAGA	CTTCCTTTTT	ACAAACAAAT	TAAGAAGAAC		
msa252409.2{85_M732}	TATCTAAATT	TAAAGAAAGA	CTTCCTTTTT	ACAAACAAAT	TAAGAAGAAC		
msa252409.2{85_M781}	TATCTAAATT	TAAAGAAAGA	CTTCCTTTTT	ACAAACAAAT	TAAGAAGAAC		
msa252409.2{85_18RS21}	TATCTAAATT	TAAAGAAAGA	CTTCCTTTTT	ACAAACAAAT	TAAGAAGAAC		
msa252409.2{85_2603}	TATCTAAATT	TAAAGAAAGA	CTTCCTTTTT	ACAAACAAAT	TAAGAAGAAC		
msa252409.2{85_A909}	TATCTAAATT	TAAAGAAAGA	CTTCCTTTTT	ACAAACAAAT	TAAGAAGAAC		
msa252409.2{85_H36B}	TATCTAAATT	TAAAGAAAGA	CTTCCTTTTT	ACAAACAAAT	TAAGAAGAAC		
msa252409.2{85_JM9130013}	TATCTAAATT	TAAAGAAAGA	CTTCCTTTTT	ACAAACAAAT	TAAGAAGAAC		
msa252409.2{85_1169NT}	TATCTAAATT	TAAAGAAAGA	CTTCCTTTTT	ACAAACAAAT	TAAGAAGAAC		
Consensus	*****	*****	*****	*****	*****	*****	*****
msa252409.2{85_090.con}	901	CTTAAGGAAC	CTTCTATTGT	TGATATGGAA	GTGGGAGTTT	950	ACACAACAAC
msa252409.2{85_CJB110}	CTTAAGGAAC	CTTCTATTGT	TGATATGGAA	GTGGGAGTTT	ACACAACAAC		
msa252409.2{85_COH1}	CTTAAGGAAC	CTTCTATTGT	TGATATGGAA	GTGGGAGTTT	ACACAACAAC		
msa252409.2{85_M732}	CTTAAGGAAC	CTTCTATTGT	TGATATGGAA	GTGGGAGTTT	ACACAACAAC		
msa252409.2{85_M781}	CTTAAGGAAC	CTTCTATTGT	TGATATGGAA	GTGGGAGTTT	ACACAACAAC		
msa252409.2{85_18RS21}	CTTAAGGAAC	CTTCTATTGT	TGATATGGAA	GTGGGAGTTT	ACACAACAAC		
msa252409.2{85_2603}	CTTAAGGAAC	CTTCTATTGT	TGATATGGAA	GTGGGAGTTT	ACACAACAAC		
msa252409.2{85_A909}	CTTAAGGAAC	CTTCTATTGT	TGATATGGAA	GTGGGAGTTT	ACACAACAAC		
msa252409.2{85_H36B}	CTTAAGGAAC	CTTCTATTGT	TGATATGGAA	GTGGGAGTTT	ACACAACAAC		
msa252409.2{85_JM9130013}	CTTAAGGAAC	CTTCTATTGT	TGATATGGAA	GTGGGAGTTT	ACACAACAAC		
msa252409.2{85_1169NT}	CTTAAGGAAC	CTTCTATTGT	TGATATGGAA	GTGGGAGTTT	ACACAACAAC		
Consensus	*****	*****	*****	*****	*****	*****	*****
msa252409.2{85_090.con}	951	AAgTACTATT	GAATCAACCC	CTGTgAAAGC	gGAAGATACA	1000	AAAAATAAAT
msa252409.2{85_CJB110}	AAgTACTATT	GAATCAACCC	CTGTgAAAGC	gGAAGATACA	AAAAATAAAT		
msa252409.2{85_COH1}	AAgTACTATT	GAATCAACCC	CTGTgAAAGC	gGAAGATACA	AAAAATAAAT		
msa252409.2{85_M732}	AAgTACTATT	GAATCAACCC	CTGTgAAAGC	gGAAGATACA	AAAAATAAAT		
msa252409.2{85_M781}	AAgTACTATT	GAATCAACCC	CTGTgAAAGC	gGAAGATACA	AAAAATAAAT		
msa252409.2{85_18RS21}	AAaTACcATT	GAATCAACCC	CTGTtAAAGC	aGAAGATACA	AAAAATAAAT		
msa252409.2{85_2603}	AAaTACcATT	GAATCAACCC	CTGTtAAAGC	aGAAGATACA	AAAAATAAAT		
msa252409.2{85_A909}	AAaTACcATT	GAATCAACCC	CTGTtAAAGC	aGAAGATACA	AAAAATAAAT		
msa252409.2{85_H36B}	AAaTACcATT	GAATCAACCC	CTGTtAAAGC	aGAAGATACA	AAAAATAAAT		
msa252409.2{85_JM9130013}	AAaTACcATT	GAATCAACCC	CTGTtAAAGC	aGAAGATACA	AAAAATAAAT		
msa252409.2{85_1169NT}	AAgTACTATT	GAATCAACCC	CTGTgAAAGC	gGAAGATACA	AAAAATAAAT		
Consensus	**_***_***	*****	****-*****	-*****	*****	*****	*****
msa252409.2{85_090.con}	1001	CAACTGATAA	AACACAAaCa	CAAAATGGTC	AGGTTGCGGA	1050	AAATAGTCAA
msa252409.2{85_CJB110}	CAACTGATAA	AACACAAaCa	CAAAATGGTC	AGGTTGCGGA	AAATAGTCAA		
msa252409.2{85_COH1}	CAACTGATAA	AACACAAaCa	CAAAATGGTC	AGGTTGCGGA	AAATAGTCAA		
msa252409.2{85_M732}	CAACTGATAA	AACACAAaCa	CAAAATGGTC	AGGTTGCGGA	AAATAGTCAA		
msa252409.2{85_M781}	CAACTGATAA	AACACAAaCa	CAAAATGGTC	AGGTTGCGGA	AAATAGTCAA		
msa252409.2{85_18RS21}	CAACTGATAA	AACACAAaCa	CAAAATGGTC	AGGTTGCGGA	AAATAGTCAA		
msa252409.2{85_2603}	CAACTGATAA	AACACAAaCa	CAAAATGGTC	AGGTTGCGGA	AAATAGTCAA		
msa252409.2{85_A909}	CAACTGATAA	AACACAAmCa	CAAAATGGTC	AGGTTGCGGA	AAATAGTCAA		
msa252409.2{85_H36B}	CAACTGATAA	AACACAAaCa	CAAAATGGTC	AGGTTGCGGA	AAATAGTCAA		
msa252409.2{85_JM9130013}	CAACTGATAA	AACACAAaCa	CAAAATGGTC	AGGTTGCGGA	AAATAGTCAA		
msa252409.2{85_1169NT}	CAACTGATAA	AACACAAaCc	CAAAATGGTC	AGGTTGCGGA	AAATAGTCAA		
Consensus	*****	*****~*	*****	*****	*****	*****	*****
msa252409.2{85_090.con}	1051	GGACAAACAA	ATAACTCAAA	TACTAATCAA	CAAGG...AC	1100	AACAGATAGC

Table 88: Comparative Sequences relating to SAG0477

msa252409.2{85_CJB110}	GGACAAACAA	ATAACTCAA	TACTAATCAA	CAAGG...AC	AACAGATAGC
msa252409.2{85_COH1}	GGACAAACAA	ATAACTCAA	TACTAATCAA	CAAGG...AC	AACAGATAGC
msa252409.2{85_M732}	GGACAAACAA	ATAACTCAA	TACTAATCAA	CAAGG...AC	AACAGATAGC
msa252409.2{85_M781}	GGACAAACAA	ATAACTCAA	TACTAATCAA	CAAGG...AC	AACAGATAGC
msa252409.2{85_18RS21}	GGACAAACAA	ATAACTCAA	TACTAATCAA	CAAGG...AC	AACAGATAGC
msa252409.2{85_2603}	GGACAAACAA	ATAACTCAA	TACTAATCAA	CAAGG...AC	AACAGATAGC
msa252409.2{85_A909}	GGACAAACAA	ATAACTCAA	TACTAATCAA	CAAGG...AC	AACAGATAGC
msa252409.2{85_H36B}	GGACAAACAA	ATAACTCAA	TACTAATCAA	CAAGG...AC	AACAGATAGC
msa252409.2{85_JM9130013}	GGACAAACAA	ATAACTCAA	TACTAATCAA	CAAGG...AC	AACAGATAGC
msa252409.2{85_1169NT}	GGACAAACAA	ATAACTCAA	TACTAATCAA	CAAGGacaAC	AACAGATAGC
Consensus	*****	*****	*****	*****	*****

	1101		1134
msa252409.2{85_090.con}	AACaGAGCAG	GCACCcAACC	CTCAAAATGT
msa252409.2{85_CJB110}	AACaGAGCAG	GCACCcAACC	CTCAAAATGT
msa252409.2{85_COH1}	AACaGAGCAG	GCACCcAACC	CTCAAAATGT
msa252409.2{85_M732}	AACaGAGCAG	GCACCcAACC	CTCAAAATGT
msa252409.2{85_M781}	AACaGAGCAG	GCACCcAACC	CTCAAAATGT
msa252409.2{85_18RS21}	AACaGAGCAG	GCACCcAACC	CTCAAAATGT
msa252409.2{85_2603}	AACaGAGCAG	GCACCcAACC	CTCAAAATGT
msa252409.2{85_A909}	AACaGAGCAG	GCACCcAACC	CTCAAAATGT
msa252409.2{85_H36B}	AACaGAGCAG	GCACCcAACC	CTCAAAATGT
msa252409.2{85_JM9130013}	AACaGAGCAG	GCACCcAACC	CTCAAAATGT
msa252409.2{85_1169NT}	AACgGAGCAG	GCACCcAACC	CTCAAAATGT
Consensus	***-*****	*****-****	*****

SEQ ID NO. 8812

STRAIN 2603 frame: 1

PKKKSDTPEKEEVVLTEWQKRNLEFLKKRKEDEEEQKRINEKLRLDKRSKLNISPEEPQ
 NTKIKKLHFPKISRPKIEKKQKKEKIVNSLAKTNRI RTAPIFVVAFLVILVSVFLLTPF
 SKQKTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQ
 FPNKFHIQVQENKI IAYAHTKQGYQPVLETGKKADPVNSSEL PKHFLTINLDKEDSIKLL
 IKDLKALDPDLISEIQVISLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKN
 LKEPSIVDMEVGVTITNTIESTPVKAEDTKNKSTDKTQTQNGQVAENSQGTNNSTNQ
 QGQQIATEQAPNPQNVN

SEQ ID NO. 8813

STRAIN H36B frame: 1

PKKKSDTPEKEEVVLTEWQKRNLEFLKKRKEDEEEQKRINEKLRLDKRSKLNISPEEPQ
 NTKIKKLHFPKISRPKIEKKQKKEKIVNSLAKTNRI RTAPIFVVAFLVILVSVFLLTPF
 SKQKTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQ
 FPNKFHIQVQENKI IAYAHTKQGYQPVLETGKKADPVNSSEL PKHFLTINLDKEDSIKLL
 IKDLKALDPDLISEIQVISLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKN
 LKEPSIVDMEVGVTITNTIESTPVKAEDTKNKSTDKTQTQNGQVAENSQGTNNSTNQ
 QGQQIATEQAPNPQNVN

SEQ ID NO. 8814

STRAIN 18RS21 frame: 1

PKKKSDTPEKEEVVLTEWQKRNLEFLKKRKEDEEEQKRINEKLRLDKRSKLNISPEEPQ
 NTKIKKLHFPKISRPKIEKKQKKEKIVNSLAKTNRI RTAPIFVVAFLVILVSVFLLTPF
 SKQKTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQ
 FPNKFHIQVQENKI IAYAHTKQGYQPVLETGKKADPVNSSEL PKHFLTINLDKEDSIKLL
 IKDLKALDPDLISEIQVISLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKN
 LKEPSIVDMEVGVTITNTIESTPVKAEDTKNKSTDKTQTQNGQVAENSQGTNNSTNQ
 QGQQIATEQAPNPQNVN

SEQ ID NO. 8815

STRAIN M732 frame: 1

PKKKSDTPEKEEVVLTEWQKRNLEFLKKRKEDEEEQKRINEKLRLDKRSKLNISPEEPQ
 NTKIKKLHFPKISRPKIEKKQKKEKIVNSLAKTNRI RTAPIFVVAFLVILVSVFLLTPF
 SKQKTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQ
 FPNKFHIQVQENKI IAYAHTKQGYQPVLETGKKADPVNSSEL PKHFLTINLDKEDSIKLL
 IKDLKALDPDLISEIQVISLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKN
 LKEPSIVDMEVGVTITNTIESTPVKAEDTKNKSTDKTQTQNGQVAENSQGTNNSTNQ
 QGQQIATEQAPNPQNVN

SEQ ID NO. 8816

STRAIN COH1 frame: 1

PKKKSDTPEKEEVVLTEWQKRNLEFLKKRKEDEEEQKRINEKLRLDKRSKLNISPEEPQ
 NTKIKKLHFPKISRPKIEKKQKKEKIVNSLAKTNRI RTAPIFVVAFLVILVSVFLLTPF
 SKQKTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQ
 FPNKFHIQVQENKI IAYAHTKQGYQPVLETGKKADPVNSSEL PKHFLTINLDKEDSIKLL
 IKDLKALDPDLISEIQVISLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKN
 LKEPSIVDMEVGVTITNTIESTPVKAEDTKNKSTDKTQTQNGQVAENSQGTNNSTNQ
 QGQQIATEQAPNPQNVN

SEQ ID NO. 8817

STRAIN M781 frame: 1

PKKKSDTPEKEEVVLTEWQKRNLEFLKKRKEDEEEQKRINEKLRLDKRSKLNISPEEPQ

Table 88: Comparative Sequences relating to SAG0477

NTTKIKKLHFPKISKPKIEKKQKKEKIVNSLAKTNRIRTAPIFVVAFLVILVSVFLLTPF
 SKQKTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQ
 FPNKFHIQVQENKI IAYAHTKQGYQPVLETGKKADPVNSSELPHHFLTINLDKEDSIKLL
 IKDLKALDPDLISEIQVISLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKN
 LKEPSIVDMEVGVTYTTTSTIESTPVKAEDTKNKSTDKTQTQNGQVAENSQGTNNSTNQ
 GQQIATEQAPNPQNVN

SEQ ID NO. 8818

STRAIN CJB110 frame: 1

PKKKSdTPEKEEVVLTEWQKRNLEFLKKRKEDEEEQKRINEKLRLDKRSKLNISPEEPQ
 NTKIKKLHFPKISKPKIEKKQKKEKIVNSLAKTNRIRTAPIFVVAFLVILVSVFLLTPF
 SKQKTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQ
 FPNKFHIQVQENKI IAYAHTKQGYQPVLETGKKADPVNSSELPHHFLTINLDKEDSIKLL
 IKDLKALDPDLISEIQVISLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKN
 LKEPSIVDMEVGVTYTTTSTIESTPVKAEDTKNKSTDKTQTQNGQVAENSQGTNNSTNQ
 GQQIATEQAPNPQNVN

SEQ ID NO. 8819

STRAIN 1169NT frame: 1

PKKKSdTPEKEEVVLTEWQKRNLEFLKKRKEDEEEQKRINEKLRLDKRSKLNISPEEPQ
 NTKIKKLHFPKISKPKIEKKQKKEKIVNSLAKTNRIRTAPIFVVAFLVILVSVFLLTPF
 SKQKTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQ
 FPNKFHIQVQENKI IAYAHTKQGYQPVLETGKKADPVNSSELPHHFLTINLDKEDSIKLL
 IKDLKALDPDLISEIQVISLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKN
 LKEPSIVDMEVGVTYTTTSTIESTPVKAEDTKNKSTDKTQTQNGQVAENSQGTNNSTNQ
 GQQIATEQAPNPQNVN

SEQ ID NO. 8820

STRAIN JM9130013 frame: 1

PKKKSdTPEKEEVVLTEWQKRNLEFLKKRKEDEEEQKRINEKLRLDKRSKLNISPEEPQ
 NTKIKKLHFPKISRPKIEKKQKKEKIVNSLAKTNRIRTAPIFVVAFLVILVSVFLLTPF
 SKQKTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQ
 FPNKFHIQVQENKI IAYAHTKQGYQPVLETGKKADPVNSSELPHHFLTINLDKEDSIKLL
 IKDLKALDPDLISEIQVISLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKN
 LKEPSIVDMEVGVTYTTTSTIESTPVKAEDTKNKSTDKTQTQNGQVAENSQGTNNSTNQ
 GQQIATEQAPNPQNVN

SEQ ID NO. 8821

STRAIN A909 frame: 1

PKKKSdTPEKEEVVLTEWQKRNLEFLKKRKEDEEEQKRINEKLRLDKRSKLNISPEEPQ
 NTKIKKLHFPKISRPKIEKKQKKEKIVNSLAKTNRIRTAPIFVVAFLVILVSVFLLTPF
 SKQKTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQ
 FPNKFHIQVQENKI IAYAHTKQGYQPVLETGKKADPVNSSELPHHFLTINLDKEDSIKLL
 IKDLKALDPDLISEIQVISLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKN
 LKEPSIVDMEVGVTYTTTSTIESTPVKAEDTKNKSTDKTQTQNGQVAENSQGTNNSTNQ
 GQQIATEQAPNPQNVN

SEQ ID NO. 8822

STRAIN 090 frame: 2

KKKSdTPEKEEVVLTEWQKRNLEFLKKRKEDEEEQKRINEKLRLDKRSKLNISPEEPQ
 TTKIKKLHFPKISKPKIEKKQKKEKIVNSLAKTNRIRTAPIFVVAFLVILVSVFLLTPF
 KQKTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQ
 PNKFHIQVQENKI IAYAHTKQGYQPVLETGKKADPVNSSELPHHFLTINLDKEDSIKLL
 KDLKALDPDLISEIQVISLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKN
 KEPSIVDMEVGVTYTTTSTIESTPVKAEDTKNKSTDKTQTQNGQVAENSQGTNNSTNQ
 GQQIATEQAPNPQNVN

PRETTY of: /biotmp/msa252337.2{*} January 31, 2003 03:32 ..

	1		50
msa252337.2{85_090}	~KKKSdTPEK	EEVVLTEWQK RNLEFLKKRK	EDEEEQKRIN EKLRLDKRSK
msa252337.2{85_18RS21}	PKKKSdTPEK	EEVVLTEWQK RNLEFLKKRK	EDEEEQKRIN EKLRLDKRSK
msa252337.2{85_2603}	PKKKSdTPEK	EEVVLTEWQK RNLEFLKKRK	EDEEEQKRIN EKLRLDKRSK
msa252337.2{85_A909}	PKKKSdTPEK	EEVVLTEWQK RNLEFLKKRK	EDEEEQKRIN EKLRLDKRSK
msa252337.2{85_CJB110}	PKKKSdTPEK	EEVVLTEWQK RNLEFLKKRK	EDEEEQKRIN EKLRLDKRSK
msa252337.2{85_COH1}	PKKKSdTPEK	EEVVLTEWQK RNLEFLKKRK	EDEEEQKRIN EKLRLDKRSK
msa252337.2{85_H36B}	PKKKSdTPEK	EEVVLTEWQK RNLEFLKKRK	EDEEEQKRIN EKLRLDKRSK
msa252337.2{85_JM9130013}	PKKKSdTPEK	EEVVLTEWQK RNLEFLKKRK	EDEEEQKRIN EKLRLDKRSK
msa252337.2{85_M732}	PKKKSdTPEK	EEVVLTEWQK RNLEFLKKRK	EDEEEQKRIN EKLRLDKRSK
msa252337.2{85_M781}	PKKKSdTPEK	EEVVLTEWQK RNLEFLKKRK	EDEEEQKRIN EKLRLDKRSK
msa252337.2{85_1169NT}	PKKKSdTPEK	EEVVLTEWQK RNLEFLKKRK	EDEEEQKRIN EKLRLDKRSK
Consensus	*****	*****	*****
	51		100
msa252337.2{85_090}	LNISPEEPQ	NTTKIKKLHF PKISKPKIEK	KQKKEKIVNS LAKTNRIRTA
msa252337.2{85_18RS21}	LNISPEEPQ	NTTKIKKLHF PKISrPKIEK	KQKKEKIVNS LAKTNRIRTA
msa252337.2{85_2603}	LNISPEEPQ	NTTKIKKLHF PKISrPKIEK	KQKKEKIVNS LAKTNRIRTA
msa252337.2{85_A909}	LNISPEEPQ	NTTKIKKLHF PKISrPKIEK	KQKKEKIVNS LAKTNRIRTA
msa252337.2{85_CJB110}	LNISPEEPQ	NTTKIKKLHF PKISKPKIEK	KQKKEKIVNS LAKTNRIRTA

Table 88: Comparative Sequences relating to SAG0477

msa252337.2{85_COH1}	LNISPEEPQ	NTTKIKKLHF	PKISKPKIEK	KQKKEKIVNS	LAKTNRIRTA
msa252337.2{85_H36B}	LNISPEEPQ	NTTKIKKLHF	PKISrPKIEK	KQKKEKIVNS	LAKTNRIRTA
msa252337.2{85_JM9130013}	LNISPEEPQ	NTTKIKKLHF	PKISrPKIEK	KQKKEKIVNS	LAKTNRIRTA
msa252337.2{85_M732}	LNISPEEPQ	NTTKIKKLHF	PKISKPKIEK	KQKKEKIVNS	LAKTNRIRTA
msa252337.2{85_M781}	LNISPEEPQ	NTTKIKKLHF	PKISKPKIEK	KQKKEKIVNS	LAKTNRIRTA
msa252337.2{85_1169NT}	LNISPEEPQ	NTTKIKKLHF	PKISKPKIEK	KQKKEKIVNS	LAKTNRIRTA
Consensus	*****	*****	*****	*****	*****
msa252337.2{85_090}	PIFvVAFLVI	LVSFLLTPF	SKQKTITVSG	NQHTPDDILI	EKTNIQKNDY
msa252337.2{85_18RS21}	PIFvVAFLVI	LVSFLLTPF	SKQKTITVSG	NQHTPDDILI	EKTNIQKNDY
msa252337.2{85_2603}	PIFvVAFLVI	LVSFLLTPF	SKQKTITVSG	NQHTPDDILI	EKTNIQKNDY
msa252337.2{85_A909}	PIFvVAFLVI	LVSFLLTPF	SKQKTITVSG	NQHTPDDILI	EKTNIQKNDY
msa252337.2{85_CJB110}	PIFvVAFLVI	LVSFLLTPF	SKQKTITVSG	NQHTPDDILI	EKTNIQKNDY
msa252337.2{85_COH1}	PIFvVAFLVI	LVSFLLTPF	SKQKTITVSG	NQHTPDDILI	EKTNIQKNDY
msa252337.2{85_H36B}	PIFvVAFLVI	LVSFLLTPF	SKQKTITVSG	NQHTPDDILI	EKTNIQKNDY
msa252337.2{85_JM9130013}	PIFvVAFLVI	LVSFLLTPF	SKQKTITVSG	NQHTPDDILI	EKTNIQKNDY
msa252337.2{85_M732}	PIFvVAFLVI	LVSFLLTPF	SKQKTITVSG	NQHTPDDILI	EKTNIQKNDY
msa252337.2{85_M781}	PIFvVAFLVI	LVSFLLTPF	SKQKTITVSG	NQHTPDDILI	EKTNIQKNDY
msa252337.2{85_1169NT}	PIFvVAFLVI	LVSFLLTPF	SKQKTITVSG	NQHTPDDILI	EKTNIQKNDY
Consensus	***-*****	*****	*****	*****	*****
msa252337.2{85_090}	FFSLIFKHKA	IEQRLAAEDV	WVKTAQMTYQ	FPNKFHIQVQ	ENKI IAYAHT
msa252337.2{85_18RS21}	FFSLIFKHKA	IEQRLAAEDV	WVKTAQMTYQ	FPNKFHIQVQ	ENKI IAYAHT
msa252337.2{85_2603}	FFSLIFKHKA	IEQRLAAEDV	WVKTAQMTYQ	FPNKFHIQVQ	ENKI IAYAHT
msa252337.2{85_A909}	FFSLIFKHKA	IEQRLAAEDV	WVKTAQMTYQ	FPNKFHIQVQ	ENKI IAYAHT
msa252337.2{85_CJB110}	FFSLIFKHKA	IEQRLAAEDV	WVKTAQMTYQ	FPNKFHIQVQ	ENKI IAYAHT
msa252337.2{85_COH1}	FFSLIFKHKA	IEQRLAAEDV	WVKTAQMTYQ	FPNKFHIQVQ	ENKI IAYAHT
msa252337.2{85_H36B}	FFSLIFKHKA	IEQRLAAEDV	WVKTAQMTYQ	FPNKFHIQVQ	ENKI IAYAHT
msa252337.2{85_JM9130013}	FFSLIFKHKA	IEQRLAAEDV	WVKTAQMTYQ	FPNKFHIQVQ	ENKI IAYAHT
msa252337.2{85_M732}	FFSLIFKHKA	IEQRLAAEDV	WVKTAQMTYQ	FPNKFHIQVQ	ENKI IAYAHT
msa252337.2{85_M781}	FFSLIFKHKA	IEQRLAAEDV	WVKTAQMTYQ	FPNKFHIQVQ	ENKI IAYAHT
msa252337.2{85_1169NT}	FFSLIFKHKA	IEQRLAAEDV	WVKTAQMTYQ	FPNKFHIQVQ	ENKI IAYAHT
Consensus	*****	*****	*****	*****	*****
msa252337.2{85_090}	KQGYQPVLET	GKKADPNVSS	ELPKHFLTIN	LDKEDSIKLL	IKDLKALDPD
msa252337.2{85_18RS21}	KQGYQPVLET	GKKADPNVSS	ELPKHFLTIN	LDKEDSIKLL	IKDLKALDPD
msa252337.2{85_2603}	KQGYQPVLET	GKKADPNVSS	ELPKHFLTIN	LDKEDSIKLL	IKDLKALDPD
msa252337.2{85_A909}	KQGYQPVLET	GKKADPNVSS	ELPKHFLTIN	LDKEDSIKLL	IKDLKALDPD
msa252337.2{85_CJB110}	KQGYQPVLET	GKKADPNVSS	ELPKHFLTIN	LDKEDSIKLL	IKDLKALDPD
msa252337.2{85_COH1}	KQGYQPVLET	GKKADPNVSS	ELPKHFLTIN	LDKEDSIKLL	IKDLKALDPD
msa252337.2{85_H36B}	KQGYQPVLET	GKKADPNVSS	ELPKHFLTIN	LDKEDSIKLL	IKDLKALDPD
msa252337.2{85_JM9130013}	KQGYQPVLET	GKKADPNVSS	ELPKHFLTIN	LDKEDSIKLL	IKDLKALDPD
msa252337.2{85_M732}	KQGYQPVLET	GKKADPNVSS	ELPKHFLTIN	LDKEDSIKLL	IKDLKALDPD
msa252337.2{85_M781}	KQGYQPVLET	GKKADPNVSS	ELPKHFLTIN	LDKEDSIKLL	IKDLKALDPD
msa252337.2{85_1169NT}	KQGYQPVLET	GKKADPNVSS	ELPKHFLTIN	LDKEDSIKLL	IKDLKALDPD
Consensus	*****	*****	*****	*****	*****
msa252337.2{85_090}	LISEIQVISL	ADSKTTPDLL	LLDMHDGNSI	rIPLSKFKER	LPFYKQIKKN
msa252337.2{85_18RS21}	LISEIQVISL	ADSKTTPDLL	LLDMHDGNSI	rIPLSKFKER	LPFYKQIKKN
msa252337.2{85_2603}	LISEIQVISL	ADSKTTPDLL	LLDMHDGNSI	rIPLSKFKER	LPFYKQIKKN
msa252337.2{85_A909}	LISEIQVISL	ADSKTTPDLL	LLDMHDGNSI	xIPLSKFKER	LPFYKQIKKN
msa252337.2{85_CJB110}	LISEIQVISL	ADSKTTPDLL	LLDMHDGNSI	rIPLSKFKER	LPFYKQIKKN
msa252337.2{85_COH1}	LISEIQVISL	ADSKTTPDLL	LLDMHDGNSI	rIPLSKFKER	LPFYKQIKKN
msa252337.2{85_H36B}	LISEIQVISL	ADSKTTPDLL	LLDMHDGNSI	rIPLSKFKER	LPFYKQIKKN
msa252337.2{85_JM9130013}	LISEIQVISL	ADSKTTPDLL	LLDMHDGNSI	rIPLSKFKER	LPFYKQIKKN
msa252337.2{85_M732}	LISEIQVISL	ADSKTTPDLL	LLDMHDGNSI	rIPLSKFKER	LPFYKQIKKN
msa252337.2{85_M781}	LISEIQVISL	ADSKTTPDLL	LLDMHDGNSI	rIPLSKFKER	LPFYKQIKKN
msa252337.2{85_1169NT}	LISEIQVISL	ADSKTTPDLL	LLDMHDGNSI	rIPLSKFKER	LPFYKQIKKN
Consensus	*****	*****	*****	-*****	*****
msa252337.2{85_090}	LKEPSIVDME	VGVTtTtTI	ESTPVKAEDT	KNKSTDKTQ	QNGQVAENSQ
msa252337.2{85_18RS21}	LKEPSIVDME	VGVTtTtTI	ESTPVKAEDT	KNKSTDKTQ	QNGQVAENSQ
msa252337.2{85_2603}	LKEPSIVDME	VGVTtTtTI	ESTPVKAEDT	KNKSTDKTQ	QNGQVAENSQ
msa252337.2{85_A909}	LKEPSIVDME	VGVTtTtTI	ESTPVKAEDT	KNKSTDKTQx	QNGQVAENSQ
msa252337.2{85_CJB110}	LKEPSIVDME	VGVTtTtTI	ESTPVKAEDT	KNKSTDKTQ	QNGQVAENSQ
msa252337.2{85_COH1}	LKEPSIVDME	VGVTtTtTI	ESTPVKAEDT	KNKSTDKTQ	QNGQVAENSQ
msa252337.2{85_H36B}	LKEPSIVDME	VGVTtTtTI	ESTPVKAEDT	KNKSTDKTQ	QNGQVAENSQ
msa252337.2{85_JM9130013}	LKEPSIVDME	VGVTtTtTI	ESTPVKAEDT	KNKSTDKTQ	QNGQVAENSQ
msa252337.2{85_M732}	LKEPSIVDME	VGVTtTtTI	ESTPVKAEDT	KNKSTDKTQ	QNGQVAENSQ
msa252337.2{85_M781}	LKEPSIVDME	VGVTtTtTI	ESTPVKAEDT	KNKSTDKTQ	QNGQVAENSQ
msa252337.2{85_1169NT}	LKEPSIVDME	VGVTtTtTI	ESTPVKAEDT	KNKSTDKTQ	QNGQVAENSQ
Consensus	*****	*****-*	*****	*****	*****
msa252337.2{85_090}	GQTNNSTNTQ	QGQQiatega	pnpqnv-		
msa252337.2{85_18RS21}	GQTNNSTNTQ	QGQQiatega	pnpqnv-		
msa252337.2{85_2603}	GQTNNSTNTQ	QGQQiatega	pnpqnv-		
msa252337.2{85_A909}	GQTNNSTNTQ	QGQQiatega	pnpqnv-		

Table 88: Comparative Sequences relating to SAG0477

msa252337.2{85_CJB110}	GQTNNSENTNQ	QGQQiateqa	pnpqnv~
msa252337.2{85_COH1}	GQTNNSENTNQ	QGQQiateqa	pnpqnv~
msa252337.2{85_H36B}	GQTNNSENTNQ	QGQQiateqa	pnpqnv~
msa252337.2{85_JM9130013}	GQTNNSENTNQ	QGQQiateqa	pnpqnv~
msa252337.2{85_M732}	GQTNNSENTNQ	QGQQiateqa	pnpqnv~
msa252337.2{85_M781}	GQTNNSENTNQ	QGQQiateqa	pnpqnv~
msa252337.2{85_1169NT}	GQTNNSENTNQ	QGQQiateq	apnpqnv~
Consensus	*****	****-	-----*

Table 89: Comparative Sequences relating to SAG1350

SEQ ID NO. 8901

STRAIN 2603

ATGAAAAAAGGACAAGTAAATGATACTAAGCAATCTTACTCTCTACGTAAA
 TATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCATTTCATAATGGTCACAAGTCCTGTT
 TTTGCGGATCAAACCTACATCGGTTCAAGTTAATAATCAGACAGGCACTAGTGTGGATGCT
 AATAATCTTCCAATGAGACAAGTGCGTCAAGTGTGATTACTTCCAATAATGATAGTGT
 CAAGCGTCTGATAAAGTTGTAAATAGTCAAAATACGGCAACAAAGGACATTACTACTCCT
 TTAGTAGAGACAAAGCCAATGGTGGAAAAACATTACCTGAACAAGGGAATTATGTTTAT
 AGCAAAGAAACCGAGGTGAAAAATACACCTTCAAATCAGCCCCAGTAGCTTTCTATGCA
 AAGAAAGGTGATAAAGTTTCTATGACCAAGTATTTAATAAAGATAATGTGAAATGGATT
 TCATATAAGTCTTTTGTGGCGTACGTGATACGCAGCTATTGAGTCACTAGATCCATCA
 GGAGGTTTCAGAGACTAAAGCACCTACTCCTGTAAACAAATTTCAGGAAGCAATAATCAAGAG
 AAAATAGCAACGCAAGGAAATTATACATTTTACATAAAGTAGAAGTAAAAAATGAAGCT
 AAGGTAGCGAGTCCAACCTCAATTTACATTGGACAAAGGAGACAGAATTTTTTACGACCAA
 ATACTAACTATTGAAGGAAATCAGTGGTTATCTTATAAATCATTCAATGGTGTTCGTGCT
 TTTGTTTTGTAGGTAAAGCATCTTCAGTAGAAAAAAGTGAAGATAAAGAAAAAGTGTCT
 CCTCAACCACAAGCCCGTATTACTAAAACCTGGTAGACTGACTATTTCTAACGAAAACACT
 ACAGGTTTTGATATTTAATTACGAATATTAAAGATGATAACGGTATCGCTGCTGTTAAG
 GTACCGGTTTGGACTGAACAAGGAGGGCAAGATGATATTAAATGGTATACAGCTGTAACCT
 ACTGGGGATGGCAACTACAAAGTAGCTGTATCATTGCTGACCATAAGAATGAGAAGGGT
 CTTTATAATATTCAATTTATACTACCAAGAAGCTAGTGGGACACTTGTAGGTGTAACAGGA
 ACTAAAGTGACAGTAGCTGGAACCTAATCTTCTCAAGAACCTATTGAAAAATGGTTTAGCA
 AAGACTGGTGTATATAATATTATCGGAAGTACTGAAGTAAAAAATGAAGCTAAAAATATCA
 AGTCAGACCCAAATTTACTTTAGAAAAAGGTGACAAAAATAAATTATGATCAAGTATTGACA
 GCAGATGGTTACCAAGTGGATTTCTTACAAATCTTATAGTGGTGTTCGTGCTATATTCCT
 GTGAAAAAGCTAACTACAAGTAGTGAAGAAAGCGAAAGATGAGGCGACTAAACCGACTAGT
 TATCCCAACTTACCTAAAACAGGTACCTATACATTTACTAAAACCTGTAGATGTGAAAAGT
 CAACCTAAAGTATCAAGTCCAGTGGAAATTTAATTTTCAAAGGGTGAAAAAATACATTAT
 GATCAAGTGTTAGTAGTAGATGGTCATCAGTGGATTTTATACAAGAGTTATTCCGGTATT
 CGTCGCTATATTGAAATT

SEQ ID NO. 8902

STRAIN 090

AAAAAAGGACAAGTAAATGATACTAAGCAATCTTACT
 CTCTACGTAAATATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCATTTC
 ATAATGGTCACAAGTCCTGTTTTTGGCGATCAAACCTACATCGGTTCAAGT
 TAATAATCAGACAGGCACTAGTGTGGATGCTAATAATCTTCCAATGAGA
 CAAGTGCCTCAAGTGTGATTACTTCCAATAATGATAGTGTTCAGCGTCT
 GATAAAGTTGTAAATAGTCAAAATACGGCAACAAAGGACATTACTACTCC
 TTTAGTAGAGACAAAGCCAATGGTGGAAAAACATTACCTGAACAAGGGA
 ATTATGTTTTATAGCAAGAAACCGAGGTGAAAAATACACCTTCAAATCA
 GCCCCAGTAGCTTTCTATGCAAGAAAGGTGATAAAGTTTTCTATGACCA
 AGTATTTAATAAAGATAATGTGAAATGGATTTATATAAGTCTTTTTGTG
 GCGTACGTGATACGCAGCTATTGAGTCACTAGATCCATCAGGAGGTTCA
 GAGACTAAAGCACCTACTCCTGTAAACAAATTTCAGGAAGCAATAATCAAGA
 GAAAAATAGCAACGCAAGGAAATTATACATTTTACATAAAGTAGAAGTAA
 AAAATGAAGCTAAGGTAGCGAGTCCAACCTCAATTTACATTGGACAAAGGA
 GACAGAATTTTTTACGACCAAATACTAATTTGAAGGAAATCAGTGGTT
 ATCTTATAAATCATTCAATGGTGTTCGTGTTTTGTTTTGTCTAGGTAAAG
 CATCTTCAGTAGAAAAAAGTGAAGATAAAGAAAAAGTGTCTCTCAACCA
 CAAGCCCGTATTACTAAAACCTGGTAGACTGACTATTTCTAACGAAACAAC
 TACAGGTTTTGATATTTAATTACGAATATTAAAGATGATAACGGTATCG
 CTGCTGTTAAGGTACCGGTTTTGGACTGAACAAGGAGGGCAAGATGATATT
 AAATGGTATACAGCTGTAACCTACTGGGGATGGCAACTACAAAGTAGCTGT
 ATCATTGTGCTGACCATAAGAATGAGAAGGGTCTTTATAATATTCAATTTAT
 ACTACCAAGAAGCTAGTGGGACACTTGTAGGTGTAACAGGAACTAAAGTG
 ACAGTAGCTGGAACCTAATCTTCTCAAGAACCTATTGAAAAATGGTTTAGC
 AAAGACTGGTGTTTATAATATTATCGGAAGTACTGAAGTAAAAAATGAAG
 CTAAAAATATCAAGTCAGACCCAATTTACTTTAGAAAAAGGTGACAAATA
 AATTATGATCAAGTATTGACAGCAGATGGTTACCAGTGGATTTCTTACAA
 ATCTTATAGTGGTGTTCGTGCTATATTCTGTGAAAAAGCTAACTACAA
 GTAGTGAAAAAGCGAAAGATGAGGCGACTAAACCGACTAGTTATCCCAAC
 TTACCTAAAAACAGGTACCTATACATTTACTAAAACCTGTAGATGTGAAGAG
 TCAACCTAAAGTATCAAGTCCAGTGGAAATTTAATTTTCAAAGGGTGAAA
 AAATACATTATGATCAAGTGTAGTAGTAGATGGTCATCAGTGGATTTCA
 TACAAGAGTTATTCCGGTATTTCGTGCTATATTGAAATT

SEQ ID NO. 8903

STRAIN A909

AAAAAAGGACAAGTAAATGATACTAAGCAATCTTAC
 TCTCTACGTAAATATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCATT
 CATAATGGTCACAAGTCCTGTTTTTGGCGATCAAACCTACATCGGTTCAAG
 TTAATAATCAGACAGGCACTAGTGTGGATGCTAATAATCTTCCAATGAG
 ACAAGTGCGTCAAGTGTGATTACTTCCAATAATGATAGTGTTCAGCGTC
 TGATAAAGTTGTAAATAGTCAAAATACGGCAACAAAGGACATTACTACTC
 CTTTAGTAGAGACAAAGCCAATGGTGGAAAAACATTACCTGAACAAGGG
 AATTATGTTTTATAGCAAAGAAACCGAGGTGAAAAATACACCTTCAAATC
 AGCCCCAGTAGCTTTCTATGCAAGAAAGGTGATAAAGTTTTCTATGACC
 AAGTATTTAATAAAGATAATGTGAAATGGATTTTCATATAAGTCTTTTTGT
 GGCGTACGTGATACGCAGCTATTGAGTCACTAGATCCATCAGGAGGTTTC
 AGAGACTAAAAGCACCTACTCCTGTAAACAAATTTCAGGAAGCAATAATCAAG
 AGAAAAATAGCAACGCAAGGAAATTATACATTTTACATAAAGTAGAAGTA
 AAAAATGAAGCTAAGGTAGCGAGTCCAACCTCAATTTACATTGGACAAAGG

Table 89: Comparative Sequences relating to SAG1350

AGACAGAATTTTACGACCAAATACTAACTATTGAAGGAAATCAGTGGT
TATCTTATAAATCATTCATGGTGTTCGTCTGTTTGTtTGCTAGGTAAA
GCATCTTCAGTAGAAAAAAGTGAAGATAAAGAAAAAGTGTCTCCTCAACC
ACAAGCCCGTATTACTAAACTGGTAGACTGACTATTCTAACGAAACAA
CTACAGGTTTGTATTTTAATTACGAATATTAAAGATGATAACGGTATC
GCTGCTGTAAAGGTACCGGTTTGGACTGAACAAGGAGGGCAAGATGATAT
TAAATGGTATACAGCTGTAACTACTGGGGATGGCAACTACAAAGTAGCTG
TATCATTTGCTGACCATAAGAATGAGAAGGGTCTTTATAATATTCAATTTA
TACTACCAAGAAGCTAGTGGGACACTTGTAGGTGTAACAGGAAGTAAAGT
GACAGTAGCTGGAACATAATTCTTCTCAAGAACCTATTGAAAATGGTTTAG
CAAAGACTGGTGTtTATAATATTATCGGAAGTACTGAAGTAAAAAATGAA
GCTAAAAATATCAAGTCAGACCCAATTTACTTTAGAAAAAGGTGACAAAAT
AAATTATGATCAAGTATTGACAGCAGATGGTTACCAGTGGATTTCTTACA
AATCTTATAGTGGTGTTCGTCTGCTATATTCTGTGAAAAAGCTAACTACA
AGTAGTGAAAAAGCGAAAGATGAGGCGACTAAACCGACTAGTTATCCCAA
CTTACCTAAAACAGGTACCTATACATTTACTAAAAGTGTAGATGTGAAGA
GTCAACCTAAAGTATCAAGTCCAGTGGAAATTTAATTTTCAAAGGGTGAA
AAAAATACATTATGATCAAGTGTTAGTAGTAGATGGTCATCAGTGGATTTT
ATACAAGAGTTATTCCGGTATTCTGCTGCTATATTGAAATT

SEQ ID NO. 8904

STRAIN H36B

AAAAAAGGACAAGTAAATGATACTAAGCAATCTTACT
CTCTACGTAAATATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCATT
ATAATGGTCACAAGTCCTGTTTGGCGATCAAACCTACATCGGTTCAAGT
TAATAATCAGACAGGCACTAGTGTGGATGATAATAATCTTCCAATGAGA
CAAGTGCGTCAAGTGTGATTACTTCCAATAATGATAGTGTCAAGCGTCT
GATAAAGTTGTAAATAGTCAAAATACGGCAACAAAGGACATTACTACTCC
TTTAGTAGAGACAAAGCCAATGGTGGAAAAACATTACCTGAACAAGGGA
ATTATGTTTATAGCAAAGAAACCGAGGTGAAAAATACACCTTCAAATCA
GCCCCAGTAGCTTTCTATGCAAAGAAAGGTGATAAAGTTTCTATGACCA
AGTATTTAATAAAGATAATGTGAAATGGATTTATATAAGTCTTTTGTG
GCGTACGTCGATACGCAGCTATTGAGTCACTAGATCCATCAGGAGGTTCA
GAGACTAAAGCACCTACTCTGTAAACAAATTCAGGAAGCAATAATCAAGA
GAAAATAGCAACGCAAGGAAATTATACATTTTACATAAAGTAGAAGTAA
AAAATGAAGCTAAGGTAGCGAGTCCAACCTCAATTTACATTGGACAAAGGA
GACAGAATTTTACGACCAATACTAACTATTGAAGGAAATCAGTGGTT
ATCTTATAAATCATTCAATGGTGTTCGTCTGTTTGTtTGCTAGGTAAAG
CATCTTCAGTAGAAAAAAGTGAAGATAAAGAAAAAGTGTCTCCTCAACCA
CAAGCCCGTATTACTAAAAGTGGTAGACTGACTATTTCTAACGAAACAAC
TACAGGTTTGTATTTTAATTACGAATATTAAAGATGATAACGGTATCG
CTGCTGTAAAGGTACCGGTTTGGACTGAACAAGGAGGGCAAGATGATATT
AAATGGTATACAGCTGTAACTACTGGGGATGGCAACTACAAAGTAGCTGT
ATCATTTGCTGACCATAAGAATGAGAAGGGTCTTTATAATATTCAATTTAT
ACTACCAAGAAGCTAGTGGGACACTTGTAGGTGTAACAGGAAGTAAAGTG
ACAGTAGCTGGAACATAATTCTTCTCAAGAACCTATTGAAAATGGTTTAGC
AAAGACTGGTGTtTATAATATTATCGGAAGTACTGAAGTAAAAAATGAAG
CTAAAATATCAAGTCAGACCCAATTTACTTTAGAAAAAGGTGACAAAATA
AATTATGATCAAGTATTGACAGCAGATGGTTACCAGTGGATTTCTTACAA
ATCTTATAGTGGTGTTCGTCTGCTATATTCTGTGAAAAAGCTAACTACAA
GTAGTGAAAAAGCGAAAGATGAGGCGACTAAACCGACTAGTTATCCCAAC
TTACCTAAAACAGGTACCTATACATTTACTAAAAGTGTAGATGTGAAGAG
TCAACCTAAAGTATCAAGTCCAGTGGAAATTTAATTTTCAAAGGGTGAAA
AAATACATTATGATCAAGTGTTAGTAGTAGATGGTCATCAGTGGATTTCA
TACAAGAGTTATTCCGGTATTCTGCTGCTATATTGAAATT

SEQ ID NO. 8905

STRAIN 18RS21

AAAAAAGGACAAGTAAATGATACTAAGCAATCTTACTC
TCTACGTAAATATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCATTCA
TAATGGTCACAAGTCCTGTTTGGCGATCAAACCTACATCGGTTCAAGTT
AATAATCAGACAGGCACTAGTGTGGATGCTAATAATCTTCCAATGAGAC
AAGTGCGTCAAGTGTGATTACTTCCAATAATGATAGTGTCAAGCGTCTG
ATAAAGTTGTAAATAGTCAAAATACGGCAACAAAGGACATTACTACTCCT
TTAGTAGAGACAAAGCCAATGGTGGAAAAACATTACCTGAACAAGGGAA
TTATGTTTATAGCAAAGAAACCGAGGTGAAAAATACACCTTCAAATCAG
CCCCAGTAGCTTTCTATGCAAAGAAAGGTGATAAAGTTTCTATGACCAA
GTATTTAATAAAGATAATGTGAAATGGATTTATATAAGTCTTTTGTGG
CGTACGTCGATACGCAGCTATTGAGTCACTAGATCCATCAGGAGGTTTCA
GAGCTAAAGCACCTACTCTGTAAACAAATTCAGGAAGCAATAATCAAGAG
AAAATAGCAACGCAAGGAAATTATACATTTTACATAAAGTAGAAGTAAA
AAATGAAGcTAAGGTAGCGAGTCCAACCTCAATTTACATTGGACAAAGGAG
ACAGAATTTTACGACCAATACTAACTATTGAAGGAAATCAGTGGTTA
TCTTATAAATCATTCATGGTGTTCGTCTGTTTGTtTGCTAGGTAAAGC
ATCTTCAGTAGAAAAAAGTGAAGATAAAGAAAAAGTGTCTCCTCAACCAC
AAGCCCGTATTACTAAAAGTGGTAGACTGACTATTTCTAACGAAACAAC
ACAGGTTTGTATTTTAATTACGAATATTAAAGATGATAACGGTATCGC
TGCTGTAAAGGTACCGGTTTGGACTGAACAAGGAGGGCAAGATGATATTA
AATGGTATACAGCTGTAACTACTGGGGATGGCAACTACAAAGTAGCTGTA
TCATTTGCTGACCAATAAGAAATGAGAAGGGTCTTTATAATATTCAATTTATA
CTACCAAGAAGCTAGTGGGACACTTGTAGGTGTAACAGGAAGTAAAGTGA
CAGTAGCTGGAACATAATTCTTCTCAAGAACCTATTGAAAATGGTTTAGCA
AAGACTGGTGTtTATAATATTATCGGAAGTACTGAAGTAAAAAATGAAGC

Table 89: Comparative Sequences relating to SAG1350

TAAAATATCAAGTCAGACCCAATTTACTTTAGAAAAAGGTGACAAAATAA
 ATTATGATCAAGTATTGACAGCAGATGGTTACCAGTGGATTTCTTACAAA
 TCTTATAGTGGTGTTCGTGCTATATTCTGTGAAAAAGCTAACTACAAG
 TAGTGAAAAAGCGAAAGATGAGGCGACTAAACCGACTAGTTATCCCAACT
 TACCTAAAACAGGTACCTATACATTTACTAAAACGTAGATGTGAAAAAGT
 CAACCTAAAGTATCAAGTCCAGTGGAAATTTAATTTTCAAAGGGTGAAAA
 AATACATTATGATCAAGTGTGTAGTAGTAGATGGTCATCAGTGGATTTTAT
 ACAAGAGTTATTCCGGTATTTCGTGCTATATTGAAATT

SEQ ID NO. 8906

STRAIN M732

CAAGTAAATGATaCTAAGCAATCTTACTCTCTACGTAAATATAAAATTTGG
 TTTAGCATCAGTAATTTTAGGGTCATTATAATGGTCACAAGTCCTGTTT
 TTGCGGATCAAACACATCGGTTCAAGTTAATAATCAGACAGGCACCTAGT
 GTGGATGCTAATAATTCTTCCAATGAGACAAGTGGTCAAGTGTGATTAC
 TTCCAATAATGATAGTGTTCAGCGTCTGATAAAGTTGTAAATAGTCAAA
 ATACGGCAACAAAGGACATTACTACTCTTTAGTAGAGACAAAGCCAATG
 GTGGAAAAAACATTACCTGAACAAGGAATTATGTTTATAGCAAAAGAAAC
 CGAGGTGAAAAATACACCTTCAAAATCAGCCCCAGTAGCTTTCTATGCAA
 AGAAAGGTGATAAAGTTTTCTATGACCAAGTATTTAATAAAGATAATGTG
 AAATGGATTTTATATAAGTCTTTTGGTGGCGTACGTGATACGCAGCTAT
 TGAGTCACTAGATCCATCAGGAGGTTTCAAGACTAAAGCACCTACTCCTG
 TAACAAATTCAGGAAGCAATAATCAAGAGAAAAATAGCAACGCAAGGAAAT
 TATACATTTTACATAAAGTAGAAGTAAAAAATGAAGCTAAGGTAGCGAG
 TCCAACCTCAATTTACATTGGACAAGGAGACAGAATTTTACGACCAAA
 TACTAACTatTGAAGGAAATCAGTGGTTATCTTATAAATCATTCATGGT
 GTTCGTGCTTTTGTtTtGcTAGGTAAAGCATCTTCAGTAGAAAAAACTGA
 AGATAAAGAAAAAGTGTCTCTCAACCACAAGCCCGTATTACTAAAACCTG
 GTAGACTGACTATTTCTAACGAAACAACCTACAGGTTTTGATATTTAATT
 ACGAATATTTAAGATGATAACGGTATCGCTGCTGTTAAGGTACCGGTTTG
 GACTGAACAAGGAGGGCAAGATGATATTAAATGGTATACAGCTGTAACCTA
 CTGGGGATGGCAACTACAAAGTAGCTGTATCATTTGCTGACCATAAGAAAT
 GAGAAGGGTCTTTATAATATTCATTTATACTACCAAGAAGCTAGTGGGAC
 ACTTGTAGGTGTAACAGGAACCTAAAGTGACAGTAGCTGGAACCTAATTCCT
 CTCGAAGAACCTATTGAAAATGGTTTACCAAGACTGGTGTTTATAATATT
 ATCGGAAGTACTGAAGTAAAAAATGAAGCTAAAATATCAAGTCAGACCCA
 AITTTACTTTAGAAAAAAGGTGACAAAAATAAATTATGATCAAGTATGACAG
 CAGATGGTTACCAGTGGATTTCTTACAAATCTTATAGTGGTGTTCGTGCGC
 TATATTCTGTGAAAAAGCTAACTACAAGTAGTGAAAAAGCGAAAGATGA
 GGCGACTAAACCGACTAGTTATCCCAACTTACCTAAAACAGGTACCTATA
 CATTTACTAAAACGTAGATGTGAAAAGTCAACCTAAAGTATCAAGTCCA
 GTGGAATTTAATTTTCAAAGGGTGAAAAATACATTATGATCAAGTGT
 AGTAGTAGATGGTCATCAGTGGATTTATACAAAGAGTTATTCGGGTATTC
 GTCGCTATATTGAAATT

SEQ ID NO. 8907

STRAIN COH1

AAAAAAGGACAAGTAAATGATACTAAGCAATCTTACTCTCT
 ACGTAAATATAAATTTGGTTTAGCATCAGTAATTTAGGGTCATTGATAA
 TGGTCACAAGTCCTGTTTTTGGCGATCAAACCTACATCGGTTCAAGTTAAT
 AATCAGACAGGCACTAGTGTGGATGCTAATAATTCTTCCAATGAGACAAG
 TGCGTCAAGTGTGATTACTTCCAATAATGATAGTGTTCAGCGTCTGATA
 AAGTTGTAAATAGTCAAAATACGGCAACAAAGGACATTACTACTCTTTA
 GTAGAGACAAAGCCAATGGTGGAAAAAACATTACCTGAACAAGGAATTA
 TGTTTTATAGCAAAGAAACCGAGGTGAAAAATACACCTTCAAAATCAGCCC
 CAGTAGCTTTCTATGCAAAGAAAGGTGATAAAGTTTTCTATGACCAAGTA
 TTTAATAAAGATAATGTTAAATGGATTTTATATAAGTCTTTTGGTGGCGT
 ACGTCGATACGCAGCTATTGAGTCACTAGATCCATCAGGAGGTTTCAAGAG
 CTAAAGCACCTACTCTGTAAACAAATTCAGGAAGCAATAATCAAGAGAAA
 ATAGCAACGCAAGGAAATTATACATTTTACATAAAGTAGAAGTaaAAAA
 TGAAGcTAAGGTAGCGAGTCCAACCTCAATTTACATTGGACAAAGGAGACA
 GAATTTTTTACGACCAAATACTAACTATTGAAGGAAATCAGTGGTTATCT
 TATAAATCATTCATGGTGTTCGTGTTTTGTTtTGCTAGGTAAAGCATC
 TTCAGTAGAAAAAACTGAAGATAAAGAAAAAGTGTCTCTCAACCACAAG
 CCCGTATTACTAAAACCTGGTAGACTGACTATTTCTAACGAAACAACCTACA
 GGTTTTTGATATTTAATTACGAATATTTAAAGATGATAACGGTATCGCTGC
 TGTTAAGGTACCGGTTTTGGACTGAACAAGGAGGGCAAGATGATTTAAAT
 GGTATACAGCTGTAACCTACTGGGGATGGCAACTACAAAGTAGCTGTATCA
 TTTGCTGACCATAAGAATGAGAAGGGTCTTTATAATATTCATTTATACTA
 CCAAGAAGCTAGTGGGACACTTGTAGGTGTAACAGGAACCTAAAGTGACAG
 TAGCTGGAACCTAATTCTTCTCAAGAACCTATTGAAAATGGTTTACCAAAG
 ACTGGTGTTTATAATATTATCGGAAGTACTGAAGTAAAAAATGAAGCTAA
 AATATCAAGTCAGACCCAATTTACTTTAGAAAAAAGGTGACAAAAATAAAT
 ATGATCAAGTATTGACAGCAGATGGTTACCAGTGGATTTCTTACAAATCT
 TATAGTGGTGTTCGTGCTATATTCTGTGAAAAAGCTAACTACAAGTAG
 TGAAAAAGCGAAAGATGAGGCGACTAAACCGACTAGTTATCCCAACTTAC
 CTAAAACAGGTACCTATACATTTACTAAAACGTAGATGTGAAAAAGTCAA
 CCTAAAGTATCAAGTCCAGTGGAAATTTAATTTTCAAAGGGTGAAAAAAT
 ACATTATGATCAAGTGTGTAGTAGTAGATGGTCATCAGTGGATTTATACA
 AGAGTTATTCGGGTATTTCGTGCTATATTGAAATT

SEQ ID NO. 8908

STRAIN M781

Table 89: Comparative Sequences relating to SAG1350

AAAAAAGGACAAGTAAATGATACTAAGCAATCTT
 ACTCTCTACGTAAATATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCA
 TTCATAATGGTCACAAGTCCTGTTTTGCGGATCAAACCTACATCGGTTCA
 AGTTAATAATCAGACAGGCACTAGTGTGGATGCTAATAATCTTCCAATG
 AGACAAGTGCCTCAAGTGTGATTACTTCCAATAATGATAGTGTCAAGCG
 TCTGATAAAGTTGTAAATAGTCAAAATACGGCAACAAAGGACATTACTAC
 TCCTTTAGTAGAGACAAAGCCAAATGGTGGAAAAACATTACCTGAACAAG
 GGAATTATGTTTTATAGCAAAGAAACCGAGGTGAAAAATACACCTTCAAAA
 TCAGCCCCAGTAGCTTTCTATGCAAAGAAAGGTGATAAAGTTTTCTATGA
 CCAAGTATTTAATAAAGATAATGTGAAATGGATTTTCATATAAGTCTTTTG
 GTGGCGTACGTGATACGCAGCTATTGAGTCACTAGATCCATCAGGAGGT
 TCAGAGACTAAGCAACCTACTCTCTGTAACAAATTCAGGAAGCAATAATCA
 AGAGAAAATAGCAACGCAAGGAAATATACATTTTTCACATAAAGTAGAAG
 TAAAAAATGAAGCTAAGGTAGCGAGTCCAACCTCAATTTACATTGGACAAA
 GGAGACAGAATTTTTTACGACCAAATACTAATTTGAAGGAAATCAGTG
 GTTATCTTATAAATCATTCATGGTGTTCGTCTGTTTTGTTTGTCTAGGTA
 AAGCATCTTCAGTAGAAAAAAGTGAAGATAAAGAAAAAGTGTCTCCTCAA
 CCACAAGCCCGTATTACTAAAACTGGTAGACTGACTATTTCTAACGAAAC
 AACTACAGGTTTTGATATTTTAATTACGAATATTAAGATGATAACGGTA
 TCGCTGCTGTTAAGGTACCGGTTTGGACTGAACAAGGAGGGCAAGATGAT
 ATTAAATGGTATACAGCTGTAACCTACTGGGGATGGCAACTACAAAGTAGC
 TGTATCATTTGCTGACCATAAGAATGAGAAGGGTCTTTATAATATTCATT
 TATACTACCAAGAAGCTAGTGGGACACTTGTAGGTGTAACAGGAACATAAA
 GTGACAGTAGCTGGAACATAATCTTCTCAAGAACCTATTGAAAATGGTTT
 ACCAAAGACTGGTGTTTATAATATTATCGGAAGTACTGAAGTAAAAAATG
 AAGCTAAAATATCAAGTCAGACCCAATTTACTTTAGAAAAAGGTGACAAA
 ATAAATTATGATCAAGTATTGACAGCAGATGGTTACCAGTGGATTTCTTA
 CAAATCTTATAGTGGTGTTCGTCTGCTATATTCTGTGAAAAAGCTAACTA
 CAAGTAGTGA AAAAGCGAAAGATGAGGCGACTAAACCGACTAGTTATCCC
 AACTTACCTAAAAACAGGTACCTATACATTTACTAAAACTGTAGATGTGAA
 AAGTCAACCTAAAGTATCAAGTCCAGTGGAAATTTAATTTTCAAAAGGGTG
 AAAAAATACATTATGATCAAGTGTAGTAGTAGATGGTCATCAGTGGATT
 TCATACAAGAGTTATTCCGGTATTCGTCTGCTATATTGAAATT

SEQ ID NO. 8909

STRAIN CJB110

AAAAAAGGACAAGTAAATGATACTAAGCAATCTTACTCTC
 TACGTAAATATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCATTTCATA
 ATGGTCACAAGTCCTGTTTTGCGGATCAAACCTACATCGGTTCAAGTTAA
 TAATCAGACAGGCACTAGTGTGGATGCTAATAATCTTCCAATGAGACAA
 GTGCGTCAAGTGTGATTACTTCCAATAATGATAGTGTTCAGCGTCTGAT
 AAAGTTGTAAATAGTCAAAATACGGCAACAAAGGACATTACTACTCTTT
 AGTAGAGACAAAGCCAAATGGTGGAAAAAACATTACCTGAACAAGGGAAAT
 ATGTTTATAGCAAAGAAACCGAGGTGAAAAATACACCTTCAAAATCAGCC
 CCAGTAGCTTTCTATGCAAAGAAAGGTGATAAAGTTTTCTATGACCAAGT
 ATTTAATAAAGATAATGTGAAATGGATTTTCATATAAGTCTTTTGTGGCG
 TACGTGATACGCAGCTATTGAGTCACTAGATCCATCAGGAGGTTTCAGAG
 ACTAAAGCACCTACTCTGTAAACAAATTCAGGAAGCAATAATCAAGAGAA
 AATAGCAACGCAAGGAAATATACATTTTTCACATAAAGTAGAAGTAAAAA
 ATGAAGCTAAGGTAGCGAGTCCAACCTCAATTTACATTGGACAAAGGAGAC
 AGAATTTTTTACGACCAAATACTAATTTGAAGGAAATCAGTGGTTATC
 TTATAAATCATTCATGGTGTTCGTCTGTTTTGTTTTGCTAGGTAAAGCAT
 CTTTCAAGTAGAAAAAAGTGAAGATAAAGAAAAAGTGTCTCTCTCAACCACAA
 GCCCGTATTACTAAAACTGGTAGACTGACTATTTCTAACGAAACCACTAC
 AGGTTTTGATATTTTAATTACGAATATTAAGATGATAACGGTATTCGCTG
 CTGTTAAGGTACCGGTTTGGACTGAACAAGGAGGGCAAGATGATATTAAA
 TGGTATACAGCTGTAACCTACTGGGGATGGCAACTACAAAGTAGCTGTATC
 ATTTGCTGACCATAAGAATGAGAAGGGTCTTTATAATATTTCATTTATACT
 ACCAAGAAGCTAGTGGGACACTTGTAGGTGTAACAGGAACATAAGTGACA
 GTAGCTGGAACATAATCTTCTCAAGAACCTATTGAAAATGGTTTAGCAAA
 GACTGGTGTTTATAATATTATCGGAAGTACTGAAGTAAAAAATGAAGCTA
 AAATATCAAGTCAGACCCAATTTACTTTAGAAAAAGGTGACAAAATAAAT
 TATGATCAAGTATTGACAGCAGATGGTTACCAGTGGATTTCTTACAAATC
 TTATAGTGGTGTTCGTCTGCTATATTCTGTGAAAAAGCTAACTACAAAGTA
 GTGAAAAAGCGAAAGATGAGGCGACTAAACCGACTAGTTATCCCAACTTA
 CCTAAAACAGGTACCTATACATTTACTAAAACTGTAGATGTGAAGAGTCA
 ACCTAAAGTATCAAGTCCAGTGGAAATTTAATTTTCAAAAGGGTGAAAAAA
 TACATTATGATCAAGTGTAGTAGTAGATGGTCATCAGTGGATTTATAC
 AAGAGTTATTCCGGTATTCGTCTGCTATATTGAAATT

SEQ ID NO. 8910

STRAIN 1169NT

AAAAAAGGACAAGTAAATGATACTAAGCAATCTTACTC
 TCTACGTAAATATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCATTTCATA
 TAATGGTCACAAGTCCTGTTTTGCGGATCAAACCTACATCGGTTCAAGTT
 AATAATCAGACAGGCACTAGTGTGGATGCTAATAATCTTCCAATGAGAC
 AAGTGCCTCAAGTGTGATTACTTCCAATAATGATAGTGTTCAGCGTCTG
 ATAAAGTTGTAAATAGTCAAAATACGGCAACAAAGGACATTACTACTCT
 TTAGTAGAGACAAAGCCAAATGGTGGAAAAAACATTACCTGAACAAGGGAA
 TTATGTTTTATAGCAAAGAAACCGAGGTGAAAAATACACCTTCAAAATCAG
 CCCCAGTAGCTTTCTATGCAAAGAAAGGTGATAAAGTTTTCTATGACCAA
 GTATTTAATAAAGATAATGTGAAATGGATTTTCATATAAGTCTTTTGGTGG
 CGTACGTGATACGCAGCTATTGAGTCACTAGATCCATCAGGAGGTTTCAG

Table 89: Comparative Sequences relating to SAG1350

AGACTAAAGCACCTACTCCTGTAACAAATTCAGGAAGCAATAATCAAGAG
 AAAATAGCAACGCAAGGAAATTATACATTTTTCACATAAAGTAGAAGTAAA
 AAATGAAGCTAAGGTAGCGAGTCCAACCTCAATTTACATTGGACAAAGGAG
 ACAGAAATTTTACGACCAATACTAATTAAGGAATCAGTGGTTA
 TCTTATAAATCATTCAATGGTGTTCGTCGTTTTGTTTTGCTAGGTAAAGC
 ATCTTCAGTAGAAAAAACTGAAGATAAAGAAAAAGTGTCTCCTCAACCAC
 AAGCCCGTATTACTAAAACCTGGTAGACTGACTATTTCTAACGAAACAACT
 ACAGGTTTTGATATTTTAAATTACGAATATTAAAGATGATAACGGTATCGC
 TGCTGTTAAGGTACCGGTTTTGGACTGAACAAGGAGGGCAAGATGATATTA
 AATGGTATACAGCTGTAACCTACTGGGGATGGCAACTACAAAGTAGCTGTA
 TCATTTGCTGACCATAGAAATGAGAAGGGTCTTTATAATATTCAATTTATA
 CTACCAAGAGCTAGTGGGACACTTGTAGGTGTAACAGGAACATAAGTGA
 CAGTAGCTGGAaCTAATTTCTTCTCAAGAACCTATTGAAAATGGTTTAGCA
 AAGACTGGTGTTTATAATATTATCGGAAGTACTGAAGTAAAAAATGAAGC
 TAAAAATATCAAGTCAGACCCAAATTTACTTTAGAAAAAGGTGACAAAATAA
 ATTTATGATCAAGTATTGACAGCAGATGGTTACCAAGTGGATTTCTTACAAA
 TCTTATAGTGGTGTTCGTCGCTATATTCTGTGAAAAAGCTAACTACAAAG
 TAGTGAAAAAGCGAAAGATGAGGCGACTAAACCGACTAGTTATCCCAACT
 TACCTAAAAACAGGTACCTATACATTTACTAAAACCTGTAGATGTGAAAAGT
 CAACCTAAAGTATCAAGTCCAGTGAATTTAATTTTCAAAGGGTGAAAA
 AATACATTATGATCAAGTGTAGTAGTAGATGGTCATCAGTGGATTTTCAT
 ACAAGAGTTATTCCGGTATTTCGTCGCTATATTGAAATT

SEQ ID NO. 8911

STRAIN JM9130013

AAAAAAGGACAAGTAAATGATACTAAGCAATCTTACT
 CTCTACGTAAATATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCATTC
 ATAATGGTCACAAGTCTGTTTTTGGCGATCAAACTACATCGGTTCAAGT
 TAATAATCAGACAGGCACTAGTGTGGATGCTAATAATTTCTTCCAATGAGA
 CAAGTGCCTCAAGTGTGATTACTTCCAATAATGATAGTGTCAAGCGTCT
 GATAAAGTTGTAAATAGTCAAAATACGGCAACAAAGGACATTACTACTCC
 TTTAGTAGAGACAAAGCCAATGGTGGAAAAACATTACCTGAACAAGGGA
 ATTATGTTTTATAGCAAGAAACCGAGGTGAAAAATACACCTTCAAAATCA
 GCCCCAGTAGCTTTCTATGCAAGAAAGGTGATAAAGTTTCTATGACCA
 AGTATTTAATAAAGATAATGTGAAATGGATTTTATATAAGTCTTTTTGTG
 GCGTACGTCGATACGCACTATTGAGTCACTAGATCCATCAGGAGGTTCA
 GAGACTAAAGCACCTACTCTGTAAACAAATTCAGGAAGCAATAATCAAGA
 GAAAATAGCAACGCAAGGAAATTATACATTTTTCACATAAAGTAGAAGTAA
 AAAATGAAGCTAAGGTAGCGAGTCCAACCTCAATTTACATTGGACAAAGGA
 GACAGAATTTTACGACCAATACTAATTAAGGAATCAGTGGTT
 ATCTTATAAATCATTCAATGGTGTTCGTCGTTTTGTTTTGCTAGGTAAAG
 CATCTTCAGTAGAAAAAACTGAAGATAAAGAAAAAGTGTCTCTCAACCA
 CAAGCCCGTATTACTAAAACCTGGTAGACTGACTATTTATAACGAAACAAC
 TACAGGTTTTGATATTTTAAATTACGAATATTAAAGATGATAACGGTATCG
 CTGCTGTTAAGGTACCGGTTTTGGACTGAACAAGGAGGGCAAGATGATATT
 AAATGGTATACAGCTGTAACCTACTGGGGATGGCAACTACAAAGTAGCTGT
 ATCATTTGCTGACCATAGAATGAGAAGGGTCTTTATAATATTCAATTTAT
 ACTACCAAGAAGCTAGTGGGACACTTGTAGGTGTAACAGGAACATAAGTG
 ACAGTAGCTGGAATAATTTCTTCTCAAGAACCTATTGAAAATGGTTTAGC
 AAAGACTGGTGTTTATAATATTATCGGAAGTACTGAAGTAAAAAATGAAG
 CTAATAATATCAAGTCAGACCCAAATTTACTTTAGAAAAAGGTGACAAAATA
 AATTATGATCAAGTATTGACAGCAGATGGTTACCAAGTGGATTTCTTACAA
 ATCTTATAGTGGTGTTCGTCGCTATATTCTGTGAAAAAGCTAACTACAA
 GTAGTGAAAAAGCGAAAGATGAGGCGACTAAACCGACTAGTTATCCCAAC
 TTACCTAAAACAGGTACCTATACATTTACTAAAACCTGTAGATGTGAAGAG
 TCAACCTAAAGTATCAAGTCCAGTGGAAATTTAATTTTCAAAGGGTGAAA
 AAATACATTATGATCAAGTGTAGTAGTAGATGGTCATCAGTGGATTTCA
 TACAAGAGTTATTCCGGTATTTCGTCGCTATATTGAAATT

PRETTY of: /biotmp/msa255059.2{*} February 11, 2003 08:41 ..

	1				50
msa255059.2{91_M732}	-----	CAAGTAAA	TGATACTAAG	CAATCTTACT	CTCTACGTAA
msa255059.2{91_M781}	---AAAAAAG	GACAAGTAAA	TGATACTAAG	CAATCTTACT	CTCTACGTAA
msa255059.2{91_COH1}	---AAAAAAG	GACAAGTAAA	TGATACTAAG	CAATCTTACT	CTCTACGTAA
msa255059.2{91_18RS21}	---AAAAAAG	GACAAGTAAA	TGATACTAAG	CAATCTTACT	CTCTACGTAA
msa255059.2{91_2603}	atgAAAAAAG	GACAAGTAAA	TGATACTAAG	CAATCTTACT	CTCTACGTAA
msa255059.2{91_1169NT}	---AAAAAAG	GACAAGTAAA	TGATACTAAG	CAATCTTACT	CTCTACGTAA
msa255059.2{91_090}	---AAAAAAG	GACAAGTAAA	TGATACTAAG	CAATCTTACT	CTCTACGTAA
msa255059.2{91_A909}	---AAAAAAG	GACAAGTAAA	TGATACTAAG	CAATCTTACT	CTCTACGTAA
msa255059.2{91_CJB110}	---AAAAAAG	GACAAGTAAA	TGATACTAAG	CAATCTTACT	CTCTACGTAA
msa255059.2{91_H36B}	---AAAAAAG	GACAAGTAAA	TGATACTAAG	CAATCTTACT	CTCTACGTAA
msa255059.2{91_JM9130013}	---AAAAAAG	GACAAGTAAA	TGATACTAAG	CAATCTTACT	CTCTACGTAA
Consensus	*****	*****	*****	*****	*****

	51				100
msa255059.2{91_M732}	ATATAAATTT	GGTTTAGCAT	CAGTAATTTT	AGGGTCATTC	ATAATGGTCA
msa255059.2{91_M781}	ATATAAATTT	GGTTTAGCAT	CAGTAATTTT	AGGGTCATTC	ATAATGGTCA
msa255059.2{91_COH1}	ATATAAATTT	GGTTTAGCAT	CAGTAATTTT	AGGGTCATTC	ATAATGGTCA
msa255059.2{91_18RS21}	ATATAAATTT	GGTTTAGCAT	CAGTAATTTT	AGGGTCATTC	ATAATGGTCA
msa255059.2{91_2603}	ATATAAATTT	GGTTTAGCAT	CAGTAATTTT	AGGGTCATTC	ATAATGGTCA
msa255059.2{91_1169NT}	ATATAAATTT	GGTTTAGCAT	CAGTAATTTT	AGGGTCATTC	ATAATGGTCA

Table 89: Comparative Sequences relating to SAG1350

msa255059.2{91_090}	ATATAAATTT	GGTTTAGCAT	CAGTAATTTT	AGGGTCATTC	ATAATGGTCA
msa255059.2{91_A909}	ATATAAATTT	GGTTTAGCAT	CAGTAATTTT	AGGGTCATTC	ATAATGGTCA
msa255059.2{91_CJB110}	ATATAAATTT	GGTTTAGCAT	CAGTAATTTT	AGGGTCATTC	ATAATGGTCA
msa255059.2{91_H36B}	ATATAAATTT	GGTTTAGCAT	CAGTAATTTT	AGGGTCATTC	ATAATGGTCA
msa255059.2{91_JM9130013}	ATATAAATTT	GGTTTAGCAT	CAGTAATTTT	AGGGTCATTC	ATAATGGTCA
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	CAAGTCCTGT	TTTTGCGGAT	CAAACTACAT	CGGTTCAAGT	TAATAATCAG
msa255059.2{91_M781}	CAAGTCCTGT	TTTTGCGGAT	CAAACTACAT	CGGTTCAAGT	TAATAATCAG
msa255059.2{91_COH1}	CAAGTCCTGT	TTTTGCGGAT	CAAACTACAT	CGGTTCAAGT	TAATAATCAG
msa255059.2{91_18RS21}	CAAGTCCTGT	TTTTGCGGAT	CAAACTACAT	CGGTTCAAGT	TAATAATCAG
msa255059.2{91_2603}	CAAGTCCTGT	TTTTGCGGAT	CAAACTACAT	CGGTTCAAGT	TAATAATCAG
msa255059.2{91_1169NT}	CAAGTCCTGT	TTTTGCGGAT	CAAACTACAT	CGGTTCAAGT	TAATAATCAG
msa255059.2{91_090}	CAAGTCCTGT	TTTTGCGGAT	CAAACTACAT	CGGTTCAAGT	TAATAATCAG
msa255059.2{91_A909}	CAAGTCCTGT	TTTTGCGGAT	CAAACTACAT	CGGTTCAAGT	TAATAATCAG
msa255059.2{91_CJB110}	CAAGTCCTGT	TTTTGCGGAT	CAAACTACAT	CGGTTCAAGT	TAATAATCAG
msa255059.2{91_H36B}	CAAGTCCTGT	TTTTGCGGAT	CAAACTACAT	CGGTTCAAGT	TAATAATCAG
msa255059.2{91_JM9130013}	CAAGTCCTGT	TTTTGCGGAT	CAAACTACAT	CGGTTCAAGT	TAATAATCAG
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	ACAGGCACTA	GTGTGGATGc	TAATAATTCT	TCCAATGAGA	CAAGTGCGTC
msa255059.2{91_M781}	ACAGGCACTA	GTGTGGATGc	TAATAATTCT	TCCAATGAGA	CAAGTGCGTC
msa255059.2{91_COH1}	ACAGGCACTA	GTGTGGATGc	TAATAATTCT	TCCAATGAGA	CAAGTGCGTC
msa255059.2{91_18RS21}	ACAGGCACTA	GTGTGGATGc	TAATAATTCT	TCCAATGAGA	CAAGTGCGTC
msa255059.2{91_2603}	ACAGGCACTA	GTGTGGATGc	TAATAATTCT	TCCAATGAGA	CAAGTGCGTC
msa255059.2{91_1169NT}	ACAGGCACTA	GTGTGGATGc	TAATAATTCT	TCCAATGAGA	CAAGTGCGTC
msa255059.2{91_090}	ACAGGCACTA	GTGTGGATGc	TAATAATTCT	TCCAATGAGA	CAAGTGCGTC
msa255059.2{91_A909}	ACAGGCACTA	GTGTGGATGc	TAATAATTCT	TCCAATGAGA	CAAGTGCGTC
msa255059.2{91_CJB110}	ACAGGCACTA	GTGTGGATGc	TAATAATTCT	TCCAATGAGA	CAAGTGCGTC
msa255059.2{91_H36B}	ACAGGCACTA	GTGTGGATGc	TAATAATTCT	TCCAATGAGA	CAAGTGCGTC
msa255059.2{91_JM9130013}	ACAGGCACTA	GTGTGGATGc	TAATAATTCT	TCCAATGAGA	CAAGTGCGTC
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	AAGTGTGATT	ACTTCCAATA	ATGATAGTGT	TCAAGCGTCT	GATAAAGTTG
msa255059.2{91_M781}	AAGTGTGATT	ACTTCCAATA	ATGATAGTGT	TCAAGCGTCT	GATAAAGTTG
msa255059.2{91_COH1}	AAGTGTGATT	ACTTCCAATA	ATGATAGTGT	TCAAGCGTCT	GATAAAGTTG
msa255059.2{91_18RS21}	AAGTGTGATT	ACTTCCAATA	ATGATAGTGT	TCAAGCGTCT	GATAAAGTTG
msa255059.2{91_2603}	AAGTGTGATT	ACTTCCAATA	ATGATAGTGT	TCAAGCGTCT	GATAAAGTTG
msa255059.2{91_1169NT}	AAGTGTGATT	ACTTCCAATA	ATGATAGTGT	TCAAGCGTCT	GATAAAGTTG
msa255059.2{91_090}	AAGTGTGATT	ACTTCCAATA	ATGATAGTGT	TCAAGCGTCT	GATAAAGTTG
msa255059.2{91_A909}	AAGTGTGATT	ACTTCCAATA	ATGATAGTGT	TCAAGCGTCT	GATAAAGTTG
msa255059.2{91_CJB110}	AAGTGTGATT	ACTTCCAATA	ATGATAGTGT	TCAAGCGTCT	GATAAAGTTG
msa255059.2{91_H36B}	AAGTGTGATT	ACTTCCAATA	ATGATAGTGT	TCAAGCGTCT	GATAAAGTTG
msa255059.2{91_JM9130013}	AAGTGTGATT	ACTTCCAATA	ATGATAGTGT	TCAAGCGTCT	GATAAAGTTG
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	TAAATAGTCA	AAATACGGCA	ACAAAGGACA	TTACTACTCC	TTTAGTAGAG
msa255059.2{91_M781}	TAAATAGTCA	AAATACGGCA	ACAAAGGACA	TTACTACTCC	TTTAGTAGAG
msa255059.2{91_COH1}	TAAATAGTCA	AAATACGGCA	ACAAAGGACA	TTACTACTCC	TTTAGTAGAG
msa255059.2{91_18RS21}	TAAATAGTCA	AAATACGGCA	ACAAAGGACA	TTACTACTCC	TTTAGTAGAG
msa255059.2{91_2603}	TAAATAGTCA	AAATACGGCA	ACAAAGGACA	TTACTACTCC	TTTAGTAGAG
msa255059.2{91_1169NT}	TAAATAGTCA	AAATACGGCA	ACAAAGGACA	TTACTACTCC	TTTAGTAGAG
msa255059.2{91_090}	TAAATAGTCA	AAATACGGCA	ACAAAGGACA	TTACTACTCC	TTTAGTAGAG
msa255059.2{91_A909}	TAAATAGTCA	AAATACGGCA	ACAAAGGACA	TTACTACTCC	TTTAGTAGAG
msa255059.2{91_CJB110}	TAAATAGTCA	AAATACGGCA	ACAAAGGACA	TTACTACTCC	TTTAGTAGAG
msa255059.2{91_H36B}	TAAATAGTCA	AAATACGGCA	ACAAAGGACA	TTACTACTCC	TTTAGTAGAG
msa255059.2{91_JM9130013}	TAAATAGTCA	AAATACGGCA	ACAAAGGACA	TTACTACTCC	TTTAGTAGAG
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	ACAAAGCCAA	TGGTGGAAAA	AACATTACCT	GAACAAGGGA	ATTATGTTTA
msa255059.2{91_M781}	ACAAAGCCAA	TGGTGGAAAA	AACATTACCT	GAACAAGGGA	ATTATGTTTA
msa255059.2{91_COH1}	ACAAAGCCAA	TGGTGGAAAA	AACATTACCT	GAACAAGGGA	ATTATGTTTA
msa255059.2{91_18RS21}	ACAAAGCCAA	TGGTGGAAAA	AACATTACCT	GAACAAGGGA	ATTATGTTTA
msa255059.2{91_2603}	ACAAAGCCAA	TGGTGGAAAA	AACATTACCT	GAACAAGGGA	ATTATGTTTA
msa255059.2{91_1169NT}	ACAAAGCCAA	TGGTGGAAAA	AACATTACCT	GAACAAGGGA	ATTATGTTTA
msa255059.2{91_090}	ACAAAGCCAA	TGGTGGAAAA	AACATTACCT	GAACAAGGGA	ATTATGTTTA
msa255059.2{91_A909}	ACAAAGCCAA	TGGTGGAAAA	AACATTACCT	GAACAAGGGA	ATTATGTTTA
msa255059.2{91_CJB110}	ACAAAGCCAA	TGGTGGAAAA	AACATTACCT	GAACAAGGGA	ATTATGTTTA
msa255059.2{91_H36B}	ACAAAGCCAA	TGGTGGAAAA	AACATTACCT	GAACAAGGGA	ATTATGTTTA
msa255059.2{91_JM9130013}	ACAAAGCCAA	TGGTGGAAAA	AACATTACCT	GAACAAGGGA	ATTATGTTTA
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	TAGCAAAGAA	ACCGAGGTGA	AAAATACACC	TTCAAATCA	GCCCCAGTAG
msa255059.2{91_M781}	TAGCAAAGAA	ACCGAGGTGA	AAAATACACC	TTCAAATCA	GCCCCAGTAG
msa255059.2{91_COH1}	TAGCAAAGAA	ACCGAGGTGA	AAAATACACC	TTCAAATCA	GCCCCAGTAG
msa255059.2{91_18RS21}	TAGCAAAGAA	ACCGAGGTGA	AAAATACACC	TTCAAATCA	GCCCCAGTAG
msa255059.2{91_2603}	TAGCAAAGAA	ACCGAGGTGA	AAAATACACC	TTCAAATCA	GCCCCAGTAG

Table 89: Comparative Sequences relating to SAG1350

msa255059.2{91_1169NT}	TAGCAAAGAA	ACCGAGGTGA	AAAATACACC	TTCAAAATCA	GCCCCAGTAG
msa255059.2{91_090}	TAGCAAAGAA	ACCGAGGTGA	AAAATACACC	TTCAAAATCA	GCCCCAGTAG
msa255059.2{91_A909}	TAGCAAAGAA	ACCGAGGTGA	AAAATACACC	TTCAAAATCA	GCCCCAGTAG
msa255059.2{91_CJB110}	TAGCAAAGAA	ACCGAGGTGA	AAAATACACC	TTCAAAATCA	GCCCCAGTAG
msa255059.2{91_H36B}	TAGCAAAGAA	ACCGAGGTGA	AAAATACACC	TTCAAAATCA	GCCCCAGTAG
msa255059.2{91_JM9130013}	TAGCAAAGAA	ACCGAGGTGA	AAAATACACC	TTCAAAATCA	GCCCCAGTAG
Consensus	*****	*****	*****	*****	*****
401					
msa255059.2{91_M732}	CTTCTCTATGC	AAAGAAAGGT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
msa255059.2{91_M781}	CTTCTCTATGC	AAAGAAAGGT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
msa255059.2{91_COH1}	CTTCTCTATGC	AAAGAAAGGT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
msa255059.2{91_18RS21}	CTTCTCTATGC	AAAGAAAGGT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
msa255059.2{91_2603}	CTTCTCTATGC	AAAGAAAGGT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
msa255059.2{91_1169NT}	CTTCTCTATGC	AAAGAAAGGT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
msa255059.2{91_090}	CTTCTCTATGC	AAAGAAAGGT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
msa255059.2{91_A909}	CTTCTCTATGC	AAAGAAAGGT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
msa255059.2{91_CJB110}	CTTCTCTATGC	AAAGAAAGGT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
msa255059.2{91_H36B}	CTTCTCTATGC	AAAGAAAGGT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
msa255059.2{91_JM9130013}	CTTCTCTATGC	AAAGAAAGGT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
Consensus	*****	*****	*****	*****	*****
451					
msa255059.2{91_M732}	AAAGATAATG	TgAAATGGAT	TTCATATAAG	TCTTTTgGTG	GCGTACGTCG
msa255059.2{91_M781}	AAAGATAATG	TgAAATGGAT	TTCATATAAG	TCTTTTgGTG	GCGTACGTCG
msa255059.2{91_COH1}	AAAGATAATG	TtAAATGGAT	TTCATATAAG	TCTTTTgGTG	GCGTACGTCG
msa255059.2{91_18RS21}	AAAGATAATG	TgAAATGGAT	TTCATATAAG	TCTTTTtGTG	GCGTACGTCG
msa255059.2{91_2603}	AAAGATAATG	TgAAATGGAT	TTCATATAAG	TCTTTTtGTG	GCGTACGTCG
msa255059.2{91_1169NT}	AAAGATAATG	TgAAATGGAT	TTCATATAAG	TCTTTTgGTG	GCGTACGTCG
msa255059.2{91_090}	AAAGATAATG	TgAAATGGAT	TTCATATAAG	TCTTTTtGTG	GCGTACGTCG
msa255059.2{91_A909}	AAAGATAATG	TgAAATGGAT	TTCATATAAG	TCTTTTtGTG	GCGTACGTCG
msa255059.2{91_CJB110}	AAAGATAATG	TgAAATGGAT	TTCATATAAG	TCTTTTtGTG	GCGTACGTCG
msa255059.2{91_H36B}	AAAGATAATG	TgAAATGGAT	TTCATATAAG	TCTTTTtGTG	GCGTACGTCG
msa255059.2{91_JM9130013}	AAAGATAATG	TgAAATGGAT	TTCATATAAG	TCTTTTtGTG	GCGTACGTCG
Consensus	*****	*..*****	*****	*****-***	*****
501					
msa255059.2{91_M732}	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTCA	GAGACTAAAG
msa255059.2{91_M781}	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTCA	GAGACTAAAG
msa255059.2{91_COH1}	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTCA	GAGACTAAAG
msa255059.2{91_18RS21}	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTCA	GAGACTAAAG
msa255059.2{91_2603}	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTCA	GAGACTAAAG
msa255059.2{91_1169NT}	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTCA	GAGACTAAAG
msa255059.2{91_090}	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTCA	GAGACTAAAG
msa255059.2{91_A909}	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTCA	GAGACTAAAG
msa255059.2{91_CJB110}	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTCA	GAGACTAAAG
msa255059.2{91_H36B}	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTCA	GAGACTAAAG
msa255059.2{91_JM9130013}	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTCA	GAGACTAAAG
Consensus	*****	*****	*****	*****	*****
551					
msa255059.2{91_M732}	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAATAGCA
msa255059.2{91_M781}	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAATAGCA
msa255059.2{91_COH1}	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAATAGCA
msa255059.2{91_18RS21}	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAATAGCA
msa255059.2{91_2603}	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAATAGCA
msa255059.2{91_1169NT}	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAATAGCA
msa255059.2{91_090}	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAATAGCA
msa255059.2{91_A909}	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAATAGCA
msa255059.2{91_CJB110}	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAATAGCA
msa255059.2{91_H36B}	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAATAGCA
msa255059.2{91_JM9130013}	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAATAGCA
Consensus	*****	*****	*****	*****	*****
601					
msa255059.2{91_M732}	ACGCAAGGAA	ATTATACATT	TTCACATAAA	GTAGAAGTAA	AAAATGAAGC
msa255059.2{91_M781}	ACGCAAGGAA	ATTATACATT	TTCACATAAA	GTAGAAGTAA	AAAATGAAGC
msa255059.2{91_COH1}	ACGCAAGGAA	ATTATACATT	TTCACATAAA	GTAGAAGTAA	AAAATGAAGC
msa255059.2{91_18RS21}	ACGCAAGGAA	ATTATACATT	TTCACATAAA	GTAGAAGTAA	AAAATGAAGC
msa255059.2{91_2603}	ACGCAAGGAA	ATTATACATT	TTCACATAAA	GTAGAAGTAA	AAAATGAAGC
msa255059.2{91_1169NT}	ACGCAAGGAA	ATTATACATT	TTCACATAAA	GTAGAAGTAA	AAAATGAAGC
msa255059.2{91_090}	ACGCAAGGAA	ATTATACATT	TTCACATAAA	GTAGAAGTAA	AAAATGAAGC
msa255059.2{91_A909}	ACGCAAGGAA	ATTATACATT	TTCACATAAA	GTAGAAGTAA	AAAATGAAGC
msa255059.2{91_CJB110}	ACGCAAGGAA	ATTATACATT	TTCACATAAA	GTAGAAGTAA	AAAATGAAGC
msa255059.2{91_H36B}	ACGCAAGGAA	ATTATACATT	TTCACATAAA	GTAGAAGTAA	AAAATGAAGC
msa255059.2{91_JM9130013}	ACGCAAGGAA	ATTATACATT	TTCACATAAA	GTAGAAGTAA	AAAATGAAGC
Consensus	*****	*****	*****	*****	*****
651					
msa255059.2{91_M732}	TAAGGTAGCG	AGTCCAACCTC	AATTTACATT	GGACAAAGGA	GACAGAATTT
msa255059.2{91_M781}	TAAGGTAGCG	AGTCCAACCTC	AATTTACATT	GGACAAAGGA	GACAGAATTT
msa255059.2{91_COH1}	TAAGGTAGCG	AGTCCAACCTC	AATTTACATT	GGACAAAGGA	GACAGAATTT
msa255059.2{91_18RS21}	TAAGGTAGCG	AGTCCAACCTC	AATTTACATT	GGACAAAGGA	GACAGAATTT

Table 89: Comparative Sequences relating to SAG1350

msa255059.2{91_2603}	TAAGGTAGCG	AGTCCAACCTC	AATTTACATT	GGACAAAGGA	GACAGAATTT
msa255059.2{91_1169NT}	TAAGGTAGCG	AGTCCAACCTC	AATTTACATT	GGACAAAGGA	GACAGAATTT
msa255059.2{91_090}	TAAGGTAGCG	AGTCCAACCTC	AATTTACATT	GGACAAAGGA	GACAGAATTT
msa255059.2{91_A909}	TAAGGTAGCG	AGTCCAACCTC	AATTTACATT	GGACAAAGGA	GACAGAATTT
msa255059.2{91_CJB110}	TAAGGTAGCG	AGTCCAACCTC	AATTTACATT	GGACAAAGGA	GACAGAATTT
msa255059.2{91_H36B}	TAAGGTAGCG	AGTCCAACCTC	AATTTACATT	GGACAAAGGA	GACAGAATTT
msa255059.2{91_JM9130013}	TAAGGTAGCG	AGTCCAACCTC	AATTTACATT	GGACAAAGGA	GACAGAATTT
Consensus	*****	*****	*****	*****	*****
701					
msa255059.2{91_M732}	TTTACGACCA	AATACTAACT	ATTGAAGGAA	ATCAGTGGTT	ATCTTATAAA
msa255059.2{91_M781}	TTTACGACCA	AATACTAACT	ATTGAAGGAA	ATCAGTGGTT	ATCTTATAAA
msa255059.2{91_COH1}	TTTACGACCA	AATACTAACT	ATTGAAGGAA	ATCAGTGGTT	ATCTTATAAA
msa255059.2{91_18RS21}	TTTACGACCA	AATACTAACT	ATTGAAGGAA	ATCAGTGGTT	ATCTTATAAA
msa255059.2{91_2603}	TTTACGACCA	AATACTAACT	ATTGAAGGAA	ATCAGTGGTT	ATCTTATAAA
msa255059.2{91_1169NT}	TTTACGACCA	AATACTAACT	ATTGAAGGAA	ATCAGTGGTT	ATCTTATAAA
msa255059.2{91_090}	TTTACGACCA	AATACTAACT	ATTGAAGGAA	ATCAGTGGTT	ATCTTATAAA
msa255059.2{91_A909}	TTTACGACCA	AATACTAACT	ATTGAAGGAA	ATCAGTGGTT	ATCTTATAAA
msa255059.2{91_CJB110}	TTTACGACCA	AATACTAACT	ATTGAAGGAA	ATCAGTGGTT	ATCTTATAAA
msa255059.2{91_H36B}	TTTACGACCA	AATACTAACT	ATTGAAGGAA	ATCAGTGGTT	ATCTTATAAA
msa255059.2{91_JM9130013}	TTTACGACCA	AATACTAACT	ATTGAAGGAA	ATCAGTGGTT	ATCTTATAAA
Consensus	*****	*****	*****	*****	*****
751					
msa255059.2{91_M732}	TCATTCAATG	GTGTTCTGTCG	TTTTGTTTTG	CTAGGTAAAG	CATCTTCAGT
msa255059.2{91_M781}	TCATTCAATG	GTGTTCTGTCG	TTTTGTTTTG	CTAGGTAAAG	CATCTTCAGT
msa255059.2{91_COH1}	TCATTCAATG	GTGTTCTGTCG	TTTTGTTTTG	CTAGGTAAAG	CATCTTCAGT
msa255059.2{91_18RS21}	TCATTCAATG	GTGTTCTGTCG	TTTTGTTTTG	CTAGGTAAAG	CATCTTCAGT
msa255059.2{91_2603}	TCATTCAATG	GTGTTCTGTCG	TTTTGTTTTG	CTAGGTAAAG	CATCTTCAGT
msa255059.2{91_1169NT}	TCATTCAATG	GTGTTCTGTCG	TTTTGTTTTG	CTAGGTAAAG	CATCTTCAGT
msa255059.2{91_090}	TCATTCAATG	GTGTTCTGTCG	TTTTGTTTTG	CTAGGTAAAG	CATCTTCAGT
msa255059.2{91_A909}	TCATTCAATG	GTGTTCTGTCG	TTTTGTTTTG	CTAGGTAAAG	CATCTTCAGT
msa255059.2{91_CJB110}	TCATTCAATG	GTGTTCTGTCG	TTTTGTTTTG	CTAGGTAAAG	CATCTTCAGT
msa255059.2{91_H36B}	TCATTCAATG	GTGTTCTGTCG	TTTTGTTTTG	CTAGGTAAAG	CATCTTCAGT
msa255059.2{91_JM9130013}	TCATTCAATG	GTGTTCTGTCG	TTTTGTTTTG	CTAGGTAAAG	CATCTTCAGT
Consensus	*****	*****	*****	*****	*****
801					
msa255059.2{91_M732}	AGAAAAAACT	GAAGATAAAG	AAAAAGTGTC	TCCTCAACCA	CAAGCCCGTA
msa255059.2{91_M781}	AGAAAAAACT	GAAGATAAAG	AAAAAGTGTC	TCCTCAACCA	CAAGCCCGTA
msa255059.2{91_COH1}	AGAAAAAACT	GAAGATAAAG	AAAAAGTGTC	TCCTCAACCA	CAAGCCCGTA
msa255059.2{91_18RS21}	AGAAAAAACT	GAAGATAAAG	AAAAAGTGTC	TCCTCAACCA	CAAGCCCGTA
msa255059.2{91_2603}	AGAAAAAACT	GAAGATAAAG	AAAAAGTGTC	TCCTCAACCA	CAAGCCCGTA
msa255059.2{91_1169NT}	AGAAAAAACT	GAAGATAAAG	AAAAAGTGTC	TCCTCAACCA	CAAGCCCGTA
msa255059.2{91_090}	AGAAAAAACT	GAAGATAAAG	AAAAAGTGTC	TCCTCAACCA	CAAGCCCGTA
msa255059.2{91_A909}	AGAAAAAACT	GAAGATAAAG	AAAAAGTGTC	TCCTCAACCA	CAAGCCCGTA
msa255059.2{91_CJB110}	AGAAAAAACT	GAAGATAAAG	AAAAAGTGTC	TCCTCAACCA	CAAGCCCGTA
msa255059.2{91_H36B}	AGAAAAAACT	GAAGATAAAG	AAAAAGTGTC	TCCTCAACCA	CAAGCCCGTA
msa255059.2{91_JM9130013}	AGAAAAAACT	GAAGATAAAG	AAAAAGTGTC	TCCTCAACCA	CAAGCCCGTA
Consensus	*****	*****	*****	*****	*****
851					
msa255059.2{91_M732}	TTACTAAAAC	TGGTAGACTG	ACTATTTcTA	ACGAAACAAC	TACAGGTTTT
msa255059.2{91_M781}	TTACTAAAAC	TGGTAGACTG	ACTATTTcTA	ACGAAACAAC	TACAGGTTTT
msa255059.2{91_COH1}	TTACTAAAAC	TGGTAGACTG	ACTATTTcTA	ACGAAACAAC	TACAGGTTTT
msa255059.2{91_18RS21}	TTACTAAAAC	TGGTAGACTG	ACTATTTcTA	ACGAAACAAC	TACAGGTTTT
msa255059.2{91_2603}	TTACTAAAAC	TGGTAGACTG	ACTATTTcTA	ACGAAACAAC	TACAGGTTTT
msa255059.2{91_1169NT}	TTACTAAAAC	TGGTAGACTG	ACTATTTcTA	ACGAAACAAC	TACAGGTTTT
msa255059.2{91_090}	TTACTAAAAC	TGGTAGACTG	ACTATTTcTA	ACGAAACAAC	TACAGGTTTT
msa255059.2{91_A909}	TTACTAAAAC	TGGTAGACTG	ACTATTTcTA	ACGAAACAAC	TACAGGTTTT
msa255059.2{91_CJB110}	TTACTAAAAC	TGGTAGACTG	ACTATTTcTA	ACGAAACAAC	TACAGGTTTT
msa255059.2{91_H36B}	TTACTAAAAC	TGGTAGACTG	ACTATTTcTA	ACGAAACAAC	TACAGGTTTT
msa255059.2{91_JM9130013}	TTACTAAAAC	TGGTAGACTG	ACTATTTaTA	ACGAAACAAC	TACAGGTTTT
Consensus	*****	*****	*****-*	*****	*****
901					
msa255059.2{91_M732}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTTAA
msa255059.2{91_M781}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTTAA
msa255059.2{91_COH1}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTTAA
msa255059.2{91_18RS21}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTTAA
msa255059.2{91_2603}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTTAA
msa255059.2{91_1169NT}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTTAA
msa255059.2{91_090}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTTAA
msa255059.2{91_A909}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTTAA
msa255059.2{91_CJB110}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTTAA
msa255059.2{91_H36B}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTTAA
msa255059.2{91_JM9130013}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTTAA
Consensus	*****	*****	*****	*****	*****
951					
msa255059.2{91_M732}	GGTACCGGTT	TGGACTGAAC	AAGGAGGGCA	AGATGATATT	AAATGGTATA
msa255059.2{91_M781}	GGTACCGGTT	TGGACTGAAC	AAGGAGGGCA	AGATGATATT	AAATGGTATA
msa255059.2{91_COH1}	GGTACCGGTT	TGGACTGAAC	AAGGAGGGCA	AGATGATATT	AAATGGTATA
1000					

Table 89: Comparative Sequences relating to SAG1350

msa255059.2{91_18RS21}	GGTACCGGTT	TGGACTGAAC	AAGGAGGGCA	AGATGATATT	AAATGGTATA
msa255059.2{91_2603}	GGTACCGGTT	TGGACTGAAC	AAGGAGGGCA	AGATGATATT	AAATGGTATA
msa255059.2{91_1169NT}	GGTACCGGTT	TGGACTGAAC	AAGGAGGGCA	AGATGATATT	AAATGGTATA
msa255059.2{91_090}	GGTACCGGTT	TGGACTGAAC	AAGGAGGGCA	AGATGATATT	AAATGGTATA
msa255059.2{91_A909}	GGTACCGGTT	TGGACTGAAC	AAGGAGGGCA	AGATGATATT	AAATGGTATA
msa255059.2{91_CJB110}	GGTACCGGTT	TGGACTGAAC	AAGGAGGGCA	AGATGATATT	AAATGGTATA
msa255059.2{91_H36B}	GGTACCGGTT	TGGACTGAAC	AAGGAGGGCA	AGATGATATT	AAATGGTATA
msa255059.2{91_JM9130013}	GGTACCGGTT	TGGACTGAAC	AAGGAGGGCA	AGATGATATT	AAATGGTATA
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	CAGCTGTAAC	TACTGGGGAT	GGCAACTACA	AAGTAGCTGT	ATCATTGCT
msa255059.2{91_M781}	CAGCTGTAAC	TACTGGGGAT	GGCAACTACA	AAGTAGCTGT	ATCATTGCT
msa255059.2{91_COH1}	CAGCTGTAAC	TACTGGGGAT	GGCAACTACA	AAGTAGCTGT	ATCATTGCT
msa255059.2{91_18RS21}	CAGCTGTAAC	TACTGGGGAT	GGCAACTACA	AAGTAGCTGT	ATCATTGCT
msa255059.2{91_2603}	CAGCTGTAAC	TACTGGGGAT	GGCAACTACA	AAGTAGCTGT	ATCATTGCT
msa255059.2{91_1169NT}	CAGCTGTAAC	TACTGGGGAT	GGCAACTACA	AAGTAGCTGT	ATCATTGCT
msa255059.2{91_090}	CAGCTGTAAC	TACTGGGGAT	GGCAACTACA	AAGTAGCTGT	ATCATTGCT
msa255059.2{91_A909}	CAGCTGTAAC	TACTGGGGAT	GGCAACTACA	AAGTAGCTGT	ATCATTGCT
msa255059.2{91_CJB110}	CAGCTGTAAC	TACTGGGGAT	GGCAACTACA	AAGTAGCTGT	ATCATTGCT
msa255059.2{91_H36B}	CAGCTGTAAC	TACTGGGGAT	GGCAACTACA	AAGTAGCTGT	ATCATTGCT
msa255059.2{91_JM9130013}	CAGCTGTAAC	TACTGGGGAT	GGCAACTACA	AAGTAGCTGT	ATCATTGCT
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	GACCATAAGA	ATGAGAAGGG	TCTTTATAAT	ATTCAATTTAT	ACTACCAAGA
msa255059.2{91_M781}	GACCATAAGA	ATGAGAAGGG	TCTTTATAAT	ATTCAATTTAT	ACTACCAAGA
msa255059.2{91_COH1}	GACCATAAGA	ATGAGAAGGG	TCTTTATAAT	ATTCAATTTAT	ACTACCAAGA
msa255059.2{91_18RS21}	GACCATAAGA	ATGAGAAGGG	TCTTTATAAT	ATTCAATTTAT	ACTACCAAGA
msa255059.2{91_2603}	GACCATAAGA	ATGAGAAGGG	TCTTTATAAT	ATTCAATTTAT	ACTACCAAGA
msa255059.2{91_1169NT}	GACCATAAGA	ATGAGAAGGG	TCTTTATAAT	ATTCAATTTAT	ACTACCAAGA
msa255059.2{91_090}	GACCATAAGA	ATGAGAAGGG	TCTTTATAAT	ATTCAATTTAT	ACTACCAAGA
msa255059.2{91_A909}	GACCATAAGA	ATGAGAAGGG	TCTTTATAAT	ATTCAATTTAT	ACTACCAAGA
msa255059.2{91_CJB110}	GACCATAAGA	ATGAGAAGGG	TCTTTATAAT	ATTCAATTTAT	ACTACCAAGA
msa255059.2{91_H36B}	GACCATAAGA	ATGAGAAGGG	TCTTTATAAT	ATTCAATTTAT	ACTACCAAGA
msa255059.2{91_JM9130013}	GACCATAAGA	ATGAGAAGGG	TCTTTATAAT	ATTCAATTTAT	ACTACCAAGA
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	AGCTAGTGGG	ACACTTGTAG	GTGTAACAGG	AACTAAAGTG	ACAGTAGCTG
msa255059.2{91_M781}	AGCTAGTGGG	ACACTTGTAG	GTGTAACAGG	AACTAAAGTG	ACAGTAGCTG
msa255059.2{91_COH1}	AGCTAGTGGG	ACACTTGTAG	GTGTAACAGG	AACTAAAGTG	ACAGTAGCTG
msa255059.2{91_18RS21}	AGCTAGTGGG	ACACTTGTAG	GTGTAACAGG	AACTAAAGTG	ACAGTAGCTG
msa255059.2{91_2603}	AGCTAGTGGG	ACACTTGTAG	GTGTAACAGG	AACTAAAGTG	ACAGTAGCTG
msa255059.2{91_1169NT}	AGCTAGTGGG	ACACTTGTAG	GTGTAACAGG	AACTAAAGTG	ACAGTAGCTG
msa255059.2{91_090}	AGCTAGTGGG	ACACTTGTAG	GTGTAACAGG	AACTAAAGTG	ACAGTAGCTG
msa255059.2{91_A909}	AGCTAGTGGG	ACACTTGTAG	GTGTAACAGG	AACTAAAGTG	ACAGTAGCTG
msa255059.2{91_CJB110}	AGCTAGTGGG	ACACTTGTAG	GTGTAACAGG	AACTAAAGTG	ACAGTAGCTG
msa255059.2{91_H36B}	AGCTAGTGGG	ACACTTGTAG	GTGTAACAGG	AACTAAAGTG	ACAGTAGCTG
msa255059.2{91_JM9130013}	AGCTAGTGGG	ACACTTGTAG	GTGTAACAGG	AACTAAAGTG	ACAGTAGCTG
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	GAACATAATTC	TTCTCAAGAA	CCTATTGAAA	ATGGTTTAcC	AAAGACTGGT
msa255059.2{91_M781}	GAACATAATTC	TTCTCAAGAA	CCTATTGAAA	ATGGTTTAcC	AAAGACTGGT
msa255059.2{91_COH1}	GAACATAATTC	TTCTCAAGAA	CCTATTGAAA	ATGGTTTAcC	AAAGACTGGT
msa255059.2{91_18RS21}	GAACATAATTC	TTCTCAAGAA	CCTATTGAAA	ATGGTTTAgC	AAAGACTGGT
msa255059.2{91_2603}	GAACATAATTC	TTCTCAAGAA	CCTATTGAAA	ATGGTTTAgC	AAAGACTGGT
msa255059.2{91_1169NT}	GAACATAATTC	TTCTCAAGAA	CCTATTGAAA	ATGGTTTAgC	AAAGACTGGT
msa255059.2{91_090}	GAACATAATTC	TTCTCAAGAA	CCTATTGAAA	ATGGTTTAgC	AAAGACTGGT
msa255059.2{91_A909}	GAACATAATTC	TTCTCAAGAA	CCTATTGAAA	ATGGTTTAgC	AAAGACTGGT
msa255059.2{91_CJB110}	GAACATAATTC	TTCTCAAGAA	CCTATTGAAA	ATGGTTTAgC	AAAGACTGGT
msa255059.2{91_H36B}	GAACATAATTC	TTCTCAAGAA	CCTATTGAAA	ATGGTTTAgC	AAAGACTGGT
msa255059.2{91_JM9130013}	GAACATAATTC	TTCTCAAGAA	CCTATTGAAA	ATGGTTTAgC	AAAGACTGGT
Consensus	*****	*****	*****	*****-*	*****
msa255059.2{91_M732}	GTTTATAATA	TTATCGGAAG	TACTGAAGTA	AAAAATGAAG	CTAAAATATC
msa255059.2{91_M781}	GTTTATAATA	TTATCGGAAG	TACTGAAGTA	AAAAATGAAG	CTAAAATATC
msa255059.2{91_COH1}	GTTTATAATA	TTATCGGAAG	TACTGAAGTA	AAAAATGAAG	CTAAAATATC
msa255059.2{91_18RS21}	GTTTATAATA	TTATCGGAAG	TACTGAAGTA	AAAAATGAAG	CTAAAATATC
msa255059.2{91_2603}	GTTTATAATA	TTATCGGAAG	TACTGAAGTA	AAAAATGAAG	CTAAAATATC
msa255059.2{91_1169NT}	GTTTATAATA	TTATCGGAAG	TACTGAAGTA	AAAAATGAAG	CTAAAATATC
msa255059.2{91_090}	GTTTATAATA	TTATCGGAAG	TACTGAAGTA	AAAAATGAAG	CTAAAATATC
msa255059.2{91_A909}	GTTTATAATA	TTATCGGAAG	TACTGAAGTA	AAAAATGAAG	CTAAAATATC
msa255059.2{91_CJB110}	GTTTATAATA	TTATCGGAAG	TACTGAAGTA	AAAAATGAAG	CTAAAATATC
msa255059.2{91_H36B}	GTTTATAATA	TTATCGGAAG	TACTGAAGTA	AAAAATGAAG	CTAAAATATC
msa255059.2{91_JM9130013}	GTTTATAATA	TTATCGGAAG	TACTGAAGTA	AAAAATGAAG	CTAAAATATC
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	AAGTCAGACC	CAATTTACTT	TAGAAAAAGG	TGACAAAATA	AATTATGATC
msa255059.2{91_M781}	AAGTCAGACC	CAATTTACTT	TAGAAAAAGG	TGACAAAATA	AATTATGATC

Table 89: Comparative Sequences relating to SAG1350

msa255059.2{91_COH1}	AAGTCAGACC	CAATTTACTT	TAGAAAAAGG	TGACAAAATA	AATTATGATC
msa255059.2{91_18RS21}	AAGTCAGACC	CAATTTACTT	TAGAAAAAGG	TGACAAAATA	AATTATGATC
msa255059.2{91_2603}	AAGTCAGACC	CAATTTACTT	TAGAAAAAGG	TGACAAAATA	AATTATGATC
msa255059.2{91_1169NT}	AAGTCAGACC	CAATTTACTT	TAGAAAAAGG	TGACAAAATA	AATTATGATC
msa255059.2{91_090}	AAGTCAGACC	CAATTTACTT	TAGAAAAAGG	TGACAAAATA	AATTATGATC
msa255059.2{91_A909}	AAGTCAGACC	CAATTTACTT	TAGAAAAAGG	TGACAAAATA	AATTATGATC
msa255059.2{91_CJB110}	AAGTCAGACC	CAATTTACTT	TAGAAAAAGG	TGACAAAATA	AATTATGATC
msa255059.2{91_H36B}	AAGTCAGACC	CAATTTACTT	TAGAAAAAGG	TGACAAAATA	AATTATGATC
msa255059.2{91_JM9130013}	AAGTCAGACC	CAATTTACTT	TAGAAAAAGG	TGACAAAATA	AATTATGATC
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	AAGTATTGAC	AGCAGATGGT	TACCAGTGGA	TTTCTTACAA	ATCTTATAGT
msa255059.2{91_M781}	AAGTATTGAC	AGCAGATGGT	TACCAGTGGA	TTTCTTACAA	ATCTTATAGT
msa255059.2{91_COH1}	AAGTATTGAC	AGCAGATGGT	TACCAGTGGA	TTTCTTACAA	ATCTTATAGT
msa255059.2{91_18RS21}	AAGTATTGAC	AGCAGATGGT	TACCAGTGGA	TTTCTTACAA	ATCTTATAGT
msa255059.2{91_2603}	AAGTATTGAC	AGCAGATGGT	TACCAGTGGA	TTTCTTACAA	ATCTTATAGT
msa255059.2{91_1169NT}	AAGTATTGAC	AGCAGATGGT	TACCAGTGGA	TTTCTTACAA	ATCTTATAGT
msa255059.2{91_090}	AAGTATTGAC	AGCAGATGGT	TACCAGTGGA	TTTCTTACAA	ATCTTATAGT
msa255059.2{91_A909}	AAGTATTGAC	AGCAGATGGT	TACCAGTGGA	TTTCTTACAA	ATCTTATAGT
msa255059.2{91_CJB110}	AAGTATTGAC	AGCAGATGGT	TACCAGTGGA	TTTCTTACAA	ATCTTATAGT
msa255059.2{91_H36B}	AAGTATTGAC	AGCAGATGGT	TACCAGTGGA	TTTCTTACAA	ATCTTATAGT
msa255059.2{91_JM9130013}	AAGTATTGAC	AGCAGATGGT	TACCAGTGGA	TTTCTTACAA	ATCTTATAGT
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	GGTGTTCGTC	GCTATATTCC	TGTGAAAAAG	CTAACTACAA	GTAGTGAAAA
msa255059.2{91_M781}	GGTGTTCGTC	GCTATATTCC	TGTGAAAAAG	CTAACTACAA	GTAGTGAAAA
msa255059.2{91_COH1}	GGTGTTCGTC	GCTATATTCC	TGTGAAAAAG	CTAACTACAA	GTAGTGAAAA
msa255059.2{91_18RS21}	GGTGTTCGTC	GCTATATTCC	TGTGAAAAAG	CTAACTACAA	GTAGTGAAAA
msa255059.2{91_2603}	GGTGTTCGTC	GCTATATTCC	TGTGAAAAAG	CTAACTACAA	GTAGTGAAAA
msa255059.2{91_1169NT}	GGTGTTCGTC	GCTATATTCC	TGTGAAAAAG	CTAACTACAA	GTAGTGAAAA
msa255059.2{91_090}	GGTGTTCGTC	GCTATATTCC	TGTGAAAAAG	CTAACTACAA	GTAGTGAAAA
msa255059.2{91_A909}	GGTGTTCGTC	GCTATATTCC	TGTGAAAAAG	CTAACTACAA	GTAGTGAAAA
msa255059.2{91_CJB110}	GGTGTTCGTC	GCTATATTCC	TGTGAAAAAG	CTAACTACAA	GTAGTGAAAA
msa255059.2{91_H36B}	GGTGTTCGTC	GCTATATTCC	TGTGAAAAAG	CTAACTACAA	GTAGTGAAAA
msa255059.2{91_JM9130013}	GGTGTTCGTC	GCTATATTCC	TGTGAAAAAG	CTAACTACAA	GTAGTGAAAA
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	AGCGAAAGAT	GAGGCGACTA	AACCGACTAG	TTATCCCAAC	TTACCTAAAA
msa255059.2{91_M781}	AGCGAAAGAT	GAGGCGACTA	AACCGACTAG	TTATCCCAAC	TTACCTAAAA
msa255059.2{91_COH1}	AGCGAAAGAT	GAGGCGACTA	AACCGACTAG	TTATCCCAAC	TTACCTAAAA
msa255059.2{91_18RS21}	AGCGAAAGAT	GAGGCGACTA	AACCGACTAG	TTATCCCAAC	TTACCTAAAA
msa255059.2{91_2603}	AGCGAAAGAT	GAGGCGACTA	AACCGACTAG	TTATCCCAAC	TTACCTAAAA
msa255059.2{91_1169NT}	AGCGAAAGAT	GAGGCGACTA	AACCGACTAG	TTATCCCAAC	TTACCTAAAA
msa255059.2{91_090}	AGCGAAAGAT	GAGGCGACTA	AACCGACTAG	TTATCCCAAC	TTACCTAAAA
msa255059.2{91_A909}	AGCGAAAGAT	GAGGCGACTA	AACCGACTAG	TTATCCCAAC	TTACCTAAAA
msa255059.2{91_CJB110}	AGCGAAAGAT	GAGGCGACTA	AACCGACTAG	TTATCCCAAC	TTACCTAAAA
msa255059.2{91_H36B}	AGCGAAAGAT	GAGGCGACTA	AACCGACTAG	TTATCCCAAC	TTACCTAAAA
msa255059.2{91_JM9130013}	AGCGAAAGAT	GAGGCGACTA	AACCGACTAG	TTATCCCAAC	TTACCTAAAA
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	CAGGTACCTA	TACATTTACT	AAAACGTAG	ATGTGAAaAG	TCAACCTAAA
msa255059.2{91_M781}	CAGGTACCTA	TACATTTACT	AAAACGTAG	ATGTGAAaAG	TCAACCTAAA
msa255059.2{91_COH1}	CAGGTACCTA	TACATTTACT	AAAACGTAG	ATGTGAAaAG	TCAACCTAAA
msa255059.2{91_18RS21}	CAGGTACCTA	TACATTTACT	AAAACGTAG	ATGTGAAaAG	TCAACCTAAA
msa255059.2{91_2603}	CAGGTACCTA	TACATTTACT	AAAACGTAG	ATGTGAAaAG	TCAACCTAAA
msa255059.2{91_1169NT}	CAGGTACCTA	TACATTTACT	AAAACGTAG	ATGTGAAaAG	TCAACCTAAA
msa255059.2{91_090}	CAGGTACCTA	TACATTTACT	AAAACGTAG	ATGTGAAgAG	TCAACCTAAA
msa255059.2{91_A909}	CAGGTACCTA	TACATTTACT	AAAACGTAG	ATGTGAAgAG	TCAACCTAAA
msa255059.2{91_CJB110}	CAGGTACCTA	TACATTTACT	AAAACGTAG	ATGTGAAgAG	TCAACCTAAA
msa255059.2{91_H36B}	CAGGTACCTA	TACATTTACT	AAAACGTAG	ATGTGAAgAG	TCAACCTAAA
msa255059.2{91_JM9130013}	CAGGTACCTA	TACATTTACT	AAAACGTAG	ATGTGAAgAG	TCAACCTAAA
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	GTATCAAGTC	CAGTGGAAAT	TAATTTTCAA	AAGGGTGAAA	AAATACATTA
msa255059.2{91_M781}	GTATCAAGTC	CAGTGGAAAT	TAATTTTCAA	AAGGGTGAAA	AAATACATTA
msa255059.2{91_COH1}	GTATCAAGTC	CAGTGGAAAT	TAATTTTCAA	AAGGGTGAAA	AAATACATTA
msa255059.2{91_18RS21}	GTATCAAGTC	CAGTGGAAAT	TAATTTTCAA	AAGGGTGAAA	AAATACATTA
msa255059.2{91_2603}	GTATCAAGTC	CAGTGGAAAT	TAATTTTCAA	AAGGGTGAAA	AAATACATTA
msa255059.2{91_1169NT}	GTATCAAGTC	CAGTGGAAAT	TAATTTTCAA	AAGGGTGAAA	AAATACATTA
msa255059.2{91_090}	GTATCAAGTC	CAGTGGAAAT	TAATTTTCAA	AAGGGTGAAA	AAATACATTA
msa255059.2{91_A909}	GTATCAAGTC	CAGTGGAAAT	TAATTTTCAA	AAGGGTGAAA	AAATACATTA
msa255059.2{91_CJB110}	GTATCAAGTC	CAGTGGAAAT	TAATTTTCAA	AAGGGTGAAA	AAATACATTA
msa255059.2{91_H36B}	GTATCAAGTC	CAGTGGAAAT	TAATTTTCAA	AAGGGTGAAA	AAATACATTA
msa255059.2{91_JM9130013}	GTATCAAGTC	CAGTGGAAAT	TAATTTTCAA	AAGGGTGAAA	AAATACATTA
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	TGATCAAGTG	TTAGTAGTAG	ATGGTCATCA	GTGGATTTC	TACAAGAGTT
Consensus	*****	*****	*****	*****	*****

Table 89: Comparative Sequences relating to SAG1350

msa255059.2{91_M781}	TGATCAAGTG	TTAGTAGTAG	ATGGTCATCA	GTGGATTTC	TACAAGAGTT
msa255059.2{91_COH1}	TGATCAAGTG	TTAGTAGTAG	ATGGTCATCA	GTGGATTTC	TACAAGAGTT
msa255059.2{91_18RS21}	TGATCAAGTG	TTAGTAGTAG	ATGGTCATCA	GTGGATTTC	TACAAGAGTT
msa255059.2{91_2603}	TGATCAAGTG	TTAGTAGTAG	ATGGTCATCA	GTGGATTTC	TACAAGAGTT
msa255059.2{91_1169NT}	TGATCAAGTG	TTAGTAGTAG	ATGGTCATCA	GTGGATTTC	TACAAGAGTT
msa255059.2{91_090}	TGATCAAGTG	TTAGTAGTAG	ATGGTCATCA	GTGGATTTC	TACAAGAGTT
msa255059.2{91_A909}	TGATCAAGTG	TTAGTAGTAG	ATGGTCATCA	GTGGATTTC	TACAAGAGTT
msa255059.2{91_CJB110}	TGATCAAGTG	TTAGTAGTAG	ATGGTCATCA	GTGGATTTC	TACAAGAGTT
msa255059.2{91_H36B}	TGATCAAGTG	TTAGTAGTAG	ATGGTCATCA	GTGGATTTC	TACAAGAGTT
msa255059.2{91_JM9130013}	TGATCAAGTG	TTAGTAGTAG	ATGGTCATCA	GTGGATTTC	TACAAGAGTT
Consensus	*****	*****	*****	*****	*****

	1601	1629
msa255059.2{91_M732}	ATTCCGGTAT	TCGTCGCTAT
msa255059.2{91_M781}	ATTCCGGTAT	TCGTCGCTAT
msa255059.2{91_COH1}	ATTCCGGTAT	TCGTCGCTAT
msa255059.2{91_18RS21}	ATTCCGGTAT	TCGTCGCTAT
msa255059.2{91_2603}	ATTCCGGTAT	TCGTCGCTAT
msa255059.2{91_1169NT}	ATTCCGGTAT	TCGTCGCTAT
msa255059.2{91_090}	ATTCCGGTAT	TCGTCGCTAT
msa255059.2{91_A909}	ATTCCGGTAT	TCGTCGCTAT
msa255059.2{91_CJB110}	ATTCCGGTAT	TCGTCGCTAT
msa255059.2{91_H36B}	ATTCCGGTAT	TCGTCGCTAT
msa255059.2{91_JM9130013}	ATTCCGGTAT	TCGTCGCTAT
Consensus	*****	*****

SEQ ID NO. 8912

STRAIN 2603 frame: 1

MKKGQVNDTKQSYSLRKYKFGLASVILGSFIMVTSPVFADQTTTSVQVNNQTGTSVDANNSS
 SNETSASSVITSNNDSVQASDKVVNSQNTATKDITTPLVETKPMVEKTLPEQGNVYVSKE
 TEVKNTPSKSAPVAFYAKKGDVDFYDQVFNKDNVKKWISYKSCGVRRYAAIESLDPSGGSE
 ETKAPTPTVNSGSNNQEKIATQGNVTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTI
 IEGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPPQARITKTGRLTISNETTTGTF
 DILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTITGDNKYKAVVSFADHKNEKGLYN
 IHLYYQEASGTLVGVTGKTVTVAGTNSSQEPINENGLAKTGVIYNIIGSTEVEKNEAKISSQT
 QFTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLTTSSEKAKDEATKPTSYPN
 LPKTGTYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHVDQVLVVDGHWISYKSYSGIRRY
 IEI

SEQ ID NO. 8913

STRAIN 090 frame: 1

KKKGQVNDTKQSYSLRKYKFGLASVILGSFIMVTSPVFADQTTTSVQVNNQTGTSVDANNSS
 NETSASSVITSNNDSVQASDKVVNSQNTATKDITTPLVETKPMVEKTLPEQGNVYVSKE
 EVKNTPSKSAPVAFYAKKGDVDFYDQVFNKDNVKKWISYKSCGVRRYAAIESLDPSGGSE
 TKAPTPTVNSGSNNQEKIATQGNVTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTI
 EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPPQARITKTGRLTISNETTTGTF
 ILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTITGDNKYKAVVSFADHKNEKGLYN
 HLYYQEASGTLVGVTGKTVTVAGTNSSQEPINENGLAKTGVIYNIIGSTEVEKNEAKISSQT
 FTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLTTSSEKAKDEATKPTSYPN
 LPKTGTYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHVDQVLVVDGHWISYKSYSGIRRY
 IEI

SEQ ID NO. 8914

STRAIN A909 frame: 1

KKKGQVNDTKQSYSLRKYKFGLASVILGSFIMVTSPVFADQTTTSVQVNNQTGTSVDANNSS
 NETSASSVITSNNDSVQASDKVVNSQNTATKDITTPLVETKPMVEKTLPEQGNVYVSKE
 EVKNTPSKSAPVAFYAKKGDVDFYDQVFNKDNVKKWISYKSCGVRRYAAIESLDPSGGSE
 TKAPTPTVNSGSNNQEKIATQGNVTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTI
 EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPPQARITKTGRLTISNETTTGTF
 ILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTITGDNKYKAVVSFADHKNEKGLYN
 HLYYQEASGTLVGVTGKTVTVAGTNSSQEPINENGLAKTGVIYNIIGSTEVEKNEAKISSQT
 FTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLTTSSEKAKDEATKPTSYPN
 LPKTGTYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHVDQVLVVDGHWISYKSYSGIRRY
 IEI

SEQ ID NO. 8915

STRAIN H36B frame: 1

KKKGQVNDTKQSYSLRKYKFGLASVILGSFIMVTSPVFADQTTTSVQVNNQTGTSVDANNSS
 NETSASSVITSNNDSVQASDKVVNSQNTATKDITTPLVETKPMVEKTLPEQGNVYVSKE
 EVKNTPSKSAPVAFYAKKGDVDFYDQVFNKDNVKKWISYKSCGVRRYAAIESLDPSGGSE
 TKAPTPTVNSGSNNQEKIATQGNVTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTI
 EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPPQARITKTGRLTISNETTTGTF
 ILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTITGDNKYKAVVSFADHKNEKGLYN
 HLYYQEASGTLVGVTGKTVTVAGTNSSQEPINENGLAKTGVIYNIIGSTEVEKNEAKISSQT
 FTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLTTSSEKAKDEATKPTSYPN
 LPKTGTYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHVDQVLVVDGHWISYKSYSGIRRY
 IEI

SEQ ID NO. 8916

STRAIN 18RS21 frame: 1

KKKGQVNDTKQSYSLRKYKFGLASVILGSFIMVTSPVFADQTTTSVQVNNQTGTSVDANNSS
 NETSASSVITSNNDSVQASDKVVNSQNTATKDITTPLVETKPMVEKTLPEQGNVYVSKE

Table 89: Comparative Sequences relating to SAG1350

EVKNTPSKSAPVAFYAKKGDVFDQVFNKDNVWISYKSFVGVRRYAAIESLDPSGGSE
TKAPTPVTNSGSNNQEKIATQGNVTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTI
EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPQPQARITKTGRLTISNETTTGFD
ILITNFKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTGDNVYKAVSFADHKNEKGLYNI
HLYYQEASGTLVGVTGKTVAGTNSSQEPINGLAKTGVYNIIGSTEVKNEAKISSQTQ
FTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLTSSSEKAKDEATKPTSYPNL
PKTGTFTFTKTVDVKSQPKVSSPVEFNQKGEKIHVDQVLVVDGHQWISYKSYSGIRRYI
EI

SEQ ID NO. 8917

STRAIN M732 frame: 1

QVNDTKQSYSLRKYKFGLASVILGSFIMVTSVPFADQTTSVQVNNQTGTSVDANNSSNET
SASSVITSNNDVQASDKVNSQNTATKDITPLVETKPMVEKTLPEQGNVYVSKETEVK
NTPSKSAPVAFYAKKGDVFDQVFNKDNVWISYKSFVGVRRYAAIESLDPSGGSE
TKAPTPVTNSGSNNQEKIATQGNVTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTI
EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPQPQARITKTGRLTISNETTTGFD
ILITNFKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTGDNVYKAVSFADHKNEKGLYNI
HLYYQEASGTLVGVTGKTVAGTNSSQEPINGLPKTGVYNIIGSTEVKNEAKISSQTQFTL
EKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLTSSSEKAKDEATKPTSYPNL
PKTGTFTFTKTVDVKSQPKVSSPVEFNQKGEKIHVDQVLVVDGHQWISYKSYSGIRRYI
EI

SEQ ID NO. 8918

STRAIN COH1 frame: 1

KKGQVNDTKQSYSLRKYKFGLASVILGSFIMVTSVPFADQTTSVQVNNQTGTSVDANNSS
NETSASSVITSNNDVQASDKVNSQNTATKDITPLVETKPMVEKTLPEQGNVYVSKET
EVKNTPSKSAPVAFYAKKGDVFDQVFNKDNVWISYKSFVGVRRYAAIESLDPSGGSE
TKAPTPVTNSGSNNQEKIATQGNVTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTI
EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPQPQARITKTGRLTISNETTTGFD
ILITNFKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTGDNVYKAVSFADHKNEKGLYNI
HLYYQEASGTLVGVTGKTVAGTNSSQEPINGLPKTGVYNIIGSTEVKNEAKISSQTQ
FTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLTSSSEKAKDEATKPTSYPNL
PKTGTFTFTKTVDVKSQPKVSSPVEFNQKGEKIHVDQVLVVDGHQWISYKSYSGIRRYI
EI

SEQ ID NO. 8919

STRAIN M781 frame: 1

KKGQVNDTKQSYSLRKYKFGLASVILGSFIMVTSVPFADQTTSVQVNNQTGTSVDANNSS
NETSASSVITSNNDVQASDKVNSQNTATKDITPLVETKPMVEKTLPEQGNVYVSKET
EVKNTPSKSAPVAFYAKKGDVFDQVFNKDNVWISYKSFVGVRRYAAIESLDPSGGSE
TKAPTPVTNSGSNNQEKIATQGNVTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTI
EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPQPQARITKTGRLTISNETTTGFD
ILITNFKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTGDNVYKAVSFADHKNEKGLYNI
HLYYQEASGTLVGVTGKTVAGTNSSQEPINGLPKTGVYNIIGSTEVKNEAKISSQTQ
FTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLTSSSEKAKDEATKPTSYPNL
PKTGTFTFTKTVDVKSQPKVSSPVEFNQKGEKIHVDQVLVVDGHQWISYKSYSGIRRYI
EI

SEQ ID NO. 8920

STRAIN CJB110 frame: 1

KKGQVNDTKQSYSLRKYKFGLASVILGSFIMVTSVPFADQTTSVQVNNQTGTSVDANNSS
NETSASSVITSNNDVQASDKVNSQNTATKDITPLVETKPMVEKTLPEQGNVYVSKET
EVKNTPSKSAPVAFYAKKGDVFDQVFNKDNVWISYKSFVGVRRYAAIESLDPSGGSE
TKAPTPVTNSGSNNQEKIATQGNVTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTI
EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPQPQARITKTGRLTISNETTTGFD
ILITNFKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTGDNVYKAVSFADHKNEKGLYNI
HLYYQEASGTLVGVTGKTVAGTNSSQEPINGLAKTGVYNIIGSTEVKNEAKISSQTQ
FTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLTSSSEKAKDEATKPTSYPNL
PKTGTFTFTKTVDVKSQPKVSSPVEFNQKGEKIHVDQVLVVDGHQWISYKSYSGIRRYI
EI

SEQ ID NO. 8921

STRAIN 1169NT frame: 1

KKGQVNDTKQSYSLRKYKFGLASVILGSFIMVTSVPFADQTTSVQVNNQTGTSVDANNSS
NETSASSVITSNNDVQASDKVNSQNTATKDITPLVETKPMVEKTLPEQGNVYVSKET
EVKNTPSKSAPVAFYAKKGDVFDQVFNKDNVWISYKSFVGVRRYAAIESLDPSGGSE
TKAPTPVTNSGSNNQEKIATQGNVTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTI
EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPQPQARITKTGRLTISNETTTGFD
ILITNFKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTGDNVYKAVSFADHKNEKGLYNI
HLYYQEASGTLVGVTGKTVAGTNSSQEPINGLAKTGVYNIIGSTEVKNEAKISSQTQ
FTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLTSSSEKAKDEATKPTSYPNL
PKTGTFTFTKTVDVKSQPKVSSPVEFNQKGEKIHVDQVLVVDGHQWISYKSYSGIRRYI
EI

SEQ ID NO. 8922

STRAIN JM9130013 frame: 1

KKGQVNDTKQSYSLRKYKFGLASVILGSFIMVTSVPFADQTTSVQVNNQTGTSVDANNSS
NETSASSVITSNNDVQASDKVNSQNTATKDITPLVETKPMVEKTLPEQGNVYVSKET
EVKNTPSKSAPVAFYAKKGDVFDQVFNKDNVWISYKSFVGVRRYAAIESLDPSGGSE
TKAPTPVTNSGSNNQEKIATQGNVTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTI
EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPQPQARITKTGRLTIYNETTTGFD
ILITNFKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTGDNVYKAVSFADHKNEKGLYNI
HLYYQEASGTLVGVTGKTVAGTNSSQEPINGLAKTGVYNIIGSTEVKNEAKISSQTQ

Table 89: Comparative Sequences relating to SAG1350

FTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLTTSSEKAKDEATKPTSYPNL
PKTGTYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHVDQVLVVDGHQWISYKSYSGIRRYI
EI

PRETTY of: /biotmp/msa255178.2(*) February 11, 2003 08:51 ..

	1				50
msa255178.2{91_090}	~kkgQVNDTK	QSYSLRKYKF	GLASVILGSF	IMVTSPVFAD	QTTSVQVNNQ
msa255178.2{91_18RS21}	~kkgQVNDTK	QSYSLRKYKF	GLASVILGSF	IMVTSPVFAD	QTTSVQVNNQ
msa255178.2{91_2603}	mkkgQVNDTK	QSYSLRKYKF	GLASVILGSF	IMVTSPVFAD	QTTSVQVNNQ
msa255178.2{91_A909}	~kkgQVNDTK	QSYSLRKYKF	GLASVILGSF	IMVTSPVFAD	QTTSVQVNNQ
msa255178.2{91_CJB110}	~kkgQVNDTK	QSYSLRKYKF	GLASVILGSF	IMVTSPVFAD	QTTSVQVNNQ
msa255178.2{91_H36B}	~kkgQVNDTK	QSYSLRKYKF	GLASVILGSF	IMVTSPVFAD	QTTSVQVNNQ
msa255178.2{91_JM9130013}	~kkgQVNDTK	QSYSLRKYKF	GLASVILGSF	IMVTSPVFAD	QTTSVQVNNQ
msa255178.2{91_COH1}	~kkgQVNDTK	QSYSLRKYKF	GLASVILGSF	IMVTSPVFAD	QTTSVQVNNQ
msa255178.2{91_M781}	~kkgQVNDTK	QSYSLRKYKF	GLASVILGSF	IMVTSPVFAD	QTTSVQVNNQ
msa255178.2{91_M732}	----QVNDTK	QSYSLRKYKF	GLASVILGSF	IMVTSPVFAD	QTTSVQVNNQ
msa255178.2{91_1169NT}	~kkgQVNDTK	QSYSLRKYKF	GLASVILGSF	IMVTSPVFAD	QTTSVQVNNQ
Consensus	*--*****	*****	*****	*****	*****
	51				100
msa255178.2{91_090}	TGTSVdAnNS	SNETSASSVI	TSNNDsvQAS	DKVVNSQNTA	TKDITTPLe
msa255178.2{91_18RS21}	TGTSVdAnNS	SNETSASSVI	TSNNDsvQAS	DKVVNSQNTA	TKDITTPLe
msa255178.2{91_2603}	TGTSVdAnNS	SNETSASSVI	TSNNDsvQAS	DKVVNSQNTA	TKDITTPLe
msa255178.2{91_A909}	TGTSVdAnNS	SNETSASSVI	TSNNDsvQAS	DKVVNSQNTA	TKDITTPLe
msa255178.2{91_CJB110}	TGTSVdAnNS	SNETSASSVI	TSNNDsvQAS	DKVVNSQNTA	TKDITTPLe
msa255178.2{91_H36B}	TGTSVdAnNS	SNETSASSVI	TSNNDsvQAS	DKVVNSQNTA	TKDITTPLe
msa255178.2{91_JM9130013}	TGTSVdAnNS	SNETSASSVI	TSNNDsvQAS	DKVVNSQNTA	TKDITTPLe
msa255178.2{91_COH1}	TGTSVdAnNS	SNETSASSVI	TSNNDsvQAS	DKVVNSQNTA	TKDITTPLe
msa255178.2{91_M781}	TGTSVdAnNS	SNETSASSVI	TSNNDsvQAS	DKVVNSQNTA	TKDITTPLe
msa255178.2{91_M732}	TGTSVdAnNS	SNETSASSVI	TSNNDsvQAS	DKVVNSQNTA	TKDITTPLe
msa255178.2{91_1169NT}	TGTSVdAnNS	SNETSASSVI	TSNNDsvQAS	DKVVNSQNTA	TKDITTPLe
Consensus	*****-***	*****	*****	*****	*****
	101				150
msa255178.2{91_090}	TKPMVEKTLp	EQGNYVYSKE	TEVKNTPSKS	APVAFYAKKG	DKVFYDQVFN
msa255178.2{91_18RS21}	TKPMVEKTLp	EQGNYVYSKE	TEVKNTPSKS	APVAFYAKKG	DKVFYDQVFN
msa255178.2{91_2603}	TKPMVEKTLp	EQGNYVYSKE	TEVKNTPSKS	APVAFYAKKG	DKVFYDQVFN
msa255178.2{91_A909}	TKPMVEKTLp	EQGNYVYSKE	TEVKNTPSKS	APVAFYAKKG	DKVFYDQVFN
msa255178.2{91_CJB110}	TKPMVEKTLp	EQGNYVYSKE	TEVKNTPSKS	APVAFYAKKG	DKVFYDQVFN
msa255178.2{91_H36B}	TKPMVEKTLp	EQGNYVYSKE	TEVKNTPSKS	APVAFYAKKG	DKVFYDQVFN
msa255178.2{91_JM9130013}	TKPMVEKTLp	EQGNYVYSKE	TEVKNTPSKS	APVAFYAKKG	DKVFYDQVFN
msa255178.2{91_COH1}	TKPMVEKTLp	EQGNYVYSKE	TEVKNTPSKS	APVAFYAKKG	DKVFYDQVFN
msa255178.2{91_M781}	TKPMVEKTLp	EQGNYVYSKE	TEVKNTPSKS	APVAFYAKKG	DKVFYDQVFN
msa255178.2{91_M732}	TKPMVEKTLp	EQGNYVYSKE	TEVKNTPSKS	APVAFYAKKG	DKVFYDQVFN
msa255178.2{91_1169NT}	TKPMVEKTLp	EQGNYVYSKE	TEVKNTPSKS	APVAFYAKKG	DKVFYDQVFN
Consensus	*****	*****	*****	*****	*****
	151				200
msa255178.2{91_090}	KDNVKWISYK	SfCgVRRYAA	IESLDPSGGS	ETKAPTPVTN	SGSNNOEKIA
msa255178.2{91_18RS21}	KDNVKWISYK	SfCgVRRYAA	IESLDPSGGS	ETKAPTPVTN	SGSNNOEKIA
msa255178.2{91_2603}	KDNVKWISYK	SfCgVRRYAA	IESLDPSGGS	ETKAPTPVTN	SGSNNOEKIA
msa255178.2{91_A909}	KDNVKWISYK	SfCgVRRYAA	IESLDPSGGS	ETKAPTPVTN	SGSNNOEKIA
msa255178.2{91_CJB110}	KDNVKWISYK	SfCgVRRYAA	IESLDPSGGS	ETKAPTPVTN	SGSNNOEKIA
msa255178.2{91_H36B}	KDNVKWISYK	SfCgVRRYAA	IESLDPSGGS	ETKAPTPVTN	SGSNNOEKIA
msa255178.2{91_JM9130013}	KDNVKWISYK	SfCgVRRYAA	IESLDPSGGS	ETKAPTPVTN	SGSNNOEKIA
msa255178.2{91_COH1}	KDNVKWISYK	SfCgVRRYAA	IESLDPSGGS	ETKAPTPVTN	SGSNNOEKIA
msa255178.2{91_M781}	KDNVKWISYK	SfCgVRRYAA	IESLDPSGGS	ETKAPTPVTN	SGSNNOEKIA
msa255178.2{91_M732}	KDNVKWISYK	SfCgVRRYAA	IESLDPSGGS	ETKAPTPVTN	SGSNNOEKIA
msa255178.2{91_1169NT}	KDNVKWISYK	SfCgVRRYAA	IESLDPSGGS	ETKAPTPVTN	SGSNNOEKIA
Consensus	*****	**--*****	*****	*****	*****
	201				250
msa255178.2{91_090}	TQGNyTFShK	VEVKNEAKVA	SPTQFTLDKG	DRIFYDQILT	IEGNQWLSYK
msa255178.2{91_18RS21}	TQGNyTFShK	VEVKNEAKVA	SPTQFTLDKG	DRIFYDQILT	IEGNQWLSYK
msa255178.2{91_2603}	TQGNyTFShK	VEVKNEAKVA	SPTQFTLDKG	DRIFYDQILT	IEGNQWLSYK
msa255178.2{91_A909}	TQGNyTFShK	VEVKNEAKVA	SPTQFTLDKG	DRIFYDQILT	IEGNQWLSYK
msa255178.2{91_CJB110}	TQGNyTFShK	VEVKNEAKVA	SPTQFTLDKG	DRIFYDQILT	IEGNQWLSYK
msa255178.2{91_H36B}	TQGNyTFShK	VEVKNEAKVA	SPTQFTLDKG	DRIFYDQILT	IEGNQWLSYK
msa255178.2{91_JM9130013}	TQGNyTFShK	VEVKNEAKVA	SPTQFTLDKG	DRIFYDQILT	IEGNQWLSYK
msa255178.2{91_COH1}	TQGNyTFShK	VEVKNEAKVA	SPTQFTLDKG	DRIFYDQILT	IEGNQWLSYK
msa255178.2{91_M781}	TQGNyTFShK	VEVKNEAKVA	SPTQFTLDKG	DRIFYDQILT	IEGNQWLSYK
msa255178.2{91_M732}	TQGNyTFShK	VEVKNEAKVA	SPTQFTLDKG	DRIFYDQILT	IEGNQWLSYK
msa255178.2{91_1169NT}	TQGNyTFShK	VEVKNEAKVA	SPTQFTLDKG	DRIFYDQILT	IEGNQWLSYK
Consensus	*****	*****	*****	*****	*****
	251				300
msa255178.2{91_090}	SFNGVRRFVL	LGKASSVEKT	EDKEKVSPQP	QARITKTGRL	TI\$NETTTGF
msa255178.2{91_18RS21}	SFNGVRRFVL	LGKASSVEKT	EDKEKVSPQP	QARITKTGRL	TI\$NETTTGF
msa255178.2{91_2603}	SFNGVRRFVL	LGKASSVEKT	EDKEKVSPQP	QARITKTGRL	TI\$NETTTGF
msa255178.2{91_A909}	SFNGVRRFVL	LGKASSVEKT	EDKEKVSPQP	QARITKTGRL	TI\$NETTTGF
msa255178.2{91_CJB110}	SFNGVRRFVL	LGKASSVEKT	EDKEKVSPQP	QARITKTGRL	TI\$NETTTGF

Table 89: Comparative Sequences relating to SAG1350

msa255178.2{91_H36B}	SFNGVRRFVL	LGKASSVEKT	EDKEKVSPQP	QARITKTGRL	TIaNETTTGF
msa255178.2{91_JM9130013}	SFNGVRRFVL	LGKASSVEKT	EDKEKVSPQP	QARITKTGRL	TIyNETTTGF
msa255178.2{91_COH1}	SFNGVRRFVL	LGKASSVEKT	EDKEKVSPQP	QARITKTGRL	TIaNETTTGF
msa255178.2{91_M781}	SFNGVRRFVL	LGKASSVEKT	EDKEKVSPQP	QARITKTGRL	TIaNETTTGF
msa255178.2{91_M732}	SFNGVRRFVL	LGKASSVEKT	EDKEKVSPQP	QARITKTGRL	TIaNETTTGF
msa255178.2{91_1169NT}	SFNGVRRFVL	LGKASSVEKT	EDKEKVSPQP	QARITKTGRL	TIaNETTTGF
Consensus	*****	*****	*****	*****	**-*****
msa255178.2{91_090}	DILITNIKDD	NGIAAVKVPV	WTEQGGQDDI	KWYTAVTGTD	GNVKVAVSFA
msa255178.2{91_18RS21}	DILITNIKDD	NGIAAVKVPV	WTEQGGQDDI	KWYTAVTGTD	GNVKVAVSFA
msa255178.2{91_2603}	DILITNIKDD	NGIAAVKVPV	WTEQGGQDDI	KWYTAVTGTD	GNVKVAVSFA
msa255178.2{91_A909}	DILITNIKDD	NGIAAVKVPV	WTEQGGQDDI	KWYTAVTGTD	GNVKVAVSFA
msa255178.2{91_CJB110}	DILITNIKDD	NGIAAVKVPV	WTEQGGQDDI	KWYTAVTGTD	GNVKVAVSFA
msa255178.2{91_H36B}	DILITNIKDD	NGIAAVKVPV	WTEQGGQDDI	KWYTAVTGTD	GNVKVAVSFA
msa255178.2{91_JM9130013}	DILITNIKDD	NGIAAVKVPV	WTEQGGQDDI	KWYTAVTGTD	GNVKVAVSFA
msa255178.2{91_COH1}	DILITNIKDD	NGIAAVKVPV	WTEQGGQDDI	KWYTAVTGTD	GNVKVAVSFA
msa255178.2{91_M781}	DILITNIKDD	NGIAAVKVPV	WTEQGGQDDI	KWYTAVTGTD	GNVKVAVSFA
msa255178.2{91_M732}	DILITNIKDD	NGIAAVKVPV	WTEQGGQDDI	KWYTAVTGTD	GNVKVAVSFA
msa255178.2{91_1169NT}	DILITNIKDD	NGIAAVKVPV	WTEQGGQDDI	KWYTAVTGTD	GNVKVAVSFA
Consensus	*****	*****	*****	*****	*****
msa255178.2{91_090}	DHKNEKGLYN	IHLYYQEASG	TLVGVTGTV	TVAGTNSSQE	PIENGLaKTG
msa255178.2{91_18RS21}	DHKNEKGLYN	IHLYYQEASG	TLVGVTGTV	TVAGTNSSQE	PIENGLaKTG
msa255178.2{91_2603}	DHKNEKGLYN	IHLYYQEASG	TLVGVTGTV	TVAGTNSSQE	PIENGLaKTG
msa255178.2{91_A909}	DHKNEKGLYN	IHLYYQEASG	TLVGVTGTV	TVAGTNSSQE	PIENGLaKTG
msa255178.2{91_CJB110}	DHKNEKGLYN	IHLYYQEASG	TLVGVTGTV	TVAGTNSSQE	PIENGLaKTG
msa255178.2{91_H36B}	DHKNEKGLYN	IHLYYQEASG	TLVGVTGTV	TVAGTNSSQE	PIENGLaKTG
msa255178.2{91_JM9130013}	DHKNEKGLYN	IHLYYQEASG	TLVGVTGTV	TVAGTNSSQE	PIENGLaKTG
msa255178.2{91_COH1}	DHKNEKGLYN	IHLYYQEASG	TLVGVTGTV	TVAGTNSSQE	PIENGLpKTG
msa255178.2{91_M781}	DHKNEKGLYN	IHLYYQEASG	TLVGVTGTV	TVAGTNSSQE	PIENGLpKTG
msa255178.2{91_M732}	DHKNEKGLYN	IHLYYQEASG	TLVGVTGTV	TVAGTNSSQE	PIENGLpKTG
msa255178.2{91_1169NT}	DHKNEKGLYN	IHLYYQEASG	TLVGVTGTV	TVAGTNSSQE	PIENGLaKTG
Consensus	*****	*****	*****	*****	*****-***
msa255178.2{91_090}	VYNIIGSTEV	KNEAKISSQT	QFTLEKGDKI	NYDQVLTADG	YQWISYKSYS
msa255178.2{91_18RS21}	VYNIIGSTEV	KNEAKISSQT	QFTLEKGDKI	NYDQVLTADG	YQWISYKSYS
msa255178.2{91_2603}	VYNIIGSTEV	KNEAKISSQT	QFTLEKGDKI	NYDQVLTADG	YQWISYKSYS
msa255178.2{91_A909}	VYNIIGSTEV	KNEAKISSQT	QFTLEKGDKI	NYDQVLTADG	YQWISYKSYS
msa255178.2{91_CJB110}	VYNIIGSTEV	KNEAKISSQT	QFTLEKGDKI	NYDQVLTADG	YQWISYKSYS
msa255178.2{91_H36B}	VYNIIGSTEV	KNEAKISSQT	QFTLEKGDKI	NYDQVLTADG	YQWISYKSYS
msa255178.2{91_JM9130013}	VYNIIGSTEV	KNEAKISSQT	QFTLEKGDKI	NYDQVLTADG	YQWISYKSYS
msa255178.2{91_COH1}	VYNIIGSTEV	KNEAKISSQT	QFTLEKGDKI	NYDQVLTADG	YQWISYKSYS
msa255178.2{91_M781}	VYNIIGSTEV	KNEAKISSQT	QFTLEKGDKI	NYDQVLTADG	YQWISYKSYS
msa255178.2{91_M732}	VYNIIGSTEV	KNEAKISSQT	QFTLEKGDKI	NYDQVLTADG	YQWISYKSYS
msa255178.2{91_1169NT}	VYNIIGSTEV	KNEAKISSQT	QFTLEKGDKI	NYDQVLTADG	YQWISYKSYS
Consensus	*****	*****	*****	*****	*****
msa255178.2{91_090}	GVERRYPVKK	LTTSSSEKAKD	EATKPTSYPN	LPKTGTYTFT	KTVDVKSQPK
msa255178.2{91_18RS21}	GVERRYPVKK	LTTSSSEKAKD	EATKPTSYPN	LPKTGTYTFT	KTVDVKSQPK
msa255178.2{91_2603}	GVERRYPVKK	LTTSSSEKAKD	EATKPTSYPN	LPKTGTYTFT	KTVDVKSQPK
msa255178.2{91_A909}	GVERRYPVKK	LTTSSSEKAKD	EATKPTSYPN	LPKTGTYTFT	KTVDVKSQPK
msa255178.2{91_CJB110}	GVERRYPVKK	LTTSSSEKAKD	EATKPTSYPN	LPKTGTYTFT	KTVDVKSQPK
msa255178.2{91_H36B}	GVERRYPVKK	LTTSSSEKAKD	EATKPTSYPN	LPKTGTYTFT	KTVDVKSQPK
msa255178.2{91_JM9130013}	GVERRYPVKK	LTTSSSEKAKD	EATKPTSYPN	LPKTGTYTFT	KTVDVKSQPK
msa255178.2{91_COH1}	GVERRYPVKK	LTTSSSEKAKD	EATKPTSYPN	LPKTGTYTFT	KTVDVKSQPK
msa255178.2{91_M781}	GVERRYPVKK	LTTSSSEKAKD	EATKPTSYPN	LPKTGTYTFT	KTVDVKSQPK
msa255178.2{91_M732}	GVERRYPVKK	LTTSSSEKAKD	EATKPTSYPN	LPKTGTYTFT	KTVDVKSQPK
msa255178.2{91_1169NT}	GVERRYPVKK	LTTSSSEKAKD	EATKPTSYPN	LPKTGTYTFT	KTVDVKSQPK
Consensus	*****	*****	*****	*****	*****
msa255178.2{91_090}	VSSPVEFNQ	KGEKIHYDQV	LVVDGHQWIS	YKSYSGIRRY	IEI
msa255178.2{91_18RS21}	VSSPVEFNQ	KGEKIHYDQV	LVVDGHQWIS	YKSYSGIRRY	IEI
msa255178.2{91_2603}	VSSPVEFNQ	KGEKIHYDQV	LVVDGHQWIS	YKSYSGIRRY	IEI
msa255178.2{91_A909}	VSSPVEFNQ	KGEKIHYDQV	LVVDGHQWIS	YKSYSGIRRY	IEI
msa255178.2{91_CJB110}	VSSPVEFNQ	KGEKIHYDQV	LVVDGHQWIS	YKSYSGIRRY	IEI
msa255178.2{91_H36B}	VSSPVEFNQ	KGEKIHYDQV	LVVDGHQWIS	YKSYSGIRRY	IEI
msa255178.2{91_JM9130013}	VSSPVEFNQ	KGEKIHYDQV	LVVDGHQWIS	YKSYSGIRRY	IEI
msa255178.2{91_COH1}	VSSPVEFNQ	KGEKIHYDQV	LVVDGHQWIS	YKSYSGIRRY	IEI
msa255178.2{91_M781}	VSSPVEFNQ	KGEKIHYDQV	LVVDGHQWIS	YKSYSGIRRY	IEI
msa255178.2{91_M732}	VSSPVEFNQ	KGEKIHYDQV	LVVDGHQWIS	YKSYSGIRRY	IEI
msa255178.2{91_1169NT}	VSSPVEFNQ	KGEKIHYDQV	LVVDGHQWIS	YKSYSGIRRY	IEI
Consensus	*****	*****	*****	*****	***

CLAIMS:

1. An immunogenic composition comprising a combination of GBS polypeptides, said combination consisting of two, three, four or five polypeptides, wherein each polypeptide is encoded by a GBS polynucleotide sequence which is homologous to a polynucleotide sequence of both GAS and *Streptococcus pneumoniae*.
2. The immunogenic composition of claim 1, wherein said GBS polypeptides are encoded by GBS polynucleotide sequences selected from GBS Subset 1.
3. An immunogenic composition comprising a combination of GBS polypeptides, said combination consisting of two, three, four or five polypeptides, wherein each polypeptide is encoded by a GBS polynucleotide sequence which is homologous to a polynucleotide sequence of GAS.
4. The immunogenic composition of claim 3, wherein said GBS polypeptides are encoded by GBS polynucleotide sequences selected from GBS Subset 2.
5. An immunogenic composition comprising a combination of GBS polypeptides, said combination consisting of two, three, four or five polypeptides, wherein each polypeptide is encoded by a GBS polynucleotide sequence which is homologous to a polynucleotide sequence of *Streptococcus pneumoniae*.
6. The immunogenic composition of claim 5, wherein said GBS polypeptides are encoded by GBS polynucleotide sequences selected from GBS Subset 3.
7. An immunogenic composition comprising a combination of GBS polypeptides, said combination consisting of two, three, four or five polypeptides, wherein each polypeptide is encoded by a GBS serotype polynucleotide sequence which is homologous to at least one other GBS serotype.
8. The immunogenic composition of claim 2, 4 or 6, wherein one or more of the GBS polypeptides are encoded by GBS serotype polynucleotide sequences which are homologous to at least one other GBS serotype.
9. An immunogenic composition comprising a fusion protein, wherein said fusion protein comprises a first polypeptide sequence which is encoded by a GBS serotype polynucleotide which is conserved across one or more GBS serotypes.
10. A polynucleotide sequence, or a fragment comprising at least 10 contiguous polynucleotides, selected from the sequences set forth on Tables 13 – 31 and 40 – 89.
11. The polynucleotide fragment of claim 10, wherein said fragment is derived from a GBS serotype polynucleotide sequence and is homologous to at least one additional GBS serotype polynucleotide sequence.

Figure 1

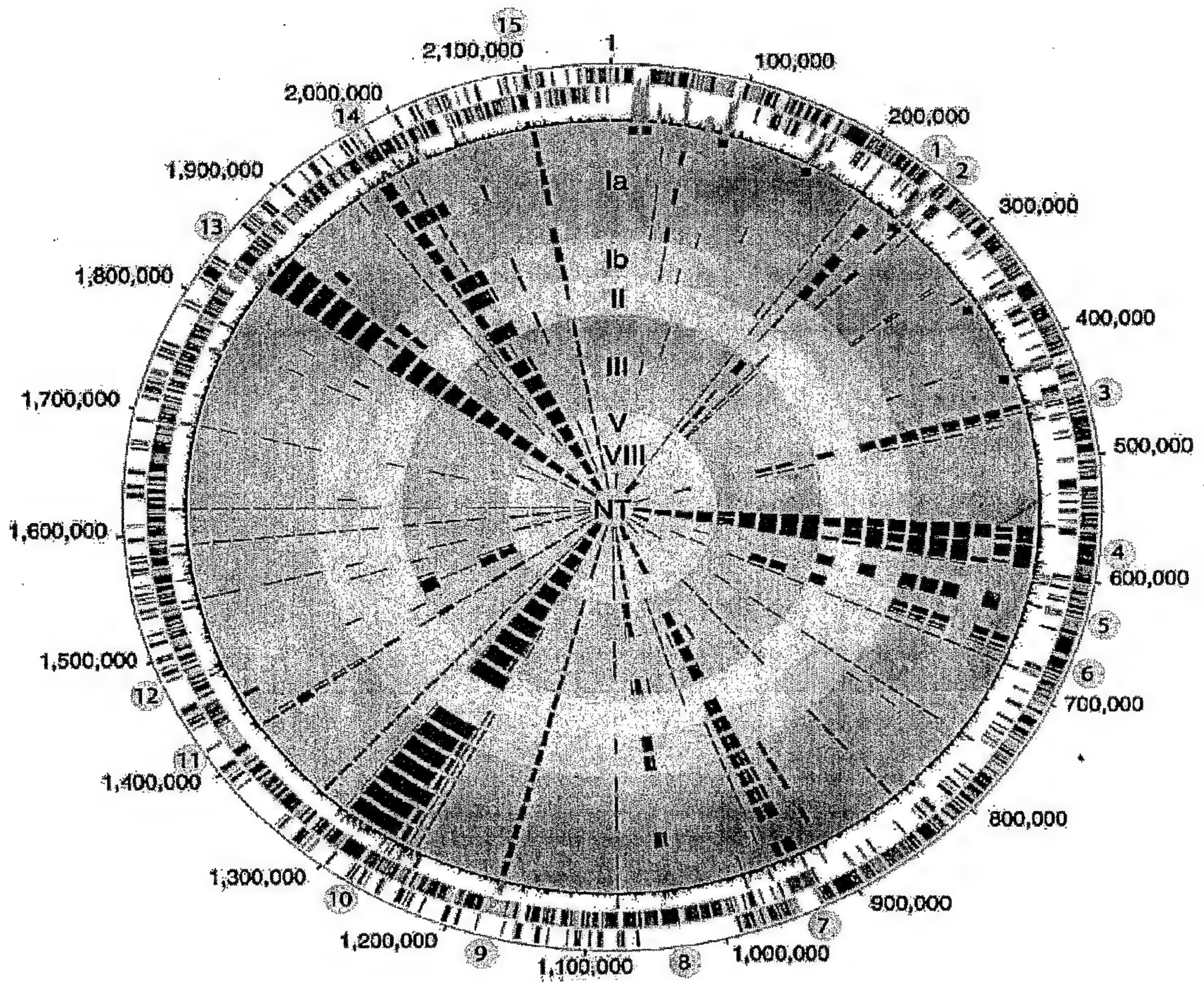


Figure 2

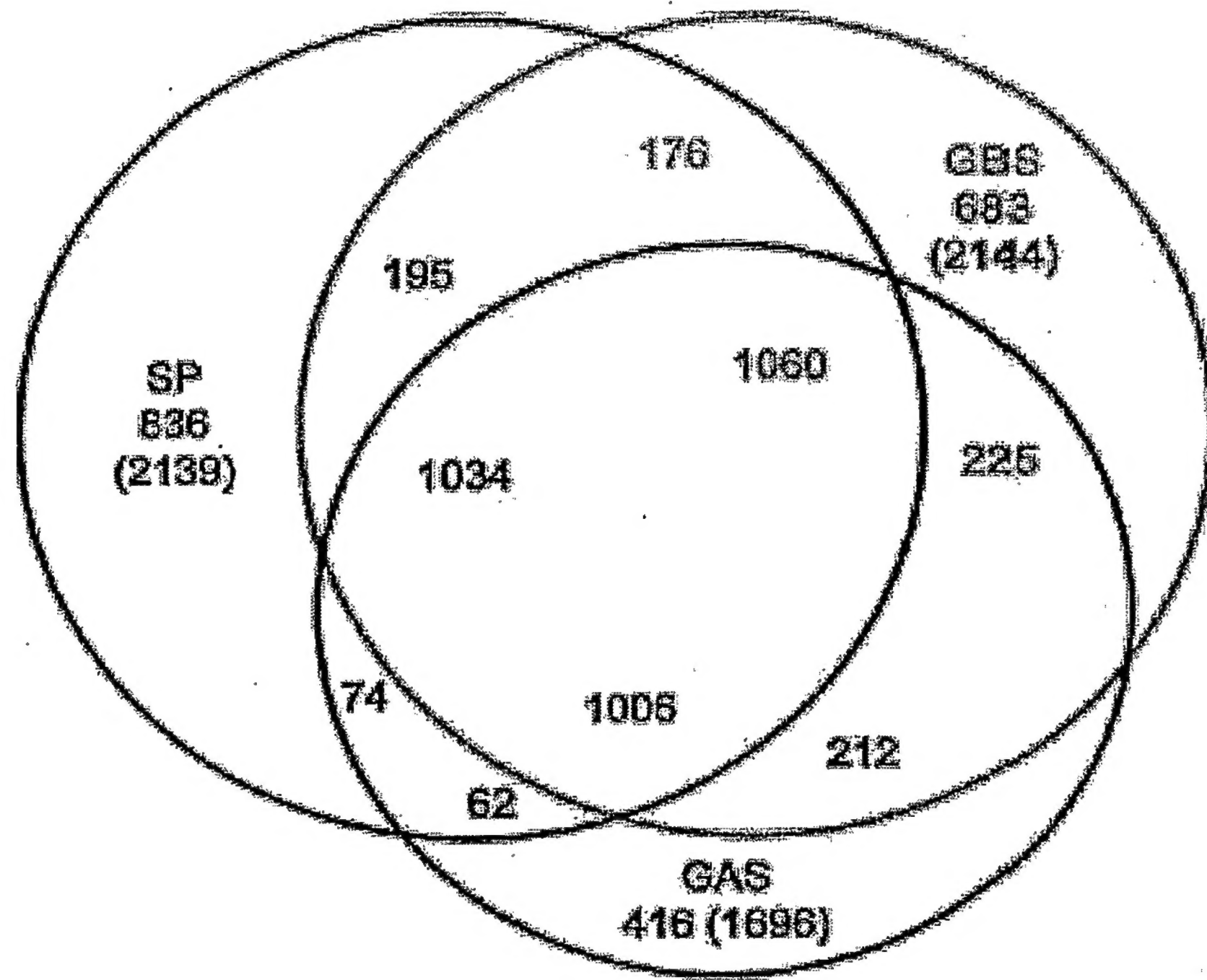
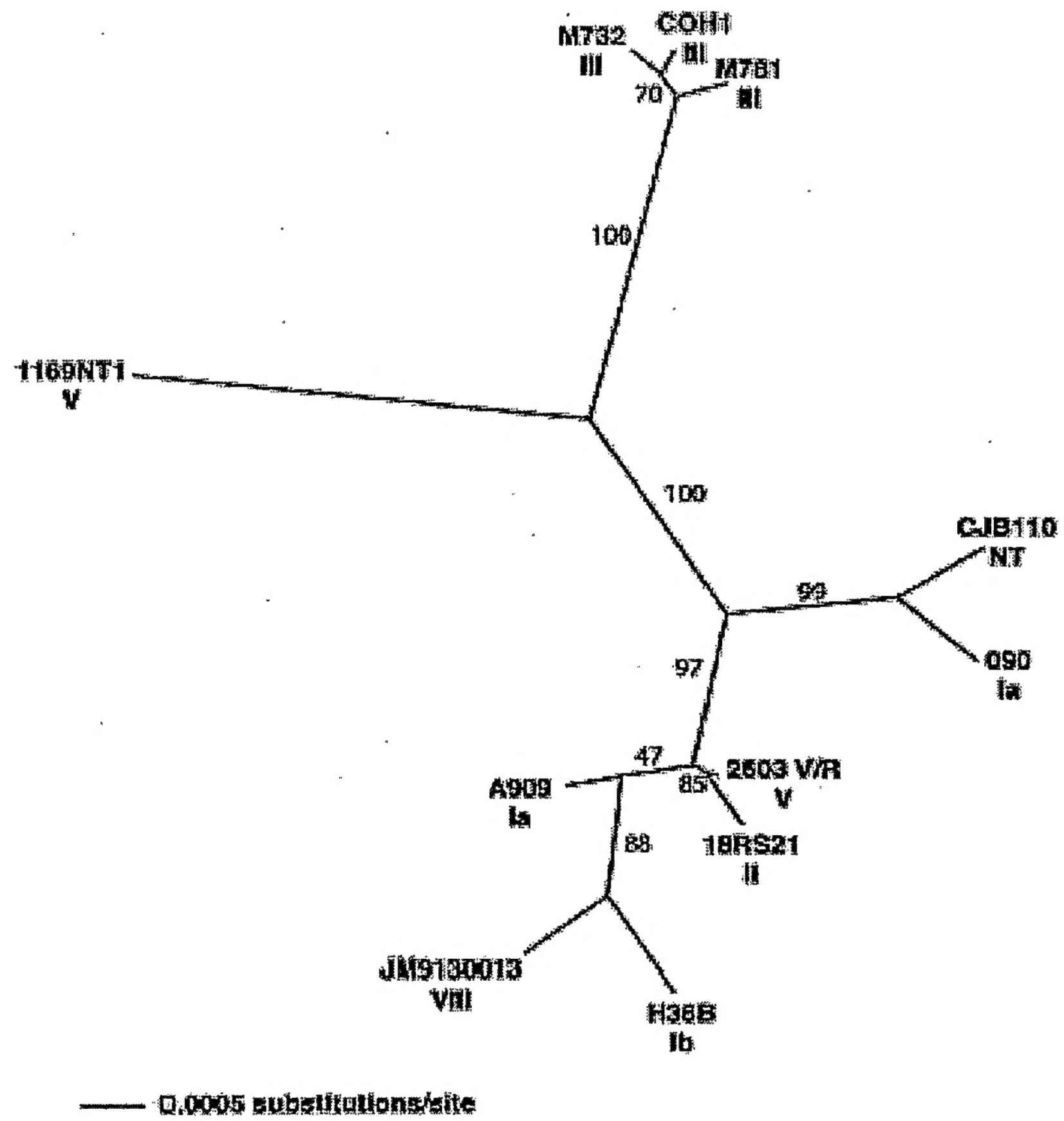


Figure 3



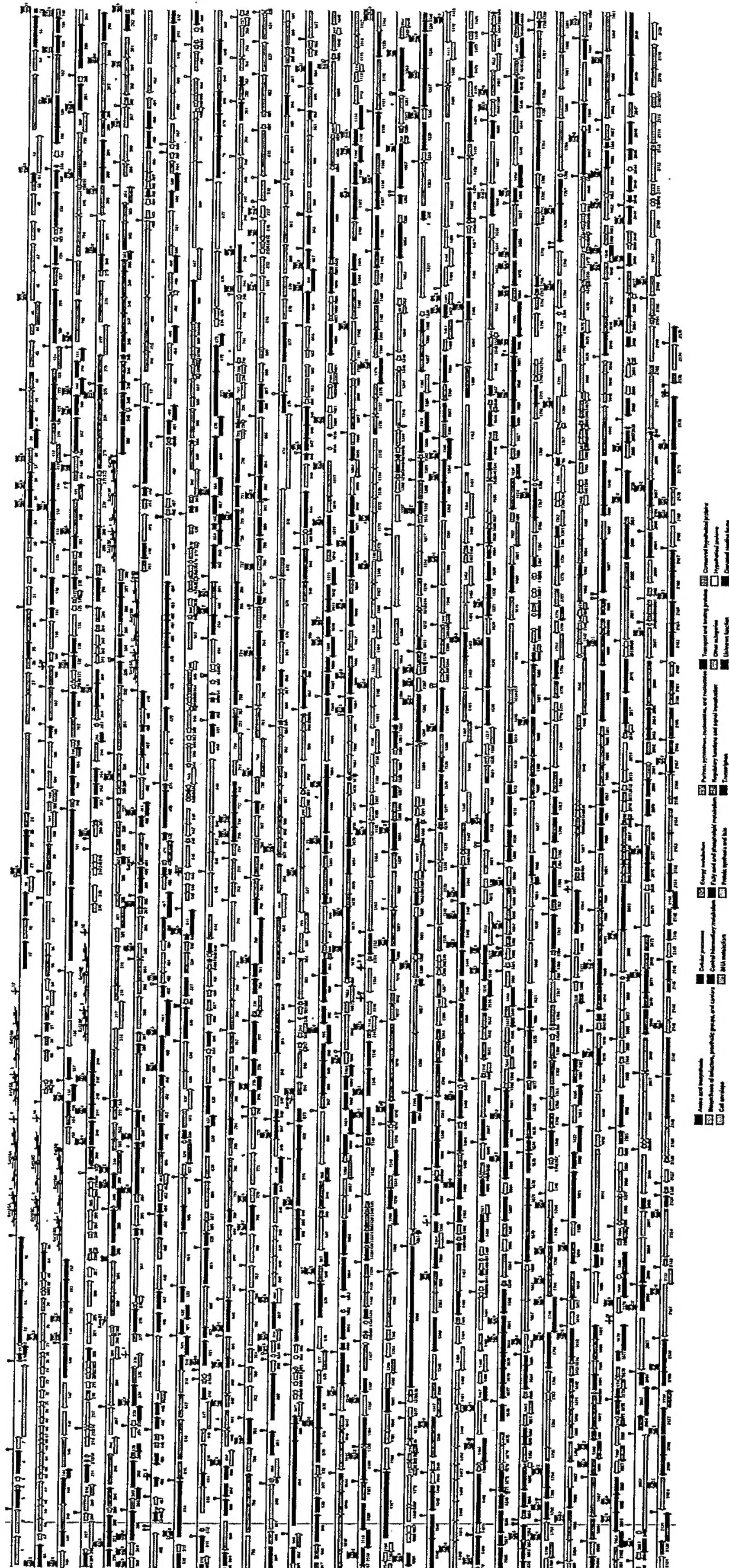


FIGURE 4

